

Connecting via Winsock to STN

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LOGINID:ssept189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\*\*\*\*\* Welcome to STN International \*\*\*\*\*

NEWS 1 Web Page for STN Seminar Schedule - N. America  
NEWS 2 JAN 02 STN pricing information for 2008 now available  
NEWS 3 JAN 16 CAS patent coverage enhanced to include exemplified  
prophetic substances  
NEWS 4 JAN 28 USPATFULL, USPAT2, and USPATOLD enhanced with new  
custom IPC display formats  
NEWS 5 JAN 28 MARPAT searching enhanced  
NEWS 6 JAN 28 USGENE now provides USPTO sequence data within 3 days  
of publication  
NEWS 7 JAN 28 TOXCENTER enhanced with reloaded MEDLINE segment  
NEWS 8 JAN 28 MEDLINE and LMEEDLINE reloaded with enhancements  
NEWS 9 FEB 08 STN Express, Version 8.3, now available  
NEWS 10 FEB 20 PCI now available as a replacement to DPCI  
NEWS 11 FEB 25 IFIREF reloaded with enhancements  
NEWS 12 FEB 25 IMSPRODUCT reloaded with enhancements  
NEWS 13 FEB 29 WPINDEX/WPIDS/WPIX enhanced with ECLA and current  
U.S. National Patent Classification  
NEWS 14 MAR 31 IFICDB, IFIPAT, and IFIUDB enhanced with new custom  
IPC display formats  
NEWS 15 MAR 31 CAS REGISTRY enhanced with additional experimental  
spectra  
NEWS 16 MAR 31 CA/CAPLUS and CASREACT patent number format for U.S.  
applications updated  
NEWS 17 MAR 31 LPCI now available as a replacement to LDPCI  
NEWS 18 MAR 31 EMBASE, EMBAL, and LEMBASE reloaded with enhancements  
NEWS 19 APR 04 STN AnaVist, Version 1, to be discontinued  
NEWS 20 APR 15 WPIDS, WPINDEX, and WPIX enhanced with new  
predefined hit display formats  
NEWS 21 APR 28 EMBASE Controlled Term thesaurus enhanced  
NEWS 22 APR 28 IMSRESEARCH reloaded with enhancements  
NEWS 23 MAY 30 INPAFAMDB now available on STN for patent family  
searching  
NEWS 24 MAY 30 DGENE, PCTGEN, and USGENE enhanced with new homology  
sequence search option  
NEWS 25 JUN 06 EPFULL enhanced with 260,000 English abstracts  
NEWS 26 JUN 06 KOREAPAT updated with 41,000 documents  
NEWS 27 JUN 13 USPATFULL and USPAT2 updated with 11-character  
patent numbers for U.S. applications  
NEWS 28 JUN 19 CAS REGISTRY includes selected substances from  
web-based collections

NEWS EXPRESS FEBRUARY 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 20 FEBRUARY 2008

NEWS HOURS STN Operating Hours Plus Help Desk Availability  
NEWS LOGIN Welcome Banner and News Items

NEWS IPC8      For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 21:14:36 ON 19 JUN 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE      TOTAL

ENTRY      SESSION

FULL ESTIMATED COST

0.21      0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 21:14:56 ON 19 JUN 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s food(p)process? and Enterococcus(p)durans

0\* FILE ADISNEWS  
4 FILE AGRICOLA  
0\* FILE ANTE  
0\* FILE AQUALINE  
5\* FILE BIOENG  
18 FILE BIOSIS  
3\* FILE BIOTECHABS  
3\* FILE BIOTECHDS  
5\* FILE BIOTECHNO  
2 FILE CABA  
20 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
4 FILE DGENE  
4 FILE EMBASE  
6\* FILE ESBIODASE  
0\* FILE FOMAD  
0\* FILE FOREGE

32 FILES SEARCHED...

7\* FILE FROSTI  
11\* FILE FSTA  
1 FILE HEALSAFE  
7 FILE IFIPAT  
0\* FILE KOSMET  
3 FILE LIFESCI  
6 FILE MEDLINE  
0\* FILE NTIS  
0\* FILE NUTRACEUT  
4\* FILE PASCAL  
0\* FILE PHARMAML

```

      2   FILE SCISEARCH
      5   FILE TOXCENTER
60 FILES SEARCHED...
      42   FILE USPATFULL
      9   FILE USPAT2
      0*   FILE WATER
      7   FILE WPIIDS
      7   FILE WPINDEX

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24 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE FOOD(P) PROCESS? AND ENTEROCOCCUS(P) DURANS

=> s l1 and (PTA-475# or PTA-476#)

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      0*   FILE AQUALINE
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      0*   FILE BIOTECHABS
      0*   FILE BIOTECHDS
      0*   FILE BIOTECHNO
      0*   FILE CEABA-VTB
      0*   FILE CIN
      0*   FILE ESBIODASE
      0*   FILE FOMAD
      0*   FILE FOREGE
      0*   FILE FROSTI
      0*   FILE FSTA
      1   FILE IFIPAT

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37 FILES SEARCHED...

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      0*   FILE NTIS
      0*   FILE NUTRACEUT
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      0*   FILE PHARMAML
      2   FILE USPATFULL
      0*   FILE WATER
      1   FILE WPIIDS

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68 FILES SEARCHED...

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      1   FILE WPINDEX

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4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L2 QUE L1 AND (PTA-475# OR PTA-476#)

=> file ifipat uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
2.60	2.81

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 21:17:15 ON 19 JUN 2008  
 COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'USPATFULL' ENTERED AT 21:17:15 ON 19 JUN 2008  
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l2

L3 3 L2

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d 14 1-3

L4 ANSWER 1 OF 3 IFIPAT COPYRIGHT 2008 IFI on STN  
AN 11124117 IFIPAT;IFIUDB;IFICDB  
TI COMPOSITION AND METHOD FOR INHIBITION OF MICROORGANISMS  
IN Doyle Michael P; Zhao Tong  
PA Unassigned Or Assigned To Individual (68000)  
PPA Georgia, University of Research Foundation Inc (Probable)  
PI US 2006073129 A1 20060406  
AI US 2003-535357 20031124  
WO 2003-US37526 20031124

20050518 PCT 371 date  
20050518 PCT 102(e) date  
PRAI US 2002-428863P 20021125 (Provisional)  
FI US 2006073129 20060406  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
ED Entered STN: 10 Apr 2006  
Last Updated on STN: 10 Apr 2006

CLMN 35

GI 1 Figure(s).

FIG. 1 illustrates the results of analyzing four probiotic isolates for their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1 Lambda ladder DNA standard, lane 2 C-192 (*L. lactis* subsp. *lactis*), lane 3 C-1-152 (*L. lactis* subsp. *lactis*), lane 4 141-1 (*E. durans*), and lane 5 152 (*E. durans*).

L4 ANSWER 2 OF 3 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)

DT Utility  
FS APPLICATION

LN.CNT 1238

INCL INCLM: 424/093.450

NCL NCLM: 424/093.450

IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]

IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 3 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of using same  
IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
Halsrud, David A., Minneapolis, MN, UNITED STATES  
PI US 20060067915 A1 20060330  
AI US 2005-233922 A1 20050922 (11)  
PRAI US 2004-612882P 20040924 (60)  
DT Utility  
FS APPLICATION



LN.CNT 1878  
 INCL INCLM: 424/093.400  
 INCL INCLM: 435/243.000  
 NCL NCLM: 424/093.400  
 NCL NCLM: 435/243.000  
 IC IPCI A01N0063-00 [I,A]  
 IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 21:14:36 ON 19 JUN 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOZ, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 21:14:56 ON 19 JUN 2008  
 SEA FOOD(P)PROCESS? AND ENTEROCOCCUS(P) DURANS

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0* FILE ADISNEWS
4 FILE AGRICOLA
0* FILE ANTE
0* FILE AQUALINE
5* FILE BIOENG
18 FILE BIOSIS
3* FILE BIOTECHABS
3* FILE BIOTECHDS
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4 FILE EMBASE
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0* FILE FOREGE
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6 FILE MEDLINE
0* FILE NTIS
0* FILE NUTRACEUT
4* FILE PASCAL
0* FILE PHARMAML
2 FILE SCISEARCH
5 FILE TOXCENTER
42 FILE USPATFULL
9 FILE USPAT2
0* FILE WATER
7 FILE WPIDS
7 FILE WPINDEX

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L1 QUE FOOD(P) PROCESS? AND ENTEROCOCCUS(P) DURANS

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 SEA L1 AND (PTA-475# OR PTA-476#)  
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0* FILE ADISNEWS
0* FILE ANTE

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0* FILE BIOENG
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0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
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0* FILE FROSTI
0* FILE FSTA
1 FILE IFIPAT
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0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
2 FILE USPATFULL
0* FILE WATER
1 FILE WPIDS
1 FILE WPINDEX
L2 QUE L1 AND (PTA-475# OR PTA-476#)
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FILE 'IFIPAT, USPATFULL' ENTERED AT 21:17:15 ON 19 JUN 2008
L3 3 S L2
L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

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=> logoff
ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF
LOGOFF? (Y)/N/HOLD:y
COST IN U.S. DOLLARS                               SINCE FILE      TOTAL
                                                    ENTRY      SESSION
FULL ESTIMATED COST                               7.72         10.53

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STN INTERNATIONAL LOGOFF AT 21:17:46 ON 19 JUN 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:  
 TERMINAL (ENTER 1, 2, 3, OR ?):2

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NEWS 1 Web Page for STN Seminar Schedule - N. America
NEWS 2 AUG 15 CAOLD to be discontinued on December 31, 2008
NEWS 3 OCT 07 EPFULL enhanced with full implementation of EPC2000
NEWS 4 OCT 07 Multiple databases enhanced for more flexible patent
           number searching
NEWS 5 OCT 22 Current-awareness alert (SDI) setup and editing
           enhanced

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NEWS 6 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT Applications

NEWS 7 OCT 24 CHEMLIST enhanced with intermediate list of pre-registered REACH substances

NEWS 8 NOV 21 CAS patent coverage to include exemplified prophetic substances identified in English-, French-, German-, and Japanese-language basic patents from 2004-present

NEWS 9 NOV 26 MARPAT enhanced with FSORT command

NEWS 10 NOV 26 MEDLINE year-end processing temporarily halts availability of new fully-indexed citations

NEWS 11 NOV 26 CHEMSAFE now available on STN Easy

NEWS 12 NOV 26 Two new SET commands increase convenience of STN searching

NEWS 13 DEC 01 ChemPort single article sales feature unavailable

NEWS 14 DEC 12 GBFULL now offers single source for full-text coverage of complete UK patent families

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS LOGIN Welcome Banner and News Items

NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGS, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s (Enterococcus durans or Lactococcus lactis) and (PTA-4759 or PTA-4758 or PTA-4760 or PTA-4761)

1 FILE IFIPAT

53 FILES SEARCHED...

2 FILE USPATFULL

1 FILE WPIDS

1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 OR PTA-4758  
OR PTA-4760 OR PTA-4761)

=> file uspatfull ifipat

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.30	1.51

FILE 'USPATFULL' ENTERED AT 16:32:25 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008  
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

=> s l1

L2 3 L1

=> d l2 1-3

L2 ANSWER 1 OF 3 USPATFULL on STN

AN 2006:86130 USPATFULL

TI Composition and method for inhibition of microorganisms

IN Doyle, Michael P, Peachtree City, GA, UNITED STATES

Zhao, Tong, Peachtree City, GA, UNITED STATES

PI US 20060073129 A1 20060406

AI US 2003-535357 A1 20031124 (10)

WO 2003-US37526 20031124

20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)

DT Utility

FS APPLICATION

LN.CNT 1238

INCL INCLM: 424/093.450

NCL NCLM: 424/093.450

IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]

IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L2 ANSWER 2 OF 3 USPATFULL on STN

AN 2006:79924 USPATFULL

TI Foaming composition of competitive exclusion microbes and method of  
using same

IN Podtburg, Teresa C., Waconia, MN, UNITED STATES

Schmidt, Bruce, Apple Valley, MN, UNITED STATES

Cords, Bruce, Inver Grove Heights, MN, UNITED STATES

Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF

Halsrud, David A., Minneapolis, MN, UNITED STATES

PI US 20060067915 A1 20060330

AI US 2005-233922 A1 20050922 (11)

PRAI US 2004-612882P 20040924 (60)

DT Utility

FS APPLICATION

LN.CNT 1878

INCL INCLM: 424/093.400

INCLS: 435/243.000

NCL NCLM: 424/093.400

NCLS: 435/243.000

IC IPCI A01N0063-00 [I,A]

IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L2 ANSWER 3 OF 3 IFIPAT COPYRIGHT 2008 IFI on STN  
 AN 11124117 IFIPAT;IFIUDB;IFICDB  
 TI Composition and method for inhibition of microorganisms  
 IN Doyle Michael P; Zhao Tong  
 PA Unassigned Or Assigned To Individual (68000)  
 PPA Georgia, University of Research Foundation Inc (Probable)  
 PI US 20060073129 A1 20060406  
 AI US 2003-535357 20031124  
 WO 2003-US37526 20031124

20050518 PCT 371 date  
 20050518 PCT 102(e) date  
 PRAI US 2002-428863P 20021125 (Provisional)  
 FI US 20060073129 20060406

DT Utility; Patent Application - First Publication  
 FS CHEMICAL

APPLICATION

ED Entered STN: 10 Apr 2006

Last Updated on STN: 10 Apr 2006

CLMN 35

GI 1 Figure(s).

FIG. 1 illustrates the results of analyzing four probiotic isolates for their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1 Lambda ladder DNA standard, lane 2 C-1-92 [*L. lactis* subsp. *lactis*], lane 3 C-1-152 [*L. lactis* subsp. *lactis*], lane 4 141-1 [*E. durans*], and lane 5 152 [*E. durans*].

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

7.72

9.23

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROFB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view  
 search error messages that display as 0\* with SET DETAIL OFF.

=> s Enterococcus durans strain 141-1

48 FILES SEARCHED...

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

=> s Enterococcus durans strain 152

58 FILES SEARCHED...

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

=> s Enterococcus drans 141-1

0 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L5 QUE ENTEROCOCCUS DRANS 141-1

=> s Enterococcus durans 141-1  
60 FILES SEARCHED...  
2 FILE USPATFULL

1 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L6 QUE ENTEROCOCCUS DURANS 141-1

=> file uspatfull  
COST IN U.S. DOLLARS SINCE FILE TOTAL  
ENTRY SESSION  
FULL ESTIMATED COST 3.90 13.13

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 16 Dec 2008 (20081216/PD)  
FILE LAST UPDATED: 16 Dec 2008 (20081216/ED)  
HIGHEST GRANTED PATENT NUMBER: US7467417  
HIGHEST APPLICATION PUBLICATION NUMBER: US20080307552  
CA INDEXING IS CURRENT THROUGH 16 Dec 2008 (20081216/UPCA)  
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 16 Dec 2008 (20081216/PD)  
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Aug 2008  
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Aug 2008

USPATFULL now includes complete International Patent Classification (IPC)  
reclassification data for the third quarter of 2008.

=> s 16  
5998 ENTEROCOCCUS  
441 DURANS  
319932 141  
5364391 1  
L7 2 ENTEROCOCCUS DURANS 141-1  
(ENTEROCOCCUS(W)DURANS(W)141(W)1)

=> d 17 1-2

L7 ANSWER 1 OF 2 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 1238  
INCL INCLM: 424/093.450  
NCL NCLM: 424/093.450  
IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]  
IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 2 OF 2 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of  
using same

IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
 Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
 Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
 Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
 Halsrud, David A., Minneapolis, MN, UNITED STATES

PI US 20060067915 A1 20060330  
 AI US 2005-233922 A1 20050922 (11)  
 PRAI US 2004-612882P 20040924 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 1878

INCL INCLM: 424/093.400  
 INCLS: 435/243.000  
 NCL NCLM: 424/093.400  
 NCLS: 435/243.000

IC IPCI A01N0063-00 [I,A]  
 IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
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FULL ESTIMATED COST

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69 FILES IN THE FILE LIST IN STINDEX

Enter SET DETAIL ON to see search term postings or to view  
 search error messages that display as 0\* with SET DETAIL OFF.

=> s Enterococcus durans 152

1 FILE AGRICOLA  
 1 FILE BIOENG  
 1 FILE BIOSIS  
 1 FILE CABA  
 2 FILE CAPLUS  
 1 FILE FROSTI  
 1 FILE FSTA  
 1 FILE HEALSAFE  
 1 FILE LIFESCI  
 1 FILE MEDLINE  
 1 FILE PASCAL  
 1 FILE SCISEARCH  
 2 FILE USPATFULL

67 FILES SEARCHED...

13 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L8 QUE ENTEROCOCCUS DURANS 152

=> file agricola bioeng biosis caba caplus frosti fsta healsafe lifesci medline  
 pascal scisearch uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
1.30	18.03

FULL ESTIMATED COST

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FILE 'BIOENG' ENTERED AT 16:38:26 ON 16 DEC 2008  
COPYRIGHT (C) 2008 Cambridge Scientific Abstracts (CSA)

FILE 'BIOSIS' ENTERED AT 16:38:26 ON 16 DEC 2008  
Copyright (c) 2008 The Thomson Corporation

FILE 'CABA' ENTERED AT 16:38:26 ON 16 DEC 2008  
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FILE 'CAPLUS' ENTERED AT 16:38:26 ON 16 DEC 2008  
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=> s l8  
L9 15 L8

=> dup rem l9  
PROCESSING COMPLETED FOR L9  
L10 3 DUP REM L9 (12 DUPLICATES REMOVED)

=> d l10 1-3

L10 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 1  
AN 2006:299263 CAPLUS  
DN 144:306860  
TI Foaming composition of benign microbes for competitive exclusion of  
undesired microbes  
IN Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;  
Halsrud, David A.  
PA USA  
SO U.S. Pat. Appl. Publ., 21 pp.



CODEN: USXXCO  
 DT Patent  
 LA English  
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

L10 ANSWER 2 OF 3 USPATFULL on STN  
 AN 2006:86130 USPATFULL  
 TI Composition and method for inhibition of microorganisms  
 IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
 Zhao, Tong, Peachtree City, GA, UNITED STATES  
 PI US 20060073129 A1 20060406  
 AI US 2003-535357 A1 20031124 (10)  
 WO 2003-US37526 20031124  
 20050518 PCT 371 date

PRAI US 2002-428863P 20021125 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 1238  
 INCL INCLM: 424/093.450  
 NCL NCLM: 424/093.450  
 IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]  
 IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 3 OF 3 AGRICOLA Compiled and distributed by the National  
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 of America. It contains copyrighted materials. All rights reserved.  
 (2008) on STN DUPLICATE 2  
 AN 2006:43066 AGRICOLA  
 DN IND43806656  
 TI Control of Listeria spp. by Competitive-Exclusion Bacteria in Floor Drains  
 of a Poultry Processing Plant.  
 AU Zhao, Tong; Podtburg, Teresa C.; Zhao, Ping; Schmidt, Bruce E.; Baker,  
 David A.; Cords, Bruce; Doyle, Michael P.  
 AV DNAL (448.3 Ap5)  
 SO Applied and environmental microbiology, 2006 May Vol. 72, no. 5 p.  
 3314-3320  
 Publisher: American Society for Microbiology  
 ISSN: 0099-2240  
 NTE Includes references  
 DT Article; (ELECTRONIC RESOURCE)  
 FS Other US  
 LA English

=> index bioscience  
 FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED  
 COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
23.94	41.97

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s Lactococcus lactis C-1-92

```
1 FILE CAPLUS
34 FILES SEARCHED...
11 FILE GENBANK
1 FILE PROMT
2 FILE USPATFULL
65 FILES SEARCHED...
```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L11 QUE LACTOCOCCUS LACTIS C-1-92

=> file caplus genbank prompt uspatfull

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.30	43.27

FILE 'CAPLUS' ENTERED AT 16:41:04 ON 16 DEC 2008  
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FILE 'PROMT' ENTERED AT 16:41:04 ON 16 DEC 2008  
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=> s l11

L12 15 L11

=> rem dup l12

DUP IS NOT VALID HERE

The DELETE command is used to remove various items stored by the system.

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field
DELETE NAMELIST MYLIST	- delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C      - delete print request
DELETE D134002C      - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER       - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l12
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L12
L13          14 DUP REM L12 (1 DUPLICATE REMOVED)
```

```
=> d l13 1-14
```

```
L13 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 1
AN  2006:299263 CAPLUS
DN  144:306860
TI  Foaming composition of benign microbes for competitive exclusion of
    undesired microbes
IN  Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;
    Halsrud, David A.
PA  USA
SO  U.S. Pat. Appl. Publ., 21 pp.
```

CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

L13 ANSWER 2 OF 14 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124

20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)

DT Utility  
FS APPLICATION  
LN.CNT 1238

INCL INCLM: 424/093.450

NCL NCLM: 424/093.450

IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]

IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L13 ANSWER 3 OF 14 PROMT COPYRIGHT 2008 Gale Group on STN

ACCESSION NUMBER: 2003:81217 PROMT  
TITLE: Natural Additives Kill Listeria.  
SOURCE: Food Ingredient News, (March 2003) Vol. 11, No. 3.  
ISSN: ISSN: 1070-1788.  
PUBLISHER: Business Communications Company, Inc.  
DOCUMENT TYPE: Newsletter  
LANGUAGE: English  
WORD COUNT: 391

\*FULL TEXT IS AVAILABLE IN THE ALL FORMAT\*

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)  
GenBank ACC. NO. (GBN): AM286415  
GenBank VERSION (VER): AM286415.1 GI:122087364  
CAS REGISTRY NO. (RN): 917704-63-3  
SEQUENCE LENGTH (SQL): 4615899  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 29 Oct 2008  
DEFINITION (DEF): *Yersinia enterocolitica* subsp. *enterocolitica* 8081 complete genome.  
KEYWORDS (ST): complete genome  
SOURCE: *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
ORGANISM (ORGN): *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
Bacteria; Proteobacteria; Gammaproteobacteria;  
Enterobacteriales; Enterobacteriaceae; *Yersinia*  
PROJECT (PJID): GenomeProject:190  
REFERENCE: 1  
AUTHOR (AU): Delihias,N.  
TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene *micF* and its target *ompF* in

Yersinia species  
 JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
 REFERENCE: 2  
 AUTHOR (AU): Thomson,N.R.; Howard,S.; Wren,B.W.; Holden,M.T.;  
 Crossman,L.; Challis,G.L.; Churcher,C.; Mungall,K.;  
 Brooks,K.; Chillingworth,T.; Feltwell,T.; Abdellah,Z.;  
 Hauser,H.; Jagels,K.; Maddison,M.; Moule,S.;  
 Sanders,M.; Whitehead,S.; Quail,M.A.; Dougan,G.;  
 Parkhill,J.; Prentice,M.B.  
 TITLE (TI): The complete genome sequence and comparative genome  
 analysis of the high pathogenicity Yersinia  
 enterocolitica strain 8081  
 JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
 REFERENCE: 3 (bases 1 to 4615899)  
 AUTHOR (AU): Thomson,N.R.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED  
 KINGDOM

# FEATURES (FEAT):

Feature Key	Location	Qualifier
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gene	complement(270..710)	/locus-tag="YE0001"
CDS	complement(270..710)	/locus-tag="YE0001" /codon-start=1 /transl-table=11 /product="putative flavoprotein" /protein-id="CAL10146.1" /db-xref="GI:122087365" /db-xref="GOA:A1JHQ8" /db-xref="InterPro:IPR001094" /db-xref="InterPro:IPR008254" /db-xref="InterPro:IPR015702" /db-xref="UniProtKB/TrEMBL:A1JHQ8" /translation="MADITLISGSLGSAEYVAE HLAEKLEAGFTTETLHGPELDEL TLDGMWLITSTHGAGDLPDNLQPLLEQIEQRRP DLSQVRFGAVGLGSSEYDTFCGAV RKLDQQLIIQGAIRVGDILEIDVIKHEIPDPAE IWKNNWNL"
misc-feature	complement(273..704)	/locus-tag="YE0001" /inference="protein motif:PFAM:PF00258" /note="Pfam match to entry PF00258 flavodoxin, Flavodoxin, score 117.3, E-value 1.9e-32"
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CDS	complement(802..1263)	/gene="asnC" /locus-tag="YE0002" /codon-start=1 /transl-table=11 /product="regulatory protein" /protein-id="CAL10147.1"

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/db-xref="InterPro:IPR000485"
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/db-xref="UniProtKB/TrEMBL:A1JHQ9"
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SAKDYPSALKKLESLEEVVEAYYT
TGHYSIFIKVMCKSIDALQQVLLINKIQTIDEIQS
TETLISLQNPIMRTIVP"
misc-feature      complement(868..1173)
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/locus-tag="YE0002"
/inference="protein
motif:PFAM:PF01037"
/notes="Pfam match to entry PF01037
ASNc-trans-reg, AsnC family, score
61.4, E-value 1.2e-15"
misc-feature      complement(1111..1191)
/gene="asnC"
/locus-tag="YE0002"
/inference="protein
motif:Prosite:PS00519"
/notes="PS00519 Bacterial
regulatory proteins, asnC family
signature."
misc-feature      complement(1129..1194)
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/notes="Predicted helix-turn-helix
motif with score 1765.000, SD 5.20
at aa 24-45, sequence
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gene              1449..2441
/gene="asnA"
/locus-tag="YE0003"
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ligase"
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/db-xref="GI:122087367"
/db-xref="GOA:A1JHR0"
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/db-xref="InterPro:IPR006195"
/db-xref="UniProtKB/Swiss-Prot:A1J
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VNKIYAAIKETEAASAEFDIKPF
LPEQIHFIHSESLRAKFPDLDAKGRERAIKELG
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DDWTSPSAEGFAGLNGDIIVWNPVLEDAFEISSM
GIRVDAEALKRQALATSDIEDRLKL
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/locus-tag="YE0003"
/inference="protein
motif:PFAM:PF03590"

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misc-feature	2055..2078	<p>/note="Pfam match to entry PF03590          AsnA, Aspartate-ammonia ligase,          score 597.7, E-value 4.6e-177"          /gene="asnA"          /locus-tag="YE0003"          /inference="protein          motif:Prosites:PS00017"          /note="PS00017 ATP/GTP-binding          site motif A (P-loop)."          /locus-tag="YE0004"          /locus-tag="YE0004"          /inference="similar to          sequence:INSDC:AE001895"          /inference="similar to          sequence:INSDC:AL646078"          /note="Similar to Ralstonia          solanacearum probable          transmembrane protein RSP0410 or          RS00867 SWALL:Q8XSQ7          (EMBL:AL646078) (224 aa) fasta          scores: E(): 7.3e-36, 46.54 38d in          217 aa, and to Deinococcus          radiodurans hypothetical protein          DR0351 SWALL:Q9RXG2          (EMBL:AE001895) (227 aa) fasta          scores: E(): 3.7e-17, 31.67 38d in          221 aa"          /codon-start=1          /transl-table=11          /product="putative membrane          protein"          /protein-id="CAL10149.1"          /db-xref="GI:122087368"          /db-xref="InterPro:IPR009781"          /db-xref="UniProtKB/TREMBL:ALJHR1"          /translation="MARFHEPLRHYSHARPLL          LSVGAGIIAYFLFLPSHFTVLLRVMVS          WNIFAWLYLLFLWLQLLRNDPKKIRLIARVQDES          ASMVLIVSMACLASILVILFELS          TANQLSGSAKAFHLVLTGMTLLVSWLLLP          TAFTHYAHFLYLSRDESDAVLPLIFPKE          VTEPTYWDFLYFSFTIGVASQTADVSTGTS          DIRRVLLQSVLSFIENMTILGLSINVG          AGLLN"          /locus-tag="YE0004"</p>
misc-feature	join(2643..2711, 2721..2777,2838..2906, 2934..3002,3192..3260)	<p>/inference="protein          motif:TMHMM:2.0"          /note="5 probable transmembrane          helices predicted for YE0004 by          TMHMM2.0 at aa 17-39, 43-61,          82-104, 114-136 and 200-222"          /locus-tag="YE0005"          /locus-tag="YE0005"          /codon-start=1          /transl-table=11          /product="conserved hypothetical          protein"          /protein-id="CAL10150.1"          /db-xref="GI:122087369"          /db-xref="InterPro:IPR002035"          /db-xref="UniProtKB/Swiss-Prot:AlJ</p>
gene CDS	complement(3276..4742) complement(3276..4742)	

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gene	6708..8435	/gene="kup" /locus-tag="YE0007" /note="synonym: trkD" /gene="kup" /locus-tag="YE0007" /codon-start=1 /transl-table=11
CDS	6708..8435	



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/protein-id="CAL10152.1"
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/db-xref="InterPro:IPR003855"
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HR6"
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VLTLLFVIQKHGTGSVGKLFAPVMLVWFLTLLAL
GLRSIIANPEVLAAALNPKWAISFF
TEYKSVSFFALGAVVLAITGVEALYADMGHFGKF
PIRLAWFTTVLPISLVLYNYFGQAL
LLKNPEAIKNPFFLLAPDWALIPLLILATLATVI
ASQAVISGVFSLTRQAVRLGYLEPP
MRIIHTSEMESGQIYIPVINWTLYLAVVLVIVGF
ERSNLAAYAGIAVTGMTVITSVL
FCTVALKNWHRNRFVYFLLVALLVIDVPMFSAN
ALKLFSGGWLPLSLGLVMFIIMTT
WKSERFSLLRRMHEHNSLEAMIASLEKSPFVRV
PGTAVYMSRAMNVIPFALLHNLKH
NKVLHDRVLLTLRTEDAPYVHNVRVTIEQLSP
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/misc-feature 6711..8432
/gene="kup"
/locus-tag="YE0007"
/inference="protein
motif:PFAM:PF02705"
/notes="Pfam match to entry PF02705
K-trans, K+ potassium transporter,
score 854.9, E-value 1.7e-254"
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6870..6938,6966..7034,
7068..7136,7194..7262,
7299..7367,7425..7493,
7566..7634,7662..7730,
7749..7802,7830..7886)
/locus-tag="YE0007"
/inference="protein
motif:TMHMM:2.0"
/notes="11 probable transmembrane
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TMHMM2.0 at aa 4-26, 55-77,
87-109, 121-143,163-185, 198-220,
240-262, 287-309, 319-341, 348-365
and 375-393"
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CDS 8606..9025
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/transl-table=11
/product="ribose permease"
/protein-id="CAL10153.1"
/db-xref="GI:122087372"
/db-xref="GOA:AlJHR8"
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/db-xref="UniProtKB/Swiss-Prot:AlJ
HR8"

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gene 9033..10535

CDS 9033..10535

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/gene="rbsA"
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sequence:UniProtKB:P04983"
/note="Similar to Escherichia coli
ribose transport ATP-binding
protein RbsA SWALL:RBSA-ECOLI
(SWALL:P04983) (501 aa) fasta
scores: E(): 2.7e-148, 85.83 38d
in 494 aa, and to Salmonella typhi
high affinity ribose transport
protein STY896 SWALL:Q8ZZR4
(EMBL:AL627280) (501 aa) fasta
scores: E(): 1.1e-147, 85.62 38d
in 494 aa"
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transport ATP-binding protein"
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/db-xref="UniProtKB/TrEMBL:AlJHS1"
/translation="MQPLLQLKGIDKAFPGVKAL
SGAALSVYPGRVMAVGENGAGKS
TMMKVLGTGIYNKDAGSQHFLGKEVVFNGPKESQE
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GREFVNHFGGIDWKKMYAEADLLARLNISYSSH
RLVGELSIGDQOMVEIAKVLSEFS
KVIIMDEPTDALTDETASLFNVIKELKAEGRGI
VYISHRLKEIFEICDDVTVFRDGO
FIAEKFPVNTLTENALIEMMVGRKLEEQYPRNLNP
RGEKRLQVKQLCGPGVENNVNFTLY
SGEILGVAGLMGAGRTLMKIIYGALPRKSGFVM
LDGREVVTHSPQDGLANGIVYISE
DRKRDGLVLGMSVKENMSLTALRYFSRSGGSLKH
ADEQQAVADFIRLFNIKTPSMEQP
IGLLSGGNQKQVAIARGLMTRPKVLILDEPTRGV
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EVLMAAAVGRDLLEK"
/gene="rbsA"
/locus-tag="YE0009"
/inference="protein
motif:PFAM:PF00005"
/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
173.1, E-value 3e-49"
/gene="rbsA"
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misc-feature 9120..9683

misc-feature 9141..9164

		/locus-tag="YE0009" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="rbsA"
misc-feature	9864..10445	/locus-tag="YE0009" /inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 134.4, E-value 1.3e-37" /gene="rbsA"
misc-feature	10218..10262	/locus-tag="YE0009" /inference="protein motif:Prosite:PS00211" /note="PS00211 ABC transporters family signature." /gene="rbsC"
gene	10623..11588	/locus-tag="YE0010" /gene="rbsC"
CDS	10623..11588	/locus-tag="YE0010" /codon-start=1 /transl-table=11 /product="putative sugar transport system, permease protein" /protein-id="CAL10155.1" /db-xref="GI:122087374" /db-xref="GOA:AlJHS2" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:AlJHS2" /translation="MSSQTINTKRWFSEWLLLEQ KSLIALLVLIADVSSLSPEFFTLN NMFNILQQTSVNAINAVGMTLVLTSGIDLSVGS LLALTGAVAAASIVGLEVNALVAVG AALALGAFVGGITGVIVAKGVQAFIATLVMMLL LRGVTMVYINGSPINTGFTDVA DT FGWFGIGRPLGIPTPIWLMAIVFIAAWYMLHHR LGRYIYALGNGESATRLSGISVDK VKIIVYSLCGLLAALAGIIEVARLSSAQPTAGTG YELDAIAAVVLGGTSLAGGKGQIV GTLIGALILGFLNNGLLNLGVSSYYQMIVKAVVI LLAVLVDNKKQ" /gene="rbsC"
sig-peptide	10623..10748	/locus-tag="YE0010" /note="Signal peptide predicted for YE0010 by SignalP 2.0 HMM (Signal peptide probability 0.969) with cleavage site probability 0.169 between residues 42 and 43" /gene="rbsC"
misc-feature	join(10686..10754, 10815..10883, 10911..10979, 10998..11066, 11124..11192, 11283..11351, 11445..11513)	/locus-tag="YE0010" /inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted for YE0010 by

		TMHMM2.0 at aa 22-44, 65-87, 97-119, 126-148,168-190, 221-243 and 275-297" /gene="rbsC" /locus-tag="YE0010" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2,Branched-chain amino acid transport system / permease component, score 3.4, E-value 7.7e-07"
misc-feature	10746..11582	
gene	11760..12647	/gene="rbsB" /locus-tag="YE0011" /note="synonyms: prlB, rbsP" /gene="rbsB" /locus-tag="YE0011" /inference="similar to sequence:UniProtKB:P02925" /inference="similar to sequence:UniProtKB:P02926" /note="Similar to Escherichia coli D-ribose-binding periplasmic protein precursor RbsB or RbsP or PrlB SWALL:RBSB-ECOLI (SWALL:P02925) (296 aa) fasta scores: E(): 1.7e-84, 84.74 38d in 295 aa, and to Salmonella typhimurium, and Salmonella typhi D-ribose-binding periplasmic protein precursor RbsB or RbsP or STM3884 or STY3894 SWALL:RBSB-SALTY (SWALL:P02926) (296 aa) fasta scores: E(): 5.6e-84, 84.06 38d in 295 aa" /codon-start=1 /transl-table=11 /product="putative D-ribose-binding periplasmic protein precursor" /protein-id="CAL10156.1" /db-xref="GI:122087375" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:ALJHS3" /translation="MKMKKLATLISVVALSATVS ANALAKDTIALVVSTLNNPFFVSM KDGAQKEADKGLYNLVILDSQNNPAKELANVQDL TVRGTKLLLINPTDSDAVGNAVKM ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM AGDYIAKKVGSDAKVIQLEGIAGA SAAREERGEFGKQSMKKNFOLLASQPADFDRTKG LNMVNQLLTAHPDVQAVFAONDEM ALGALRALQTAGKTDVLVVVFGDGTDDGIKAVESG KMGATIAQRPDQIGVIGVQTADKV LKGEKVQAVIPVDLKLVTK"
CDS	11760..12647	
sig-peptide	11760..11834	/gene="rbsB" /locus-tag="YE0011" /note="Signal peptide predicted for YE0011 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.933 between residues 25 and 26"

misc-feature	11835..12641	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 63.4, E-value 3.3e-16"
misc-feature	12432..12455	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	12811..13737	/gene="rbsK"
CDS	12811..13737	/locus-tag="YE0012" /gene="rbsK" /locus-tag="YE0012" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="CAL10157.1" /db-xref="GI:122087376" /db-xref="GOA:AlJHS4" /db-xref="InterPro:IPR002139" /db-xref="InterPro:IPR002173" /db-xref="InterPro:IPR011611" /db-xref="InterPro:IPR011877" /db-xref="UniProtKB/TrEMBL:AlJHS4" /translation="METGKLVLVGSINADHILNI EQFPRPGETVVGEQYKVAFGGKA NQAVAGRSGANIAFIACVGEDDIGDVRQLQAS DNIDTAPIEAVAGTTTGVALIFVN GEGENVIGIHAGANSAVTPEYLGRYQQQVIDADA LLMQLESPLGTVIAAAKLAKQHQT QVILNPAPARELPDELLSLVDMITPNTEAERLT GIHIEQDDDAKAAQILHDKGIAT VIITLGSRGVWLSEGGQGLVAGFKVNAVDTIAA GDTFNGALLTALLEGQAMGSAVRF AHAAAAIAVTRPGAQPSIPWRAEIDSFLQDRV"
misc-feature	12817..13701	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:PFAM:PF00294" /note="Pfam match to entry PF00294 pfkB, pfkB family carbohydrate kinase, score 298.8, E-value 4.4e-87"
misc-feature	12928..13002	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosite:PS00583" /note="PS00583 pfkB family of carbohydrate kinases signature 1."
misc-feature	13552..13593	/gene="rbsK" /locus-tag="YE0012" /inference="protein motif:Prosite:PS00584" /note="PS00584 pfkB family of carbohydrate kinases signature 2."
gene	13740..14741	/gene="rbsR"

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                                     /locus-tag="YE0012A"
                                     /inference="similar to
sequence:INSDC:AE008881"
                                     /inference="similar to
sequence:UniProtKB:P25551"
                                     /note="Similar to Escherichia
coli, and Escherichia coli O157:H7
ribose operon repressor RbsR or
b3753 or z5254 or ecs4695
SWALL:RBSR-ECOLI (SWALL:P25551)
(329 aa) fasta scores: E():
7.1e-94, 73.17 38d in 328 aa and
to Salmonella typhimurium
transcriptional repressor for rbs
operon RbsR or stm3886
SWALL:Q8ZKV7 (EMBL:AE008881) (332
aa) fasta scores: E(): 5.3e-95,
74.09 38d in 332 aa"
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                                     /db-xref="InterPro:IPR000843"
                                     /db-xref="InterPro:IPR001761"
                                     /db-xref="UniProtKB/TrEMBL:AlJHS5"
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YAPSALARSLKLNETRITIGMLVTASSNPFYAEVY
RGVERSCYERGYSLILCNTEGDI
RMSRSIETLMQKRVLDGLLMCTESHRPSQDILRC
YPSLPIIMMDWAFPEGVNDVIQDN
SLLGGEMATSYLIARGYTRIACIAGPQDKTPAKE
RLQGFQAMDRAGLPVLPDYEVAS
DFEFGGGLVAMKQLLALPQPPEAVFTSNDAVAVG
VYQALHQAGLSIPQDMAVIGYDDI
EIAQYMTPLTTIHQPKDSLGLAIDTLIHLRLNS
PEAEPQVILITPELIERGSVATR"
gene      complement(14738..16162 /locus-tag="YE0013"
)
CDS      complement(14738..16162 /locus-tag="YE0013"
)
                                     /codon-start=1
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transport protein"
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                                     /db-xref="GI:122087378"
                                     /db-xref="GOA:AlJHS6"
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                                     /db-xref="UniProtKB/TrEMBL:AlJHS6"
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ILAVSLFTLGLSLLCALSGSLPFLV
ASRVIQGVGGAMMPVARLALIRAYPRSELLPVL
NFVTIPLGLGPMGPLLGLLLVTY

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ATWHWFILNIPIGLLGIFYARKYMPDFTMPKRA
FDIIGFLLFGSSSLVMISVSLEIMG
RPDIASYLPAAVLLGGLLMLLFYIFHAKGHPNPL
IGLPLFKTRTFVSGIAGNVASRLG
TGCVPFLMPLMLQVGFYSIAIAGCMMAPTAIGS
MMAKSAVTQVLRSLGYRTVLVGIT
AIIGVLIALFAFQSPGMSPLMILPLFILGMAMS
TQFTAMNTITLADLTDNNASSGNS
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PRDGDNLIQGRNVKKVTPAKSEV"
/locus-tag="YE0013"

sig-peptide      complement(16052..16162
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                  /note="Signal peptide predicted
                  for YE0013 by SignalP 2.0 HMM
                  (Signal peptide probability 0.994)
                  with cleavage site probability
                  0.740 between residues 37 and 38"
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misc-feature      complement(join(14816..
14884,14927..14995,
15032..15100,
15128..15196,
15233..15301,
15344..15412,
15431..15499,
15527..15583,
15620..15679,
15689..15757,
15791..15859,
15869..15937,
15956..16015,
16058..16126))
                  /inference="protein
                  motif:TMHMM:2.0"
                  /note="14 probable transmembrane
                  helices predicted for YE0013 by
                  TMHMM2.0 at aa 13-35, 50-69,
                  76-98, 102-124,136-158, 162-181,
                  194-212, 222-244, 251-273,
                  288-310,323-345, 355-377, 390-412
                  and 427-449"
                  /locus-tag="YE0013"

misc-feature      complement(15830..16132
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                  /note="Pfam match to entry PF00083
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                  2.1e-06"

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CDS               complement(16237..16926
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VMQHFLILRRSLEPQACSLAINVSGKQKALLTS
LMTEMCELHAHFNRERWIOVDAQF
HQLIYEASGNPFLTSFANLFSVYHSYFRSITGD
EVIKLQHHQNIVDITILAGDSQGAL
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misc-feature      complement(16696..16875
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/inference="protein
motif:PFAM:PF00392"
/Note="Pfam match to entry PF00392
gntR, Bacterial regulatory
proteins, gntR family, score 79.0,
E-value 6.6e-21"
misc-feature      complement(16744..16818
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motif:Prosite:PS00043"
/Note="PS00043 Bacterial
regulatory proteins, gntR family
signature."
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/Note="Predicted helix-turn-helix
motif with score 1101.000, SD 2.94
at aa 38-59, sequence
PGEIELGEEQFGVSRRTAVREAVK"
gene              17506..18994
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(Y. enterocolitica 16S)"
gene              19220..19295
tRNA              19220..19295
/locus-tag="YE0014"
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/locus-tag="YE0014"
/Note="tRNA-Glu (TTC)"
/product="tRNA-Glu"
/Note="codon recognized: GAA"
gene              19674..22667
rRNA              19674..22667
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/Note="23S rRNA"
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/Note="23S rRNA"
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/Note="match to 23S-rRNA 1..2994
(Y. enterocolitica 23S
EMBL:U77925, Y. pestis KIM 98
38density, Citrobacter freundii
23S EMBL:U77928 94 38density)"
gene              22667..22908
rRNA              22667..22908
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ADFICSWLQINPSQP"
misc-feature complement(23299..23703
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/inference="protein
motif:PFAM:PF03205"
/notes="Pfam match to entry PF03205
MobB, Molybdopterin guanine
dinucleotide synthesis protein B,
score 184.3, E-value 1.3e-52"
misc-feature complement(23662..23685
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/inference="protein
motif:Prosite:PS00017"
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site motif A (P-loop)."
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gene complement(23718..24317
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CDS complement(23718..24317
)

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protein"

gene 25856..26479  
CDS 25856..26479

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FTVFPSVGGQRYEIDNLDQLEWVGRYLGRHQVQ  
SDALFVARSTIGIEYLTETPRLQ  
ASSELVPAKQDKFLAATDLLISTIKQYWHTDWQ  
FLRLHGDCHPGNILWRDGPMPFVDL  
DDARNGFAVQDLWMLLHGERREQLIQDLILLEAY  
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/db-xref="InterPro:IPR012335"  
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EEKITPLMFEGVQKTQTQVTPDDIRNVFIKAGVS  
GEEFDALNSFVVKSLVYQQQKAA  
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sig-peptide 25856..25912

/gene="dsbA"  
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/note="Signal peptide predicted  
for YE0020 by SignalP 2.0 HMM  
(Signal peptide probability 1.000)  
with cleavage site probability  
0.992 between residues 19 and 20"  
/gene="dsbA"  
/locus-tag="YE0020"

misc-feature 25856..26476

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gene	27070..29868	
CDS	27070..29868	

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misc-feature	27580..27900	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF01367" /note="Pfam match to entry PF01367 5-3-exonuclease, 5'-3' exonuclease, C-terminal SAM fold, score 194.5, E-value 1.1e-55"
misc-feature	28048..28629	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF01612" /note="Pfam match to entry PF01612 3-5-exonuclease, 3'-5' exonuclease, score 229.0, E-value 4.4e-66"
misc-feature	28717..29862	/gene="polA" /locus-tag="YE0021" /inference="protein motif:PFAM:PF00476" /note="Pfam match to entry PF00476 DNA-pol-A, DNA polymerase family A, score 698.2, E-value 2.6e-207"
misc-feature	29338..29397	/gene="polA" /locus-tag="YE0021" /inference="protein motif:Prosite:PS00447" /note="PS00447 DNA polymerase family A signature."
misc-RNA	30017..30134	/note="Spot 42 RNA (RF00021) as predicted by Rfam, score 91.54, positions 1 to 118"
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CDS	complement(30302..30955	/locus-tag="YE0022"
	)	
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misc-feature	complement(30830..30853)	LDTWFESEIPPEVMIDEYDDEEGK" /locus-tag="YE0022"
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CDS	31718..32284	/protein-id="CAL10168.1" /db-xref="GI:122087387" /db-xref="InterPro:IPR007336" /db-xref="UniProtKB/Swiss-Prot:A1J HT5" /translation="MKQPNKAPRADRAAPKGTAT PKRHHKTRVELDIEARERKRQKRA SGNRSGARTNIEGSKNGTSTQAEKDPRIKSKVP VPLVVESKAKAKLTKPKVAKVEAK PRLTPEEELTKLENDERLDALLDRLDNDEVLSKE DQAYVDLTLDRLDALMEQLGIELG DDEDEEREEREKPEDILKLLKSGNPKDTF"
gene	32467..33840	/gene="hemN" /locus-tag="YE0024"
CDS	32467..33840	/gene="hemN" /locus-tag="YE0024" /codon-start=1 /transl-table=11 /product="oxygen-independent coproporphyrinogen III oxidase" /protein-id="CAL10169.1" /db-xref="GI:122087388" /db-xref="GOA:A1JHT6" /db-xref="InterPro:IPR004558" /db-xref="InterPro:IPR006638" /db-xref="InterPro:IPR007197" /db-xref="InterPro:IPR010723" /db-xref="UniProtKB/TrEMBL:A1JHT6" /translation="MSENAVVDLSLIQKYNYS GPRYTSYPTALEFSEYDESAFQQA VKRYQPRLSLYVHIPFCHKLCYFCGCNKLVT RQ QHKADEYLAVLEKEIRQRAALFAG RQVSQMHWGGGGTPTYLNKQTQIHLNLLREN FDF LPGAEQSIEVDPREIELDVLDDL R AEGFNRLSMGVQDFNKEVQRLVNRQDE DFIFAL IARAKALGFNSTNDLIYGLPKQT PESFAFTLKRVAELNPDRSLVFNIAHLPSL FAAQ RKIKDADLPTAEQRDLILQHTISF LTESGYQFIGMDHFARPDDELAIAQREGK LHRNF QGYTTQGESDLLGLGVSAISMLGD SYAQNEKDLKTYAVVEQRGNALWRGLTMT EDDC LRRDVIKTLICNFQISYQPIEQHY GIRFADYFAEDFELLTPFEHDGLVERDDK SIRVT PRGRLLIRNICMCFDIYLRQKARK QQFSRVI"
misc-feature	32761..33522	/gene="hemN" /locus-tag="YE0024"

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Coproporphyrinogen III oxidase,
score 555.2, E-value 2.8e-164"
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/Note="Synonyms: glnG, glnT"
CDS       complement(33989..35401
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/Note="Pfam match to entry PF02954
HTH-8, Bacterial regulatory
protein, Fis family, score 64.1,
E-value 2e-16"
misc-feature complement(34007..34072
)
/locus-tag="YE0025"
/Note="Predicted helix-turn-helix
motif with score 1763.000, SD 5.19
at aa 444-465, sequence
GHKQEAARLLGWGRNTLTRKLK"
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Sigma54-activat,Sigma-54
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E-value 1.1e-146"
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/note="PS00676 Sigma-54
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/inference="protein
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region A signature."
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/inference="protein
motif:PFAM:PF00072"
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E-value 7.8e-42"
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CDS complement(35409..36458 /gene="ntrB"
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                    /inference="protein
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                    gyrase B-, and HSP90-like ATPase,
                    score 104.0, E-value 1.9e-28"
misc-feature      complement(35877..36074 /gene="ntrB"
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                    /inference="protein
                    motif:PFAM:PF00512"
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                    (phosphoacceptor) domain, score
                    64.0, E-value 2.1e-16"
gene              complement(36607..38016 /gene="glnA"
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CDS               complement(36607..38016 /gene="glnA"
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misc-feature	complement(36868..37713)	/gene="glnA"  /locus-tag="YE0027" /inference="protein" motif:PFAM:PF00120" /note="Pfam match to entry PF00120 gln-synt, Glutamine synthetase, catalytic domain, score 563.6, E-value 8.6e-167"
misc-feature	complement(37195..37242)	/gene="glnA"  /locus-tag="YE0027" /inference="protein" motif:Prosite:PS00181" /note="PS00181 Glutamine synthetase putative ATP-binding region signature."
misc-feature	complement(37729..37977)	/gene="glnA"  /locus-tag="YE0027" /inference="protein" motif:PFAM:PF03951" /note="Pfam match to entry PF03951 gln-synt-N, Glutamine synthetase, beta-Grasp domain, score 169.3, E-value 4.1e-48"
misc-feature	complement(37813..37869)	/gene="glnA"  /locus-tag="YE0027" /inference="protein" motif:Prosite:PS00180" /note="PS00180 Glutamine synthetase signature 1."
gene	complement(38201..38311)	/locus-tag="YE0028"
CDS	complement(38201..38311)	/locus-tag="YE0028"  /inference="similar to sequence:INSDC:AJ414141" /note="Poor database matches. Similar to the N-terminal region of Yersinia pestis possible membrane protein YPO0025 SWALL:Q8ZJR4 (EMBL:AJ414141) (52 aa) fasta scores: E(): 1.8e-12, 80.55 38d in 36 aa. Doubtful CDS" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAL10173.1" /db-xref="GI:122087392"

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gene	38529..40352	
CDS	38529..40352	
misc-feature	38535..39122	
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misc-feature	39711..39977	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00679" /note="Pfam match to entry PF00679 EFG-C, Elongation factor G C-terminus, score 112.3, E-value 6e-31"
gene	40648..41235	/locus-tag="YE0030"
CDS	40648..41235	/locus-tag="YE0030" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10175.1" /db-xref="GI:122087394" /db-xref="GOA:A1JHU2" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006402" /db-xref="UniProtKB/TrEMBL:A1JHU2" /translation="MLYIFDLGNVIVDIDFKRVL GVWSKLSVPLATLSERFTMGVVF QQHERGEISDEDFARQLSDEMGLSLSFQFAEGW QAVFVALRPEVISIMOKLRAEGHR VVVLSNTNRLHCNYWPQHYPEVAAAADHMYLSQD LGMKRPARIYQHVLSAENIPAEQ AVFFDDVEANIVAARIEGITGIHVTDRKVIPAYF S"
misc-feature	40648..41208	/locus-tag="YE0030" /inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 61.6, E-value 1.1e-15"
gene	41328..42218	/gene="rnb" /locus-tag="YE0031"
CDS	41328..42218	/gene="rnb" /locus-tag="YE0031" /codon-start=1 /transl-table=11 /product="ribonuclease BN" /protein-id="CAL10176.1" /db-xref="GI:122087395" /db-xref="GOA:A1JHU3" /db-xref="InterPro:IPR004664" /db-xref="InterPro:IPR017039" /db-xref="UniProtKB/Swiss-Prot:A1J HU3" /translation="MASFLRFLRSASLKPYPITFG RMLYTRIDKDLTMLAGHLAYVSL LSLVPLVTVIFALFAAFPMFADISIKLKAFIFTN FMPATGDIQNYLEQFVANSNRM VVGTCGLIVTALLLIYSVDSVLNIIWRSKVHRSL

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misc-feature	join(41442..41510, 41628..41687, 41748..41816, 41874..41933, 41967..42035, 42063..42131)	/locus-tag="YE0031" /inference="protein motif:TMHMM:2.0" /notes="6 probable transmembrane helices predicted for YE0031 by TMHMM2.0 at aa 39-61, 101-120, 141-163, 183-202, 214-236 and 246-268" /locus-tag="YE0032" /locus-tag="YE0032" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10177.1" /db-xref="GI:122087396" /db-xref="GOA:AJHU4" /db-xref="InterPro:IPR003732" /db-xref="UniProtKB/Swiss-Prot:A1J HU4" /translation="MIALIQRLSANVVVDGEV GEIGPGLLILGVEQQDTEOKAQR LCEKVLGYRIFGDENDKMNINVKQAGGSVLVVSQ FTLVADTQKMRPFSFSGASPAEA DRLYQYFVACQREHGVTETGLFAADMVSLVND GPVTFWLQI"
gene	42225..42662	
CDS	42225..42662	
misc-feature	42306..42659	/locus-tag="YE0032" /inference="protein motif:PFAM:PF02580" /notes="Pfam match to entry PF02580 DUF154, Uncharacterized ACR, COG1490, score 261.8, E-value 6e-76" /locus-tag="YE0033" /locus-tag="YE0033" /codon-start=1 /transl-table=11 /product="conserved membrane protein" /protein-id="CAL10178.1" /db-xref="GI:122087397" /db-xref="GOA:AJHU5"
gene	42914..43837	
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misc-feature 43184..43249
/locus-tag="YE0033"
/notes="Predicted helix-turn-helix
motif with score 1005.000, SD 2.61
at aa 91-112, sequence
MTLESVARQEGVKRVVCSAREDA"
misc-feature 43517..43585
/locus-tag="YE0033"
/inference="protein
motif:TMHMM:2.0"
/notes="1 probable transmembrane
helix predicted for YE0033 by
TMHMM2.0 at aa 202-224"
repeat-region 44408..45116
/notes="repeat unit encoding a
LuxR-family transcriptional
regulator"
gene 44431..45117
CDS 44431..45117
/locus-tag="YE0035"
/locus-tag="YE0035"
/inference="similar to
sequence:INSDC:AE004433"
/inference="similar to
sequence:INSDC:AE004564"
/notes="Similar to Pseudomonas
aeruginosa probable
transcriptional regulator PA1347
SWALL:Q9I3Z7 (EMBL:AE004564) (230
aa) fasta scores: E(): 3e-09,
30.43 id in 207 aa, and to the
C-terminal region of Vibrio
cholerae LuxR family
transcriptional regulator VCA1078
SWALL:Q9KKM5 (EMBL:AE004433) (319
aa) fasta scores: E(): 2.2e-10,
27.53 38d in 207 aa"
/codon-start=1
/transl-table=11
/product="LuxR family
transcription regulatory protein"
/protein-id="CAL10179.1"
/db-xref="GI:122087398"
/db-xref="GOA:A1JHU6"
/db-xref="InterPro:IPR000792"

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/db-xref="InterPro:IPR011991"
/db-xref="InterPro:IPR013656"
/db-xref="UniProtKB/TrEMBL:AJJHU6"
/translation="MEASLFNSLKMLIKFWECSS
EPWGVKDNQSRVYANNRLHKLFA
LPDKFVSMEGRTDGLPTPISEFELEFQEHDKVK
LLQDRVTSVEIHAWNGHSYYPYF
FDKYPLIDHGVSGQGISHSRPVEDVILTHLNKI
KVPISLILTPPSDLFSKREWEVLF
YILHSFSSMEIATKLHLSSITVDNIIQKIYKKIG
ISGRQQLVDVYCYENKINNYVPQSF
FEYSGSFPLV"
misc-feature 44872..45069 /locus-tag="YE0035"
/inference="protein
motif:PFAM:PF00196"
/notes="Pfam match to entry PF00196
GerE, Bacterial regulatory
proteins, luxR family, score 41.3,
E-value 1.4e-09"
misc-feature 44926..44991 /locus-tag="YE0035"
/notes="Predicted helix-turn-helix
motif with score 1060.000, SD 2.80
at aa 166-187, sequence
FSSMEIATKLHLSSITVDNIIQ"
repeat-region 45117..45833 /notes="repeat unit encoding a
LuxR-family transcriptional
regulator"
gene 45147..45833 /locus-tag="YE0036"
CDS 45147..45833 /locus-tag="YE0036"
/inference="similar to
sequence:INSDC:AE004433"
/inference="similar to
sequence:INSDC:AE004564"
/notes="Similar to Pseudomonas
aeruginosa probable
transcriptional regulator PA1347
SWALL:Q9I3Z7 (EMBL:AE004564) (230
aa) fasta scores: E():
2.2e-09,30.37 38d in 214 aa, and
to the C-terminal region of Vibrio
cholerae LuxR family
transcriptional regulator VCA1078
SWALL:Q9KKM5 (EMBL:AE004433) (319
aa) fasta scores: E(): 6.6e-13,
30.43 38d in 207 aa"
/codon-start=1
/transl-table=11
/product="LuxR family
transcription regulatory protein"
/protein-id="CAL10180.1"
/db-xref="GI:122087399"
/db-xref="GOA:AJJHU7"
/db-xref="InterPro:IPR000792"
/db-xref="InterPro:IPR011991"
/db-xref="UniProtKB/TrEMBL:AJJHU7"
/translation="MDKPLKNQLEILIRFWERSS
EPWGARDNQSRFIYSNDRHHKLLG
LSDKYNLEGRDSELPSPTAAFQMEFQAHRKVE
LSQERITSVEIHEDWGLSYLKNPF
CDKYPLIDESGVSGQIFHVRPVEDIILSRLTKI
KAPTSLTFTPPSKLFTKREWEVLF
YILHSYSSKDIKKLHISPTVSNTQSVYRKVG

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		VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM" /locus-tag="YE0036" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.3, E-value 5.5e-12"
misc-feature	45588..45785	
		/locus-tag="YE0036" /note="Predicted helix-turn-helix motif with score 2073.000, SD 6.25 at aa 166-187, sequence YSSKDIAKKLHISPRTVSNITQ" /note="repeat unit encoding a LuxR-family transcriptional regulator"
misc-feature	45642..45707	
repeat-region	45834..46549	
gene	45863..46549	
CDS	45863..46549	/locus-tag="YE0037" /locus-tag="YE0037" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3.6e-10,30.47 38d in 210 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 4.2e-10, 27.94 38d in 229 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10181.1" /db-xref="GI:122087400" /db-xref="GOA:AlJHU8" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:AlJHU8" /translation="MGETLKNQLEILIRFWEHSS EPWQIKDSQSRYYANPRSHKLLS LPAKYNMGRDLGELPSPISEFQAEFQRQDRQVE LLQDRITSAEIHIVDGKSYLTPFF CDKYPLIDENGISQGVICHARPVHNMLTRLNKI KAPTSLTFTPPSKLFTKRENEVLF YILHSYSSKDIAKKLHLSARTVSNITQSVYRKVG VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM"
misc-feature	46304..46501	/locus-tag="YE0037" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"

misc-feature	46358..46423	/locus-tag="YE0037" /note="Predicted helix-turn-helix motif with score 1813.000, SD 5.36 at aa 166-187, sequence YSSKDIAKKLHLSARTVSNITQ"
repeat-region	46550..47265	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	46579..47265	/locus-tag="YE0038"
CDS	46579..47265	/locus-tag="YE0038" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 1e-09, 31.28 id in 211 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 4.1e-10, 27.94 38d in 229 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10182.1" /db-xref="GI:122087401" /db-xref="GOA:AlJHU9" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TREMBL:AlJHU9" /translation="MGETLKNQLEILIRFWEHSS EPWQIKDSQSRYYANPRTHKLLS LPAYNMEGRDLGELPSPISFEQAEFQRQDRQVE LLQDRITSAEIHIVDGKSYLTFF CDKYLIDYEGISQGVICHDRPVHNLMLTRLNKI KAPTSLTFTTPPSKLFKRENEVLF YILHSYSSKDIAKKLHLSARTVSNITQSVYRKVG VSNKRQIVDYCYENKINNYVPQSF FEYSGSFPLM" /locus-tag="YE0038" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"
misc-feature	47020..47217	/locus-tag="YE0038" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 46.4, E-value 4.3e-11"
misc-feature	47074..47139	/locus-tag="YE0038" /note="Predicted helix-turn-helix motif with score 1813.000, SD 5.36 at aa 166-187, sequence YSSKDIAKKLHLSARTVSNITQ"
repeat-region	47266..47965	/note="repeat unit encoding a LuxR-family transcriptional regulator"
gene	47294..47980	/locus-tag="YE0039"



CDS	47294..47980	<pre> /locus-tag="YE0039" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3.8e-08,29.04 38d in 210 aa, and to Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 2.9e-10, 28.5 id in 214 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10183.1" /db-xref="GI:122087402" /db-xref="GOA:ALJHV0" /db-xref="InterPro:IPR000014" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:ALJHV0" /translation="MDKPLKNQLEILIRFWERSS EPWAIKDNQSKFIYANRRVYKLFN LPNKYTLEGRLDGEIPTPSADQDEFQQDQRQVE LSQDRVTSVDIQLYDGFSYFTPYF SDKYPLIDENGVSQGVICHARPVDIMLTHLNKI KVPTSLIFTPPSKLFTKRENEVLV YILHSYSSKDLAEKLHLSPTVSNIIQSVYRKAG VSNKRQIVDYCYENKINNYVPQSF FEYSKSFPLM" </pre>
misc-feature	47735..47932	<pre> /locus-tag="YE0039" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 43.2, E-value 3.9e-10" </pre>
misc-feature	47789..47854	<pre> /locus-tag="YE0039" /note="Predicted helix-turn-helix motif with score 2197.000, SD 6.67 at aa 166-187, sequence YSSKDLAEKLHLSPTVSNIIQ" </pre>
gene	complement(48077..49786)	<pre> /locus-tag="YE0040" </pre>
CDS	complement(48077..49786)	<pre> /locus-tag="YE0040" /codon-start=1 /transl-table=11 /product="possible exported protein" /protein-id="CAL10184.1" /db-xref="GI:122087403" /db-xref="InterPro:IPR007844" /db-xref="UniProtKB/TrEMBL:ALJHV1" /translation="MKFLGKVLTLTLLLVLSIV </pre>

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LCYVLLQTSWAAGWLSRWVSDNSE
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LQNGSLTLNNSSTPLPLQADTLRLNMAINTTIE
PQNKAGQWKVTGQQVTGGLIPWQP
LPGNSLGENAQFQFSAGSLTINGITAEKLYLQGS
IQKNALTLNFGADIAQOELTGNA
SQSADGSLVLDRLRLSNIRLQTPATLEDVWNTFL
QLPPIITLKRFDLIDARVEGKNWAF
NDLDTLKNITFKQGDWQSDGELSINAGDIKKG
NIHLIDPIATFTLSPAGVAINFOFS
TRWQDGLLRAQGNWLRDShRLQDELTLVALVYT
LPTDWKQQWQOTLPNWLSEVYISK
LNANRNLIDISPDFFQITSLDAAGTNLLAKN
HQWGVWGSGLMLNAGNATFNKNDV
RRPSLALSANEQQITVSDLSFTKEGLLEATATI
DQTSGRALSLALTGRVDNLILQN
WGWFALPLQGLGNLKLRSIGNLTADKPLKPTING
SLQATDNHGQQVNTMQNGEVHGV AGQ"
/locus-tag="YE0040"

sig-peptide    complement(49694..49786
)

/note="Signal peptide predicted
for YE0040 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability
0.986 between residues 31 and 32"
/locus-tag="YE0040"

misc-feature    complement(49700..49768
)

/inference="protein
motif:TMHMM:2.0"
/note="1 probable transmembrane
helix predicted for YE0040 by
TMHMM2.0 at aa 7-29"
/locus-tag="YE0041"

gene            complement(49933..51318
)

CDS             complement(49933..51318
)

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permease"
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/db-xref="GOA:A1JHV2"
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/db-xref="InterPro:IPR006043"
/db-xref="InterPro:IPR017588"
/db-xref="UniProtKB/TrEMBL:A1JHV2"
/translation="MSTQSAELNTPQATTHPSE
LIYRLEDRPPLAQTLPACQHLA
MFVAVITPGLLICQALGLPAEDTORIISMFLAS
GLASLLQIKTWGPGVSGLLSIQGT
SFNFVSPLMGGLALKNGGADIPTMMAALFGTLM
VASCTEILSRFLHLARRIITPLV
SGIVVMIIGLSLIQVGLTISGGGYGAMSDHTFGS
PKNLMLAGAVLVVILLNRQNPY
LRVASLVIAMAVGYLLAWTLGMLPESRPVVDAL
ITIPTPLYGLSFDWNLLVPLMLI
FMVTSLETIGDITATSDVSEQVPHGPLYMKRLKG
GVLANGLNSMLSAVENTFPNCSFG
QNNGVQLTGVASRYVGFVVALMLIVLGLFAVA
GFVQHIFEPEVLGGATLVMFGTIAA

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SGVRIVSRETLNRRRAIMIALSLAVGMGVAQQPL
ILQFAPDWIKTLLSSGIAAGGITA
IVLNLIFPQEK"
misc-feature      complement(join(49948.. /locus-tag="YE0041"
50007,50035..50103,
50122..50190,
50203..50271,
50473..50541,
50599..50667,
50686..50745,
50788..50856,
50875..50943,
50971..51039,
51127..51195))

/inference="protein
motif:TMHMM:2.0"
/notes="11 probable transmembrane
helices predicted for YE0041 by
TMHMM2.0 at aa 42-64, 94-116,
126-148, 155-177,192-211, 218-240,
260-282, 350-372, 377-399, 406-428
and 438-457"
misc-feature      complement(50038..51225 /locus-tag="YE0041"
)

/inference="protein
motif:PFAM:PF00860"
/notes="Pfam match to entry PF00860
xan-ur-permease,Permease family,
score 528.7, E-value 2.8e-156"
misc-feature      complement(50137..50199 /locus-tag="YE0041"
)

/inference="protein
motif:Prosite:PS01116"
/notes="PS01116 Xanthine/uracil
permeases family signature."
misc-feature      complement(50689..50736 /locus-tag="YE0041"
)

/inference="protein
motif:Prosite:PS00038"
/notes="PS00038 Myc-type,
'helix-loop-helix' dimerization
domain signature."
misc-feature      complement(50899..50931 /locus-tag="YE0041"
)

/inference="protein
motif:Prosite:PS00013"
/notes="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
misc-feature      complement(51202..51234 /locus-tag="YE0041"
)

/inference="protein
motif:Prosite:PS00013"
/notes="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
gene              51557..52771
/locus-tag="YE0042"
/notes="synonym: gltC"
CDS               51557..52771
/locus-tag="YE0042"
/codon-start=1

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carrier protein"
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/db-xref="GOA:AlJHV3"
/db-xref="InterPro:IPR004445"
/db-xref="UniProtKB/TrEMBL:AlJHV3"
/translation="MFHLDTYGTLVAACLVL LLG
RKLQTVTPFLKKYTIPEPVAGLL
VAFMMLLMQKTLGWEISFDMSLKDPLMLAFFATI
GLNANLASLRAGGKALSVFVFVVV
GLLLMQNAIGIALAKLMGLDPLMGLLAGSITLSG
GHGTGAWSKVVERYGFENATEV
AMACATFGLVLGGLIGGPVARYLVKHSSTPDGTP
EDSEIPSAFEKPSAGRMITSLVLT
ETIAMIAICLMVGQVISAGLQGMFELPTFVCVL
FVGVLISNTLSAIGFYKVFDRVVS
VLGNVLSLSFLAMALMSLKLWELASLALPMLVIL
SVQALAMALYAIFVTYRLMGKNYD
AAVLAAGHCGFGLGATPTAIANMQAITDRFGPSH
LAFVLVPMVGAFIDIVNVIVIKL
YLLLPFPAVVG"
misc-feature      51560..52654
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                    /locus-tag="YE0042"
                    /inference="protein
motif:PFAM:PF03616"
                    /note="Pfam match to entry PF03616
Glt-symporter, Sodium/glutamate
symporter, score 808.3, E-value
1.8e-240"
misc-feature      join(51566..51619,
51653..51706,
51764..51817,
51836..51904,
52025..52093,
52193..52261,
52289..52357,
52376..52432,
52460..52528,
52562..52630,
52658..52726)
                    /locus-tag="YE0042"
                    /inference="protein
motif:TMHMM:2.0"
                    /note="11 probable transmembrane
helices predicted for YE0042 by
TMHMM2.0 at aa 4-21, 33-50, 70-87,
94-116,157-179, 213-235, 245-267,
274-292, 302-324, 336-358 and
368-390"
gene              complement(52840..54921
)
                    /gene="recG"
                    /locus-tag="YE0043"
CDS              complement(52840..54921
)
                    /gene="recG"
                    /locus-tag="YE0043"
                    /codon-start=1
                    /transl-table=11
                    /product="ATP-dependent DNA
helicase"
                    /protein-id="CAL10187.1"

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/db-xref="GOA:A1JHV4"
/db-xref="InterPro:IPR001650"
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/db-xref="InterPro:IPR004609"
/db-xref="InterPro:IPR011545"
/db-xref="InterPro:IPR014001"
/db-xref="InterPro:IPR014021"
/db-xref="UniProtKB/TrEMBL:A1JHV4"
/translation="MKGRLLDAVPLSTLSGVGAS
QAGKLAKMGLTIQDLLHLPLRY
EDRTRLRYRIGDLLPLSVTVEGEVLRSDISFGRR
RMMTCQISDGSGLTLRFFNFNAA
MKNLSLSPGKHVIAYGEAKRGNTGPEIIHPEYRVH
GENIGVELQESLTPVYPTTEGIRQ
ATLRKLIDQALAMDSSVIAELLPIELSRSLISL
PEAIHILHRPPADIQLADLEQGKH
PAQRRLIMEELLAHNLSMLAVRAGAAQSYRALPLL
PEEQKKRRFLAALPFTPTHAQQRV
VAEIEQDMTHSYPMRLIQGDVGSGKTLVAALAA
LRAIAHGKQVALMAPTELLAEQHA
NTFRQWLEPLGLEVGWLAGKQKGKARLAQQEAVA
SGQVSMVVGTHAMFQEQVQFSGLA
LVIIIDEQHRFGVQHRLALWEKGEQGFHPHQLIM
TATPIPRTLAMTAYADLDTSTVIDE
LPPGRTPVTITVAIPDTRRSVDVIQRVKNACLEGR
QAYVWVCTLIEESELLEAAAEVTC
EELKIALPEIKVGLVHGRMGKPEKQAVMLAFKQG
ELQLLVATTVIEVGVDVFNASLMI
IDNPERLGLAQLHLRGRVGRGAVASHCVLLYKT
PLSKTAQMRLQLVRDSNDGFVIAQ
RDLEIRGPGELLGTRQTGSAEFKVADLLRDQAMI
PEVQRVARHLHQQYFEHAQALIER
WLPERTRYTNA"
/gene="recG"

sig-peptide      complement(54856..54921
)
/locus-tag="YE0043"
/note="Signal peptide predicted
for YE0043 by SignalP 2.0 HMM
(Signal peptide probability 0.878)
with cleavage site probability
0.798 between residues 22 and 23"
/gene="recG"

misc-feature      complement(53155..53373
)
/locus-tag="YE0043"
/inference="protein
motif:PFAM:PF00271"
/note="Pfam match to entry PF00271
helicase-C, Helicase conserved
C-terminal domain, score 79.9,
E-value 3.4e-21"
/gene="recG"

misc-feature      complement(53545..54147
)
/locus-tag="YE0043"
/inference="protein
motif:PFAM:PF00270"
/note="Pfam match to entry PF00270
DEAD, DEAD/DEAH box helicase,
score 123.2, E-value 3.1e-34"
/gene="recG"

misc-feature      complement(54013..54036
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/locus-tag="YE0043"

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/inference="protein
motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
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misc-feature complement(54514..54738)  
) /gene="recG"

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/locus-tag="YE0043"
/inference="protein
motif:PFAM:PF01336"
/note="Pfam match to entry PF01336
tRNA-anti, OB-fold nucleic acid
binding domain, score 34.6,
E-value 1.5e-07"
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gene complement(54922..55614)  
) /gene="trmH"

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/locus-tag="YE0044"
/note="synonym: spoU"
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CDS complement(54922..55614)  
) /gene="trmH"

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/transl-table=11
/product="tRNA
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e"
/protein-id="CAL10188.1"
/db-xref="GI:122087407"
/db-xref="GOA:AlJHV5"
/db-xref="InterPro:IPR001537"
/db-xref="UniProtKB/TrEMBL:AlJHV5"
/translation="MNPQRYARICEMLATRQPD
LTVCLEEVHKPHNVSAIIRTADAVG
IHQIHAIWPTPAMYTRLSSAAGSNWVQVKTHSH
ITDAITHLKSQGMQILATHLSDKA
VDFREIDYTRPTCILMGQEKIGISKEALAMADKD
IIIPMIGMVQSLNVSVASALILIY
AQRQRQNAAGMYQRTQSVLSEDEQQRLLFEGGYPV
LAQVAKRKGLPQFYIDEQGQVIAD
AQWWSAMQSTES"
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misc-feature complement(55138..55560)  
) /gene="trmH"

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/locus-tag="YE0044"
/inference="protein
motif:PFAM:PF00588"
/note="Pfam match to entry PF00588
SpoU-methylase, SpoU rRNA
Methylase family, score 188.6,
E-value 6.6e-54"
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gene complement(55620..57722)  
) /gene="spoT"

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/locus-tag="YE0045"
/locus-tag="YE0045"
/codon-start=1
/transl-table=11
/product="guanosine-3',5'-bisbis(d
iphosphate) 3'-pyrophosphydrolase"
/protein-id="CAL10189.1"
/db-xref="GI:122087408"
/db-xref="GOA:AlJHV6"
/db-xref="InterPro:IPR003607"
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CDS complement(55620..57722)  
) /gene="spoT"

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/db-xref="InterPro:IPR004095"
/db-xref="InterPro:IPR004811"
/db-xref="InterPro:IPR006674"
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/db-xref="InterPro:IPR012675"
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/translation="MYLFESLNLLIQRYLP EEQI
KRLQAYLVARDAHEGQTRSSGEP
YITHPVAVACILAEMRLDYETLMAALLHDVIEDT
PATYQDMEQLFGKSV AELVEGVSK
LDKLNFRDKKEAQAEFRKMIMAMVQDIRVILIK
LADRTNMRTLGLSLRPDKRRRIAR
ETLEIYSPLAHLRIGIHLKTELEELGFEALYPNR
YRVIKEVVKAARGNRKEMIQKILA
EIEGRLTEAGIPCRVSGREKHLYSIYCKMNLKEQ
RFHSIMDIYAFRVIVKEVDTCYRV
LGQAHSPLYKPRPGRVKDYIAIPKANGYQSLHTSL
IGPHGVFPVEVQIRTEDMDQMAENG
VAAHWAYKEQGESGTTAQIRAQRMQSLLELQQS
AGSSFEFIESVSKDLFPDEIYVFT
PEGRIVELPAGATPVDFAVAVHTDIGHACVGARV
DRQPYPLSQPLSSGQTVEIITAPG
ARPNAAWLNLFVVSSKARAKIRQLLKNLKRDESVS
LGRLLLNHALGNRKLSDIPEENI
KHELDRLMKLATLDDLAEIGLGNAMSVVAKNLL
GDPSTLATSGTRNLAIKGADGVLI
TFAKCCRPVPGDPIIAHISPGKGLVIHHESCRNI
RGYQKEPEKFMAVEWDQETEQEFI
AEIKVDMFNQQGALANLTAAINAAESNIQSLNTE
EKDGRVYSAFIRLTTRDRVHLANI
MRKIRIMPVVVKVSRNRN"

misc-feature      complement(55629..55850) /gene="spoT"
)

/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF01842"
/note="Pfam match to entry PF01842
ACT, ACT domain, score 15.3,
E-value 0.097"

misc-feature      complement(56382..56573) /gene="spoT"
)

/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF02824"
/note="Pfam match to entry PF02824
TGS, TGS domain, score 110.2,
E-value 2.6e-30"

misc-feature      complement(57291..57590) /gene="spoT"
)

/locus-tag="YE0045"
/inference="protein
motif:PFAM:PF01966"
/note="Pfam match to entry PF01966
HD, HD domain, score 74.5, E-value
1.4e-19"

misc-feature      complement(57561..57593) /gene="spoT"
)

/locus-tag="YE0045"
/inference="protein
motif:Prosites:PS00013"
/note="PS00013 Prokaryotic
membrane lipoprotein lipid

```

```

gene      complement(57741..58016) attachment site."
                                           /gene="rpoZ"
                                           /locus-tag="YE0046"
CDS       complement(57741..58016) /gene="rpoZ"
                                           /locus-tag="YE0046"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="DNA-directed RNA
polymerase, omega chain"
                                           /protein-id="CAL10190.1"
                                           /db-xref="GI:122087409"
                                           /db-xref="GOA:AlJHV7"
                                           /db-xref="InterPro:IPR003716"
                                           /db-xref="InterPro:IPR006110"
                                           /db-xref="UniProtKB/Swiss-Prot:AlJ
HV7"
                                           /translation="MARVTVQDAVEKIGNRFDLV
LVAARRARQIQSGGKDALVPEEND
KVTVIALREIEEGLITNQILDVREERQEQQEQA
EIQAVTAIAEGRR"
misc-feature complement(57822..57983) /gene="rpoZ"
                                           /locus-tag="YE0046"
                                           /inference="protein
motif:PFAM:PF01192"
                                           /note="Pfam match to entry PF01192
RNA-pol-Rpb6, RNA polymerase Rpb6,
score 78.8, E-value 7.6e-21"
gene      complement(58071..58694) /gene="gmk"
                                           /locus-tag="YE0047"
                                           /note="synonym: spoR"
CDS       complement(58071..58694) /gene="gmk"
                                           /locus-tag="YE0047"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="guanylate kinase"
                                           /protein-id="CAL10191.1"
                                           /db-xref="GI:122087410"
                                           /db-xref="GOA:AlJHV8"
                                           /db-xref="InterPro:IPR008144"
                                           /db-xref="InterPro:IPR008145"
                                           /db-xref="InterPro:IPR017665"
                                           /db-xref="UniProtKB/TrEMBL:AlJHV8"
                                           /translation="MVQGTLYIVSAPSGAGKSSL
IQALLKTQPLYDTQVSISSHTRAK
RPGENHGEHYFFVSKKEEFCMIDDDAFLEHAKVF
ENYGYGTSRLAIEQVLATGVDVFLD
IDWQGAQQIRAKMPTARSIFILPPSKEELDRRLR
GRGQDSEEVIAKMAQAVAEMTHY
AEYDYLVNDDFNALSDLKTIIRAERLRLGRQK
QRHDALITKLLAD"
misc-feature complement(58260..58574) /gene="gmk"
                                           /locus-tag="YE0047"
                                           /inference="protein
motif:PFAM:PF00625"
                                           /note="Pfam match to entry PF00625
Guanylate-kin, Guanylate kinase,

```



misc-feature	complement(58524..58577)	score 198.3, E-value 7.9e-57" /gene="gmk"  /locus-tag="YE0047" /inference="protein" motif:Prosite:PS00856" /note="PS00856 Guanylate kinase signature." /gene="gmk"
misc-feature	complement(58641..58664)	 /locus-tag="YE0047" /inference="protein" motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0048" /locus-tag="YE0048" /codon-start=1 /transl-table=11 /product="putative DNA ligase" /protein-id="CAL10192.1" /db-xref="GI:122087411" /db-xref="GOA:AJJHV9" /db-xref="InterPro:IPR001679" /db-xref="InterPro:IPR003583" /db-xref="InterPro:IPR004150" /db-xref="InterPro:IPR012340" /db-xref="InterPro:IPR013839" /db-xref="InterPro:IPR013840" /db-xref="UniProtKB/Swiss-Prot:AJJ HV9" /translation="MNVHKMKILSLMVSFISWQ ARAESVCPWESEERMSGEMHLEK QLDQWNIAHYHQGISPIADDIYDQLQDKLHRWRL CLGLPKTDNRPFIGNGKMLHPVA HTGLKKLKDEAALISWMTGRKNLWVPKIDGVAV TLVYQAGKLTQVLSRGNGLGQNW ADKAPFISAIPQYIASAPPLLTQGEVFLQMEGH QQAQSGGANARASVAGALMRKSVS PLLAKLGIFIWAWPDGPKSMVEKSRLQEMGFPL TAHYSEPVISSSDVALWRDRWFKM PLPFVTDGVVIRQENVPAGRYWQATPGNWSVAWK YPPQQITEIKDIHFTVGRGTKIT AILQVIPVKIDDKWIRRVNIGSIARWKQWDIVPG DQVITISLAGQGIPRLDKVIWRVSQ RQEI VPPDADKFHQLTCFRRLPFCECEPQFLSRLA WLSGTINGLDMQSVGNGLWRELIIH GFINGLLDWLSLSVEQIAAVPGIGQGQRAEKIYQQ FORARQQPFSQWLQALGFPGQIPL DTSWHSRLRQRSIAEWRLMPGIGQVRAKQINHFLLH HPEVQMMADFLSQQGIAGFSPEE"
gene	58977..60674	
CDS	58977..60674	
sig-peptide	58977..59045	/locus-tag="YE0048" /note="Signal peptide predicted for YE0048 by SignalP 2.0 HMM (Signal peptide probability 0.991) with cleavage site probability 0.950 between residues 23 and 24"
misc-feature	59073..59918	/locus-tag="YE0048" /inference="protein" motif:PFAM:PF01653" /note="Pfam match to entry PF01653 DNA-ligase-N, NAD-dependent DNA

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ligase adenylation domain, score
109.4,E-value 4.4e-30"
/misc-feature 59922..60176 /locus-tag="YE0048"
/inference="protein
motif:PFAM:PF03120"
/note="Pfam match to entry PF03120
DNA-ligase-OB,NAD-dependent DNA
ligase OB-fold domain, score
73.6,E-value 2.7e-19"
gene complement(60692..61309 /locus-tag="YE0049"
)
CDS complement(60692..61309 /locus-tag="YE0049"
)

/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="CAL10193.1"
/db-xref="GI:122087412"
/db-xref="InterPro:IPR005115"
/db-xref="UniProtKB/TrEMBL:A1JHW0"
/translation="MLLSVLYIIGITAEAMTGAL
AAGRRQMDMFGVIIASATAIGGG
SVRDMLLGHYPPLGWVKHPEYIVIVAVAAIVITWM
APLMKHLRHLFLVLDAIGLIVFSI
IGAQIALDMGHSSTIIAAIAAVITGVFGVLRDMF
CNCIPLVFQKEIYAGISFAAAWIY
IALQYTPLSHN*VVVITLVTGLSARLLALRFRLG
LPVFKYEHSEH"

/misc-feature complement(join(60743..
60796,60824..60892,
60911..60979,
60989..61048,
61067..61120,
61157..61225,
61244..61297)) /locus-tag="YE0049"

/inference="protein
motif:TMHMM:2.0"
/note="7 probable transmembrane
helices predicted for YE0049 by
TMHMM2.0 at aa 5-22, 29-51, 64-81,
88-107,111-133, 140-162 and
172-189"
/misc-feature complement(60791..61045 /locus-tag="YE0049"
)

/inference="protein
motif:PFAM:PF03458"
/note="Pfam match to entry PF03458
UPF0126, UPF0126 domain, score
130.6, E-value 1.9e-36"
/misc-feature complement(61046..61303 /locus-tag="YE0049"
)

/inference="protein
motif:PFAM:PF03458"
/note="Pfam match to entry PF03458
UPF0126, UPF0126 domain, score
138.7, E-value 6.7e-39"
gene 61529..62080 /locus-tag="YE0050"
CDS 61529..62080 /locus-tag="YE0050"

/inference="similar to
sequence:INSDC:AE005109"
/note="Poor database matches.

```

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Similar to an internal region of
Halobacterium sp. hypothetical
protein VNG2239c SWALL:Q9HN60
(EMBL:AE005109) (308 aa) fasta
scores: E(): 2.7, 29.37 38d in 143
aa. Possible alternative
translational start sites"
/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="CAL10194.1"
/db-xref="GI:122087413"
/db-xref="UniProtKB/TrEMBL:AJJHW1"
/translation="MMIILPDCRVTHPMVAFISI
SSFISVGGFFMSQCIQSFOYRAVLL
AGIAAVGVLLSGCDVRIGQANTATIKASPTCIK
GEPMTQTTLTYFGLNRPHGPFVISAT
EWQSFVDNDVTSRFDGLTVIDAKGQWLNGDGTV
AKENSKALVLIHKADKETAETLR
ARYKQQFAQESVMRVDAAVCVDF"
/locus-tag="YE0050"

misc-feature      join(61565..61624,
61634..61702)

/inference="protein
motif:TMHMM:2.0"
/note="2 probable transmembrane
helices predicted for YE0050 by
TMHMM2.0 at aa 13-32 and 36-58"

gene              complement(62176..63360
)
/locus-tag="YE0051"
/note="synonym: cru"
/locus-tag="YE0051"
/locus-tag="YE0051"
/inference="similar to
sequence:INSDC:AL627274"
/inference="similar to
sequence:UniProtKB:P33031"
/note="Similar to Escherichia coli
nucleoside permease NupC or Cru
SWALL:NUPC-ECOLI (SWALL:P33031)
(400 aa) fasta scores: E():
4.2e-106, 71.75 38d in 400 aa, and
to Salmonella typhi nucleoside
permease STY2650 SWALL:Q8Z4X4
(EMBL:AL627274) (400 aa) fasta
scores: E(): 7.5e-106,71.75 38d in
400 aa"
/codon-start=1
/transl-table=11
/product="nucleoside permease"
/protein-id="CAL10195.1"
/db-xref="GI:122087414"
/db-xref="GOA:AJJHW2"
/db-xref="InterPro:IPR002668"
/db-xref="InterPro:IPR008276"
/db-xref="InterPro:IPR011642"
/db-xref="InterPro:IPR011657"
/db-xref="UniProtKB/TrEMBL:AJJHW2"
/translation="MLQILHFLALIAIAVLALL
ASHDRKNIKLRYIFQLLIIEIALA

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YFFLHSESGLGAIKYFAGLFESLMKFASIGTSFV
FGGMNEQGLAFIFLNVLCPIIFVS
ALIGILQHFRIPLIIRVIGTLLSKVNGMGKLES
FNAVSTLILGQSENFIAKGIAD
ISPRMYTMAATAMSTVSMISVAYMTMLEPKFV
VTALILNMFSTFIVLSIINPYPT
EEPELKLNNLHEDQSFEMLEGEYILAGFKIAMII
AAMLIGFIAIISAINALESTLFHI
SFQGVGLGYLFYPLALLIGIPTQDALHAGSIMATK
LVANEFVAMIELKKVAAEISPRGL
GILSVFLVSFANFASIGIVAGAIKGLNEQQGNV
SRFLGLLVYGSTLVLLSATIAGL VL"

misc-feature      complement(62179..63357
)
                    /gene="nupC"
                    /locus-tag="YE0051"
                    /inference="protein"
                    motif:PFAM:PF01773"
                    /note="Pfam match to entry PF01773
                    Nucleoside-tra2, Na+ dependent
                    nucleoside transporter, score
                    597.4, E-value 5.8e-177"

misc-feature      complement(join(62182..
62250,62293..62361,
62476..62544,
62572..62640,
62716..62784,
62794..62862,
63037..63105,
63214..63273,
63292..63351))
                    /gene="nupC"
                    /locus-tag="YE0051"
                    /inference="protein"
                    motif:TMHMM:2.0"
                    /note="9 probable transmembrane
                    helices predicted for YE0051 by
                    TMHMM2.0 at aa 4-23, 30-49,
                    86-108, 167-189,193-215, 241-263,
                    273-295, 334-356 and 371-393"

gene              63619..64512
CDS               63619..64512
                    /locus-tag="YE0052"
                    /locus-tag="YE0052"
                    /inference="similar to
                    sequence:INSDC:Y09701"
                    /inference="similar to
                    sequence:UniProtKB:P76082"
                    /note="Similar to Escherichia coli
                    probable enoyl-CoA hydratase PaaF
                    SWALL:PAAF-ECOLI (SWALL:P76082)
                    (255 aa) fasta scores: E():
                    2.5e-06, 27.66 38d in 253 aa, and
                    to Xanthomonas campestris RpfF
                    protein, mutants of which are
                    unable to produce a diffusible
                    extracellular factor which
                    regulates synthesis of
                    extracellular enzymes and
                    modulates virulence SWALL:O05175
                    (EMBL:Y09701) (289 aa) fasta
                    scores: E(): 1.2e-27, 34.02 38d in
                    288 aa"
                    /codon-start=1
                    /transl-table=11
                    /product="enoyl-CoA

```

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hydratase/isomerase family
protein"
/protein-id="CAL10196.1"
/db-xref="GI:122087415"
/db-xref="GOA:AlJHW3"
/db-xref="InterPro:IPR001753"
/db-xref="UniProtKB/TrEMBL:AlJHW3"
/translation="MFNSLIGWNMMNINLPSCRS
FTEAGHLSQISAYYEEGRNTLWML
LRAHPRPCFNLELIENIMTLAQAAKESKLPIDFW
VTGSVVPNMFNVGGDLNFFAQMIK
NRKREALMAYARACVDCVHAASRGFDTGAISIAM
IEGSALGGGFEAALAHFVLAQTT
ARMGFPEIAFNLFPGMGYSLVARKAGMRVAEQI
IWTGESHAAEWYESRGLVDKLFQF
GDYAIATRTFIDTIRPKLNGMRAMVRVRQVLQL
TRSELMIDITEDWVDSAFSIEPKDI
AYIERLVMLQDRHTSGMPKAI"
misc-feature      63745..64269
                    /locus-tag="YE0052"
                    /inference="protein
motif:PFAM:PF00378"
                    /note="Pfam match to entry PF00378
ECH, Enoyl-CoA hydratase/isomerase
family, score 25.7, E-value
2.7e-10"
gene              complement(64538..66532 /locus-tag="YE0053"
                    )
CDS               complement(64538..66532 /locus-tag="YE0053"
                    )
                    /inference="similar to
sequence:INSDC:AL627270"
                    /inference="similar to
sequence:UniProtKB:P77334"
                    /note="Similar to Escherichia coli
hypothetical protein YciR
SWALL:YCIR-ECOLI (SWALL:P77334)
(661 aa) fasta scores: E():
3.9e-156, 60.61 38d in 650 aa, and
to Salmonella typhi hypothetical
protein STY1349 SWALL:Q8Z7D0
(EMBL:AL627270) (660 aa) fasta
scores: E(): 1.3e-152,60.24 38d in
654 aa"
                    /codon-start=1
                    /transl-table=11
                    /product="putative signalling
protein"
                    /protein-id="CAL10197.1"
                    /db-xref="GI:122087416"
                    /db-xref="GOA:AlJHW4"
                    /db-xref="InterPro:IPR000014"
                    /db-xref="InterPro:IPR000160"
                    /db-xref="InterPro:IPR001633"
                    /db-xref="InterPro:IPR013767"
                    /db-xref="UniProtKB/TrEMBL:AlJHW4"
                    /translation="MFQDQDTSILNTYFGTHRPF
WRLAFDSQALELSAIKEIANIAIP
LNSVQTMKIRSLTGITASLDIEIYGHPLHLHL
VGRKINDKEWGGTASAYADTESVA
RDLVMLGSFAEQVVSSEANSVIVILDKDGCVQRFN
HLSEEYTGKKEQDVIGKNVYDLFM
TAKEGASSRKNIIEGFQRGASYEAERWVNTVKKG

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RLFLFRNKVFVHSGSGKNERYLICS
GTDITKERRAQERLRI LANTDMITGLPNRHAIHE
RINSAIQTRGDSVVGIIYLDLDFN
KKVNDHYGHMFGRDLKDVSLAILSLCLGDNEMLA
RLGGDEFIVLVENATLDLLEITQ
RILNRMKLPFRIGLIEVYTGCSIGIALCPEHGDT
LENIIRSADTAMYTAKHEGKQYTS
IFSQQMNKKVSEYVWLDTNLRKAIEQHQLQIFYQ
PKISTKTGKVLGVEALVRWLSPER
GLIAPQEFISYAESGLIRPLGKWWLQTSMQQAV
DWKKRGINLRIAVNV SARQLIDEA
IVTSFIESLEACELESSLVDVELTESCLIDNEDA
AINIMKQLRHLGAQVHLDDFGTGY
SSLSQLARIPIDAIKLDQSFVRHIDTNPISQSLV
RAIIVVAEALKMQVIAEGVETKEE
EEFLDSIGVDEKQGFYAKPMPADKLEHWLVTQH
PHLLD"
misc-feature    complement(64586..65323 /locus-tag="YE0053"
)
                /inference="protein
                motif:PFAM:PF00563"
                /note="Pfam match to entry PF00563
                EAL, EAL domain, score 401.0,
                E-value 7.4e-118"
misc-feature    complement(65363..65839 /locus-tag="YE0053"
)
                /inference="protein
                motif:PFAM:PF00990"
                /note="Pfam match to entry PF00990
                GGDEF, GGDEF domain ,score 195.5,
                E-value 5.2e-56"
misc-feature    complement(66056..66205 /locus-tag="YE0053"
)
                /inference="protein
                motif:PFAM:PF00989"
                /note="Pfam match to entry PF00989
                PAS, PAS domain, score 22.5,
                E-value 8.3e-06"
gene            complement(67055..67885 /locus-tag="YE0055"
)
CDS             complement(67055..67885 /locus-tag="YE0055"
)
                /inference="similar to
                sequence:INSDC:AE007569"
                /inference="similar to
                sequence:INSDC:AE010879"
                /note="Similar to Methanosarcina
                acetivorans metallo-beta-lactamase
                superfamily protein MA1962
                SWALL:AA05365 (EMBL:AE010879)
                (280 aa) fasta scores: E(): 3e-44,
                44.84 38d in 281 aa, and to
                Clostridium acetobutylicum
                metal-dependent hydrolase of the
                beta-lactamase superfamily II
                CAC0535 SWALL:Q97LM2
                (EMBL:AE007569) (268 aa) fasta
                scores: E(): 2.8e-41,41.66 38d in
                276 aa"
                /codon-start=1
                /transl-table=11
                /product="metallo-beta-lactamase

```

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superfamily protein"
/protein-id="CAL10198.1"
/db-xref="GI:122087417"
/db-xref="GOA:AJJHW5"
/db-xref="InterPro:IPR001279"
/db-xref="UniProtKB/TrEMBL:AJJHW5"
/translation="MQLTVLVDNNTLIDKYLTAE
PGVCYHLKIDGKTYLFDTGYSDFV
LRNAAALIGIDISDIDSVIIISHGHNDHSGWGLIHLA
QYLDRTNYPVSVKKIKLVAHPNAFV
PKYHEDKSIKANLPADSYPSFFERINQTVYYLT
DNLFLGEIVRSNDFEGLHPIGKT
INCCGHEVDVDFIDDSAIVYTSPEGIVIIITGCSH
SGICNIIDYAIKVTGDKRIRAVIG
GFHLLNAETSTLTRTSDFYKQLNAQALYPCHCTD
LKAKIALAGAVDIEEVGVGMVLNF"
misc-feature    complement(67139..67837 /locus-tag="YE0055"
)
/inference="protein
motif:PFAM:PF00753"
/notes="Pfam match to entry PF00753
lactamase-B, Metallo-beta-lactamase
superfamily, score 11.7, E-value
0.00023"
misc-feature    complement(67406..67429 /locus-tag="YE0055"
)
/inference="protein
motif:Prosite:PS00017"
/notes="PS00017 ATP/GTP-binding
site motif A (P-loop)."
gene            complement(68287..69150 /locus-tag="YE0057"
)
CDS             complement(68287..69150 /locus-tag="YE0057"
)
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAL10199.1"
/db-xref="GI:122087418"
/db-xref="InterPro:IPR005229"
/db-xref="InterPro:IPR013527"
/db-xref="InterPro:IPR013551"
/db-xref="UniProtKB/TrEMBL:AJJHW6"
/translation="MIRSMATAYARRDIKGEWGSA
AWELRSVNQRYLETYIRLPEQFRS
LEPVIRERIRGLTRGKIECNLRFELDNAQSSLI
ILNEKLAKQLVEAGNWWVKMQSDEG
EINPVDILRWPGVMAAEEQDLDAISTELMQALDI
VLDDFIIISRETEGAALKALIEQRL
DGVSAEIVKVRAPHNILQWQERLLNKLLEAAQV
QLENTLRLEQELVLMAQRVDVAEEL
DRLEAHVKETHNLIKKEAVGRRDLFMMQEFNRE
SNTLAKSINAIEVNSAIELKVLII
EQMREQIQNIE"
misc-feature    complement(68686..69147 /locus-tag="YE0057"
)
/inference="protein
motif:PFAM:PF03755"
/notes="Pfam match to entry PF03755
YicC-N-term, YicC-like family,
N-terminal region, score 272.9,

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gene	69277..69993	E-value 2.8e-79" /gene="rph" /locus-tag="YE0058" /gene="rph" /locus-tag="YE0058" /codon-start=1 /transl-table=11 /product="ribonuclease PH" /protein-id="CAL10200.1" /db-xref="GI:122087419" /db-xref="GOA:AlJHW7" /db-xref="InterPro:IPR001247" /db-xref="InterPro:IPR002381" /db-xref="InterPro:IPR015847" /db-xref="UniProtKB/Swiss-Prot:AlJHW7" /translation="MRPADRAAQVVRPLTLTRNY TKHAEGSVLVEFGDTKVLCTATVE EGVPRFLKGGQGWITAEYGMFLPRSTHSRNAREAA AKGKQGGRTLEIQRILIARSLRAAV DLKKLGFTITLDCDVLQADGGTRTASISGACVA LADALNKLVASGKLANFPMKGLVA AVSVGIVKGEALCDLEYVEDSAAETDMNVMMED GRMIEVQGTAEGEPPFSHEELLTLL ALARGGIETIFQAQKAALAQ"
misc-feature	69304..69705	/gene="rph" /locus-tag="YE0058" /inference="protein motif:PFAM:PF01138" /note="Pfam match to entry PF01138 RNase-PH, 3' exoribonuclease family, domain 1, score 196.1, E-value 3.5e-56"
misc-feature	69622..69660	/gene="rph" /locus-tag="YE0058" /inference="protein motif:Prosite:PS01277" /note="PS01277 Ribonuclease PH signature."
misc-feature	69745..69948	/gene="rph" /locus-tag="YE0058" /inference="protein motif:PFAM:PF03725" /note="Pfam match to entry PF03725 RNase-PH-C, 3' exoribonuclease family, domain 2, score 73.9, E-value 2.2e-19"
gene	70145..70786	/gene="pyrE" /locus-tag="YE0059" /gene="pyrE" /locus-tag="YE0059" /codon-start=1 /transl-table=11 /product="orotate phosphoribosyltransferase" /protein-id="CAL10201.1" /db-xref="GI:122087420" /db-xref="GOA:AlJHW8" /db-xref="InterPro:IPR000836" /db-xref="InterPro:IPR002375" /db-xref="InterPro:IPR004467" /db-xref="UniProtKB/Swiss-Prot:AlJ
CDS	70145..70786	



```

HW8"
/translation="MKAYQREFIEFALNKQVLKF
GEFTLKSGRISPYFFNAGLFTNGL
ELAKLGRFYAAALMDCGVEFDLLFGPAYKGIPIA
TTTAVALAEEHNNRDLPCFNRKEA
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Pribosyltran,Phosphoribosyl
transferase domain, score 103.2,
E-value 3.2e-28"
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/locus-tag="YE0059"
/inference="protein
motif:Prosite:PS00103"
/note="PS00103 Purine/pyrimidine
phosphoribosyl transferases
signature."
gene complement(70864..71460
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CDS complement(70864..71460
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protein"
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misc-feature complement(71275..71418
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motif:PFAM:PF00440"
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tetR, Bacterial regulatory
proteins, tetR family, score 41.0,
E-value 1.7e-09"
misc-feature complement(71287..71379
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/inference="protein

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regulatory proteins, tetR family
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motif with score 1905.000, SD 5.68
at aa 32-53, sequence
ITTAKLAAANVGVEAALYRHFP"
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/note="synonyms: dnaS, sof"
CDS complement(71581..72036
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HX0"
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motif:PFAM:PF00692"
/note="Pfam match to entry PF00692
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E-value 1.3e-51"
gene complement(72017..73204
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CDS complement(72017..73204
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metabolism flavoprotein"
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DPVRFISNQSSGKMGFAIAQAAAA
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misc-feature    complement(72860..73201 /gene="dfp"
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CDS             73442..74110
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                HX2"
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                NPEITQKFLQNILSHREREIFLVMFLDNQHRVIR
                HEEMFTGTISSVEIHPREIVREAL
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misc-feature    73733..74107
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                /inference="protein
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                /note="Pfam match to entry PF04002
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                score 263.4, E-value 2e-76"

misc-feature    73952..73969
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                /locus-tag="YE0063"
                /inference="protein
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CDS	74374..74610	
misc-feature	74380..74562	/gene="rpmB" /locus-tag="YE0064" /inference="protein motif:PFAM:PF00830" /note="Pfam match to entry PF00830 Ribosomal-L28,Ribosomal L28 family, score 133.2, E-value 3.1e-37"
gene	74622..74789	/gene="rpmG" /locus-tag="YE0065" /gene="rpmG" /locus-tag="YE0065" /codon-start=1 /transl-table=11 /product="50S ribosomal protein L33" /protein-id="CAL10207.1" /db-xref="GI:122087426" /db-xref="GOA:AlJHR4" /db-xref="InterPro:IPR001705" /db-xref="UniProtKB/Swiss-Prot:AlJHR4" /translation="MAKGVREKIKLVSSAGTGHF YTTIKNKRIKPEKLELKKFDPVVR QHVIYKEAKIK"
CDS	74622..74789	
misc-feature	74637..74780	/gene="rpmG" /locus-tag="YE0065" /inference="protein motif:PFAM:PF00471" /note="Pfam match to entry PF00471 Ribosomal-L33,Ribosomal protein L33, score 94.5, E-value 1.3e-25"
misc-feature	74682..74741	/gene="rpmG" /locus-tag="YE0065" /inference="protein motif:Prosite:PS00582" /note="PS00582 Ribosomal protein L33 signature." /gene="mutM" /locus-tag="YE0066" /note="synonym: fpg" /gene="mutM"
gene	74876..75685	
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LRYTDPRRRFGAWLWAKDLETSNVLAHLGPEPLSD
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NKVVVGVGNIYASESLFTAGILPERAAGSLTETE
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/note="Pfam match to entry PF01149
Fapy-DNA-glyco, Formamidopyrimidine
-DNA glycosylase, score 483.1,
E-value 1.4e-142"
gene complement(75792..76271 /gene="coad"
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/locus-tag="YE0067"
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CDS complement(75792..76271 /gene="coad"
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adenyltransferase"
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HR9"
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RHGGDITPFLPAPVTKALMTKLA"
misc-feature complement(75870..76268 /gene="coad"
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motif:PFAM:PF01467"
/note="Pfam match to entry PF01467
CTP-transf-2,Cytidylyltransferase,
score 151.3, E-value 1.1e-42"
gene      complement(76268..77050
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CDS       complement(76268..77050
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YPREQYRYNDDLHVHESLDGSGSAKV
ILLAGDLLHLTCRDFFAFQRKQLNYAQAWANQRH
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sig-peptide complement(76961..77050
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/note="Signal peptide predicted
for YE0068 by SignalP 2.0 HMM
(Signal peptide probability 0.844)
with cleavage site probability
0.843 between residues 30 and 31"
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motif:PFAM:PF00535"
/note="Pfam match to entry PF00535
Glycos-transf-2,Glycosyl
transferase, score 88.5, E-value
8.8e-24"
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/note="synonym: waaA"
CDS       complement(77051..78328
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HVYLPYDLPGSVNRFLDQVNPKLVIIMETELWPN
LINALHRRKIPLVIANARLSARSA
AGYKKIGSFIRMMLQRITLAAQNQEDGDRFIEL
GLRRSQLTVTGSCLKFDISVTPELA
ARAVTLRRQWAPHRPVWIATSTHDGEETILLEAH
RQLLQQFPTLLLLILVPRHPERFFK
AIELTQKAGLSYTLRSKGEVPSSTQVVIGDTMG
ELMLLYGIADLAFVGGSLVERGGH
NPLEAAAAHAIPVLMGPHTFNFKIDICAKLEQAEG
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misc-feature complement(77126..77638
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/note="Pfam match to entry PF00534
Glycos-transferase-1, Glycosyl
transferases group 1, score 20.0,
E-value 1.6e-06"
gene complement(78869..79834
) /gene="rfaC"

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/note="synonyms: rfa-2, waaC"
CDS complement(78869..79834
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ITRIAGVRHGPDCKSAREPFASWYFNCRHEIDT
KQHAVERIRQLFAKSLGYDKPESV
GDYIAIQRFLNELPNDTGOYLVLHATTRDSKHW
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GAKAVVSVDTGLSHLTAALDRPNI
TLFGPTDPLIGGYGKNQIAVISEQKSMDDITAE
TIMARLETIS"
misc-feature complement(78884..79612
) /gene="rfaC"

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Glyco-transf-9, Glycosyltransferase
family 9 (heptosyltransferase),
score 316.4, E-value 2.1e-92"
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CDS      complement(79834..80898) /gene="rfaF"
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TGYDRAYVLPNSFKSALIPYFSGI
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ALAYDKERIHSAADDLPQFLLPWQL
QVQDEETAEITASFNLNNRP IIGFCPGA EFGPA
KRWPHYHYAALAKQLIDTGYQVIL
LGSAKDNEAGEEIRQALDESAREYCLNLAGQTSL
DQAVVMIAACNAVVSNDSGMLHVA
AALNKPLVALYGPSSPDFTPLSDKATVIRLITG
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misc-feature complement(79927..80694) /gene="rfaF"
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Glyco-transf-9, Glycosyltransferase
family 9 (heptosyltransferase),
score 372.2, E-value 3.5e-109"
gene      complement(80929..81861) /gene="rfad"
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CDS      complement(80929..81861) /gene="rfad"
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GENPKLFSGSENFKRDFIYVGDDVA
DVNLWFQNGVSGIFNCGTGRAESFQAVADAVVD
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misc-feature      complement(80932..81858) /gene="rfaD"
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motif:PFAM:PF01370"
/note="Pfam match to entry PF01370
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epimerase/dehydratase family,
score -1.0,E-value 2.2e-13"

gene      82105..83316 /gene="kbl"
CDS      82105..83316 /locus-tag="YE0073"
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SFLGMEDAILYSSCFDANGGLFETLLGPEDIAIS
DALNHASIIDGVRLCKAKRYRYAN
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misc-feature      82339..83283 /gene="kbl"
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/inference="protein
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/note="Pfam match to entry PF00155
aminotran-1-2,Aminotransferase
class I and II, score 260.1,
E-value 1.9e-75"

misc-feature      82840..82869 /gene="kbl"
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CDS	83341..84366	
misc-feature	83359..84360	
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gene	complement(84557..85582	
CDS	) complement(84557..85582	
	)	

Salmonella typhi putative exported protein STY4089 SWALL:Q8Z2F2 (EMBL:AL627280) (320 aa) fasta scores: E(): 1.3e-64,62.46 38d in 325 aa"

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/db-xref="InterPro:IPR006837"  
/db-xref="UniProtKB/TrEMBL:ALJHX9"  
/translation="MRYFNTHRLIIVSTLLIANT  
SLAGKLSIVIDDFGYRPQENKVL  
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LPMAPLSKQPLERDTLQPLMSSEE  
IQRIRQAVNNVPYATGMNNHMGSAITSSLPGMQ  
KVMQVLEHYQLYFLDSVTIGNSQA  
SRAAEGTGKVKIKRKVLDSDSQAIAIRQGFNRA  
VELARRNGSAIAIGHPHPATIKVL  
QQMLPQLPADIVLVKASALLNEFPVHNITGHNNSG  
SGTVSPGKSKPRDPAKGORLKAIAK  
QCNAKASYAPEKIYADKMFIILGESLMQSPAVTF  
VQKHQQYFPPAVPVTPEKSTIE KPAENP"  
/locus-tag="YE0075"

sig-peptide complement(85514..85582)  
)  
/note="Signal peptide predicted for YE0075 by SignalP 2.0 HMM (Signal peptide probability 0.995) with cleavage site probability 0.979 between residues 23 and 24"

misc-feature complement(84800..84823)  
)  
/locus-tag="YE0075"  
/inference="protein  
motif:Prosite:PS00017"  
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."

gene complement(85606..86760)  
)  
/locus-tag="YE0076"

CDS complement(85606..86760)  
)  
/locus-tag="YE0076"  
/codon-start=1  
/transl-table=11  
/product="putative membrane protein"  
/protein-id="CAL10218.1"  
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/db-xref="InterPro:IPR002886"  
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/db-xref="UniProtKB/TrEMBL:ALJHY0"  
/translation="MKTIQQDIAEKEKSVQQQKQ  
QRSALLDQLKQQENTIAQASRLR  
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SKQLDAAFKQGGHSGQLQLILSGEE  
SQRSERILAYFSYLNARQKSIEELKQTRTDL  
EKKTLEQKKNQKVLLEDEQKAQQQ  
KLEARTARKKTLTSLEVSLEKDDQGLAELKLN  
SRLRDQIAKAEREAKARAEREAKE  
AARVREQVKAQEQAQKKTGSSYKPSSESERSLMAR  
TGGLGRPGGQAVWPVRGNVTHRFG

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EALQGELRWKGMVISAPEGSEVKAIADGRVLLAD
WLQYGLVVVVEHGKGDMSLYGYN
QSALVNVGAQVKAGQPITALVGTSGGQGEPSLYFE
IRRQGQAVNPQPWLGR"
misc-feature    complement(85618..85866    /locus-tag="YE0076"
)
                /inference="protein
                motif:PFAM:PF01551"
                /note="Pfam match to entry PF01551
                Peptidase-M37, Peptidase family
                M23/M37, score 118.8, E-value
                6.8e-33"
gene            complement(86983..88530 /locus-tag="YE0077"
)
CDS             complement(86983..88530 /locus-tag="YE0077"
)
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                /transl-table=11
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                independent phosphoglycerate
                mutase"
                /protein-id="CAL10219.1"
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                /db-xref="UniProtKB/Swiss-Prot:A1J
                HY1"
                /translation="MSSTKKPLVLITLDGYGHRE
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                TLIAASGLDVGLPDGQMGNSEVGHVNLGAGRIVY
                QDLIRLDKEIKDGDEFFTNPTLTA
                VDKAVKAGKAVHIMGLLSAGGVHSHEDHILAMVE
                LAAKRGATAIYLFHFLDGRDTPFR
                SAEPSPKRFTEKFAALGKGRIASIIGRYYAMDRD
                NRWDRVQLAYDLLTQAKGEFTADN
                AVVGLQAAYARNENDEFVKPTVIAAGEPDAAAMN
                DGDALIFMNFRAFRARQITRTFVN
                ADFDGFKRDKVNVNFGDFIMLTXYAADIKVACAYP
                PASLENTFGEWLMKHDKTQLRISE
                TEKYAHVTFYNGGVVEEPFKGEDRILINSPKVAT
                YDLQPEMSSAELTEKLVGAIASGK
                YDVIIICNYPNGDMVHGTGDYDAAVKAVETLDNCI
                EQVVAQVAVDQQLITADHGNAE
                QMRDPATGQAHTAHTSLPVPLIYVGNKEVKKAVEG
                GKSLDIAPTMLSLMEMEIPQEMTG KPLFIVE"
misc-feature    complement(87058..87411 /locus-tag="YE0077"
)
                /inference="protein
                motif:PFAM:PF01676"
                /note="Pfam match to entry PF01676
                Metalloenzyme, Metalloenzyme
                superfamily, score 186.2, E-value
                3.5e-53"
gene            88772..89206
CDS             88772..89206
                /locus-tag="YE0078"
                /locus-tag="YE0078"
                /codon-start=1
                /transl-table=11
                /product="putative membrane
                protein"

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		/protein-id="CAL10220.1" /db-xref="GI:122087439" /db-xref="InterPro:IPR001763" /db-xref="UniProtKB/TrEMBL:AlJHY2" /translation="MLQEI MQFISQHPVLSLAWV ALFVAVIFTSFKTTL SKVKEITRG EATRLINKEDAVVVDIRTRDDYRKGHIASSINLL PSDIKNGNLAELEKHKQAPVIVVC ATGTTSRASAE LLNKAGFERVFTLKEGISG#SGE NLPLARGK"
misc-feature	88808..88864	/locus-tag="YE0078" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0078 by TMHMM2.0 at aa 13-31"
misc-feature	88895..89179	/locus-tag="YE0078" /inference="protein motif:PFAM:PF00581" /note="Pfam match to entry PF00581 Rhodanese, Rhodanese-like domain, score 76.3, E-value 4.1e-20"
gene	89256..89504	/gene="grxC" /locus-tag="YE0079"
CDS	89256..89504	/gene="grxC" /locus-tag="YE0079" /codon-start=1 /transl-table=11 /product="glutaredoxin" /protein-id="CAL10221.1" /db-xref="GI:122087440" /db-xref="GOA:AlJHY3" /db-xref="InterPro:IPR002109" /db-xref="InterPro:IPR011767" /db-xref="InterPro:IPR011900" /db-xref="InterPro:IPR012335" /db-xref="InterPro:IPR014025" /db-xref="UniProtKB/TrEMBL:AlJHY3" /translation="MAKIEIYTKATCPFCHRAKA LLNSKGAAFHEIAIDNDPAKREEM IARSGRTTVPQVFIDGQHIGGCCD LHALDARGGL DP LL"
misc-feature	89262..89435	/gene="grxC" /locus-tag="YE0079" /inference="protein motif:PFAM:PF00462" /note="Pfam match to entry PF00462 glutaredoxin, Glutaredoxin, score 85.5, E-value 7.3e-23"
misc-feature	89271..89321	/gene="grxC" /locus-tag="YE0079" /inference="protein motif:Prosites:PS00195" /note="PS00195 Glutaredoxin active site."
gene	89596..90066	/gene="secB" /locus-tag="YE0080"
CDS	89596..90066	/gene="secB" /locus-tag="YE0080" /codon-start=1 /transl-table=11 /product="protein-export protein"

		/protein-id="CAL10222.1" /db-xref="GI:122087441" /db-xref="GOA:AlJHY4" /db-xref="InterPro:IPR003708" /db-xref="UniProtKB/Swiss-Prot:AlJHY4" /translation="MSEQNNTEMAFQIQRIYTKD ISFEAPNAPQVQQDWQPEVKLDL DIASSQLAEDVYEVVLRVTASLGEETAFLCEV QGGIFSIAGIDGTLAHLGAYC PNILFPYARECITSLVSRGTFPQLNLAPVNFDA FMNYLQQQAEGEGAEQRQDA" /gene="secB" /locus-tag="YE0080" /inference="protein motif:PFAM:PF02556" /note="Pfam match to entry PF02556 SecB, Preprotein translocase subunit SecB, score 338.5, E-value 4.8e-99"
misc-feature	89596..90033	
gene	90066..91085	/gene="gpsA" /locus-tag="YE0081" /gene="gpsA" /locus-tag="YE0081" /codon-start=1 /transl-table=11 /product="glycerol-3-phosphate dehydrogenase" /protein-id="CAL10223.1" /db-xref="GI:122087442" /db-xref="GOA:AlJHY5" /db-xref="InterPro:IPR006109" /db-xref="InterPro:IPR006168" /db-xref="InterPro:IPR011128" /db-xref="InterPro:IPR013328" /db-xref="InterPro:IPR016040" /db-xref="UniProtKB/Swiss-Prot:AlJHY5" /translation="MNTTHASMTVIGAGSYGTAL AITLARNGHQVVLWGHDPKHIQTL QODRCNQAFLPDVPFDTLLLETDLARALASRD VLVVVPSPHVFAGAVLNQLKPHLRPD ARIVWATKGLEAETGRLLADVAREVLGESIPLAV VSGPTFAKELAAGLPTAIALASTD VQFSEDLQQLHCGKSRVYSNPDFIGVQLGGAV KNVIAIGAGMSDGIGFGANARTAL ITRGLAEMTRLGSALGADPSTFMGMAGLDLVLT CTDNQSRNRRFGIMLGQGLGVQEA QDKIGQVVEGYRNTKEVLALAQNRNGVEMPITEQI YQVLYSHKNAREALTLTGRTKKD EKSGI"
CDS	90066..91085	
sig-peptide	90066..90128	/gene="gpsA" /locus-tag="YE0081" /note="Signal peptide predicted for YE0081 by SignalP 2.0 HMM (Signal peptide probability 0.931) with cleavage site probability 0.910 between residues 21 and 22"
misc-feature	90078..91046	/gene="gpsA" /locus-tag="YE0081" /inference="protein motif:PFAM:PF01210" /note="Pfam match to entry PF01210"

		NAD-Gly3P-dh, NAD-dependent glycerol-3-phosphate dehydrogenase, score 543.4, E-value 1e-160"
misc-feature	90639..90704	/gene="gpsA" /locus-tag="YE0081" /inference="protein motif:Prosite:PS00957" /note="PS00957 NAD-dependent glycerol-3-phosphate dehydrogenase signature."
gene	91211..92032	/gene="cysE" /locus-tag="YE0082"
CDS	91211..92032	/gene="cysE" /locus-tag="YE0082" /codon-start=1 /transl-table=11 /product="serine acetyltransferase" /protein-id="CAL10224.1" /db-xref="GI:122087443" /db-xref="GOA:AJJHY6" /db-xref="InterPro:IPR001451" /db-xref="InterPro:IPR005881" /db-xref="InterPro:IPR010493" /db-xref="UniProtKB/TrEMBL:AJJHY6" /translation="MSSEELVWSSIKSEARL AECEPLASFFHATLLKHENLGSA LSYILANKLANPIMPATIAIREVVEDAYRADAQMI VSAARDILAVRLRDPVADKYSTPL LYLKGFFHALQAYRIGHWLWQDRKALAIYLNQNV SVAFGVDIHPAATIGCGIMLDHAT GIVIGETAVVENDVSIQSVTLGGTGKTSGDRHP KIREGVMIGAGAKILGNIEVGRGA KIGAGSVVLQAVPPHTTAAGVPARIVGKPESDKP SLDMDQHFNQGVSHGFETGDI"
misc-feature	91613..91666	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 4.6, E-value 12"
misc-feature	91709..91762	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 10.4, E-value 2.2"
misc-feature	91787..91840	/gene="cysE" /locus-tag="YE0082" /inference="protein motif:PFAM:PF00132" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 9.3, E-value 3"
misc-feature	91814..91900	/gene="cysE" /locus-tag="YE0082"

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/inference="protein
motif:Prosite:PS00101"
/note="PS00101 Hexapeptide-repeat
containing-transferases
signature."
misc-feature    91841..91894    /gene="cysE"
                                   /locus-tag="YE0082"
                                   /inference="protein
motif:PFAM:PF00132"
                                   /note="Pfam match to entry PF00132
hexapep, Bacterial transferase
hexapeptide (four repeats), score
11.9,E-value 1"
gene            complement(92213..92716    /locus-tag="YE0083"
)
CDS             complement(92213..92716    /locus-tag="YE0083"
)
                                   /codon-start=1
                                   /transl-table=11
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methyltransferase"
                                   /protein-id="CAL10225.1"
                                   /db-xref="GI:122087444"
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                                   /db-xref="InterPro:IPR001537"
                                   /db-xref="InterPro:IPR004440"
                                   /db-xref="InterPro:IPR016914"
                                   /db-xref="UniProtKB/TrEMBL:AlJHY7"
                                   /translation="MLNIVLFEEPEIPPNTGNIIR
LCANTGCQLHLIKPLGFTWDDKRL
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GTNPARLFALTTKGTPAHSVNYO
VNDYLLFGPETRGLPSNVLDALPAQQKIRIPMLA
ASRSNMNLSNAVSVVVYEAWRQLGY PGALLKE"
misc-feature    complement(92261..92716    /locus-tag="YE0083"
)
                                   /inference="protein
motif:PFAM:PF00588"
                                   /note="Pfam match to entry PF00588
SpoU-methylase, SpoU rRNA
Methylase family, score 180.0,
E-value 2.6e-51"
gene            92988..93986    /locus-tag="YE0084"
CDS             92988..93986    /locus-tag="YE0084"
                                   /codon-start=1
                                   /transl-table=11
                                   /product="bifunctional regulatory
protein/DNA repair protein"
                                   /protein-id="CAL10226.1"
                                   /db-xref="GI:122087445"
                                   /db-xref="GOA:AlJHY8"
                                   /db-xref="InterPro:IPR000005"
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                                   /db-xref="InterPro:IPR004026"
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                                   /db-xref="InterPro:IPR011991"
                                   /db-xref="InterPro:IPR014048"
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                                   /db-xref="UniProtKB/TrEMBL:AlJHY8"
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NIEFYADNDAAELAGYRPCRRCRP
TQLSQAQQHAEKISQACRLIEQAETPFTLDLAA

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misc-feature	92991..93122	
		/locus-tag="YE0084" /inference="protein motif:Prosites:PS00041" /note="PS00041 Bacterial regulatory proteins, araC family signature."
misc-feature	93153..93284	
		/locus-tag="YE0084" /inference="protein motif:PFAM:PF00165" /note="Pfam match to entry PF00165 HTH-AraC, Bacterial regulatory helix-turn-helix proteins, araC family, score 47.7, E-value 1.7e-11"
misc-feature	93165..93299	
		/locus-tag="YE0084" /note="Predicted helix-turn-helix motif with score 1245.000, SD 3.43 at aa 71-92, sequence FTLDALAAELNLSfHfHRLfK"
misc-feature	93198..93263	
		/locus-tag="YE0084" /inference="protein motif:PFAM:PF00165" /note="Pfam match to entry PF00165 HTH-AraC, Bacterial regulatory helix-turn-helix proteins, araC family, score 15.0, E-value 0.062"
misc-feature	93309..93446	
		/locus-tag="YE0084" /inference="protein motif:PFAM:PF02870" /note="Pfam match to entry PF02870 Methyltransf-1N,6-O-methylguanine DNA methyltransferase, ribonuclease-like domain, score 25.9, E-value 6.2e-05"
misc-feature	93462..93698	
		/locus-tag="YE0084" /inference="protein motif:PFAM:PF01035" /note="Pfam match to entry PF01035 Methyltransf-1,6-O-methylguanine DNA methyltransferase, DNA binding domain, score 172.2, E-value 5.7e-49"
misc-feature	93702..93968	
		/locus-tag="YE0084" /inference="protein motif:Prosites:PS00374" /note="PS00374"
misc-feature	93855..93875	

		Methylated-DNA--protein-cysteine methyltransferase active site."
gene	complement(94056..95432)	/gene="cpxA"
CDS	complement(94056..95432)	/locus-tag="YE0085" /gene="cpxA"  /locus-tag="YE0085" /codon-start=1 /transl-table=11 /product="two component sensor kinase" /protein-id="CAL10227.1" /db-xref="GI:122087446" /db-xref="GOA:AlJHY9" /db-xref="InterPro:IPR003594" /db-xref="InterPro:IPR003660" /db-xref="InterPro:IPR003661" /db-xref="InterPro:IPR004358" /db-xref="InterPro:IPR005467" /db-xref="UniProtKB/TrEMBL:AlJHY9" /translation="MINSLTARIFAIFWFTLALV LMLVLMVPKLDSRQMTTLDDSEQR QGTMLQHQIEAELASDPANDLMMWRRLYRAIEKW APPGQHLVLVTTTEGRVIGARHEM QMVRNFIGQSDNSDQPKKKYGRVEMVGFPSIRD GEDNYQLYLLRPASSPQSDFINLM FDRPLLLLIATMLISAPLLLLWLAWSLAKPARKLK NAADDVARGNLKQHPELESGPQEF LATGASFNQMISALDRMVVAQQRLISDISHELRT PLTRLQALATLMRRRHGEGKELER IEMEAQRLDSMINDLLVLRSQHKNELHREPIKA NELWSEVLENAQFEADQMCKTLEV TAPPGPWTLFGNPAALDSALENIVRNALRYSHHH IAVAFSSDNQGITITVDDDGFGVS PEDREQIFRPFFYRTDEARDRESGGTGLGLAIVET AVNQHRGWVRAEDSPLGLRLLIW LPLHPLKV"
sig-peptide	complement(95355..95432)	/gene="cpxA"  /locus-tag="YE0085" /note="Signal peptide predicted for YE0085 by SignalP 2.0 HMM (Signal peptide probability 0.757) with cleavage site probability 0.304 between residues 26 and 27"
misc-feature	complement(94071..94400)	/gene="cpxA"  /locus-tag="YE0085" /inference="protein motif:PFAM:PF02518" /note="Pfam match to entry PF02518 HATPase-c, Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase, score 133.2, E-value 3.1e-37"
misc-feature	complement(94533..94721)	/gene="cpxA"  /locus-tag="YE0085" /inference="protein motif:PFAM:PF00512" /note="Pfam match to entry PF00512 HisKA, His Kinase A (phosphoacceptor) domain, score

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misc-feature    complement(94731..94943
)
65.3, E-value 8.7e-17"
/locus-tag="YE0085"
/inference="protein
motif:PFAM:PF00672"
/notes="Pfam match to entry PF00672
HAMP, HAMP domain ,score 52.4,
E-value 6.6e-13"
misc-feature    complement(join(94872..
94940,95352..95420))
/locus-tag="YE0085"
/inference="protein
motif:TMHMM:2.0"
/notes="2 probable transmembrane
helices predicted for YE0085 by
TMHMM2.0 at aa 5-27 and 165-187"
gene            complement(95429..96127
)
/locus-tag="YE0086"
CDS              complement(95429..96127
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/codon-start=1
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/db-xref="GI:122087447"
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/db-xref="InterPro:IPR001867"
/db-xref="UniProtKB/TrEMBL:AlJHZ0"
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ARGSDLDRVLGLGLGADDYLAKPF
NDRELVARIRAILRRSNWSEQQNVDDQAPITLV
DCLQLNFGREQEASFEGQSLELTGT
EFTLLYLLAQHLGQVVSREHLSQEVLGKRLTPFD
RAIDMHISNLRRKLPDRKDGLPWF
KTLRGRGYLMVSET"
misc-feature    complement(95453..95671
)
/locus-tag="YE0086"
/inference="protein
motif:PFAM:PF00486"
/notes="Pfam match to entry PF00486
trans-reg-C,Transcriptional
regulatory protein, C terminal,
score 110.2, E-value 2.5e-30"
misc-feature    complement(95771..96124
)
/locus-tag="YE0086"
/inference="protein
motif:PFAM:PF00072"
/notes="Pfam match to entry PF00072
response-reg, Response regulator
receiver domain, score 152.2,
E-value 5.9e-43"
gene            96348..96812
/locus-tag="YE0087"

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CDS	96348..96812	<pre> /gene="cpXP" /locus-tag="YE0087" /codon-start=1 /transl-table=11 /product="putative exported protein" /protein-id="CAL10229.1" /db-xref="GI:122087448" /db-xref="GOA:A1JHZ1" /db-xref="InterPro:IPR012899" /db-xref="UniProtKB/TrEMBL:A1JHZ1" /translation="MASMLVIGSQAAFAADKTGA TDGWCHGDDGAMNNKKDGRGHHNMF DGLNLTEQQRQQMRDLMRQSRQDQPRVDLADREA MHKLITADKFDEAAVRAQAEKMSK DQIDRQVEMAKVRNQMFNLLTPEQKAALNQKHQQ RIEKMQQAPAAQSSAQK" </pre>
sig-peptide	96348..96389	<pre> /gene="cpXP" /locus-tag="YE0087" /note="Signal peptide predicted for YE0087 by SignalP 2.0 HMM (Signal peptide probability 0.647) with cleavage site probability 0.643 between residues 14 and 15" </pre>
gene	96944..97846	
CDS	96944..97846	<pre> /locus-tag="YE0088" /locus-tag="YE0088" /codon-start=1 /transl-table=11 /product="putative integral membrane protein" /protein-id="CAL10230.1" /db-xref="GI:122087449" /db-xref="GOA:A1JHZ2" /db-xref="InterPro:IPR002524" /db-xref="UniProtKB/Swiss-Prot:A1J HZ2" /translation="MDPQYARLVKAAALSATVLA SILLIIKIFAWHTGSVSLAALV DSLVDLAASLTNLFVVVRYSLQPADEEHTFGHGKA ESLAALAQSMFISGSALFLFLTGF OHLASPEPLQDPGLGIWVTLLIALFSTLILVTFQR WVVRKTQSQAIRADMLHYQSDVMM NGAILIALALSWYGFHRADALFALGIGAYILYSA LRMGYEAVQALLDRALPDDEERQEI INIVTSWPGVIGAHDLRTROSGETRFIQLHLEME DMLPLMEAHLADQVERALLHREFP GADILIHQDPTAVVPKERHAHWEL" </pre>
sig-peptide	96944..97066	<pre> /locus-tag="YE0088" /note="Signal peptide predicted for YE0088 by SignalP 2.0 HMM (Signal peptide probability 0.831) with cleavage site probability 0.693 between residues 41 and 42" </pre>
misc-feature	join(96977..97045, 97055..97123, 97181..97249, 97292..97360, 97415..97468, 97481..97540)	<pre> /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane </pre>

		helices predicted for YE0088 by TMHMM2.0 at aa 12-34, 38-60, 80-102, 117-139, 158-175 and 180-199" /locus-tag="YE0088" /inference="protein motif:PFAM:PF01545" /note="Pfam match to entry PF01545 Cation-efflux, Cation efflux family, score 354.0, E-value 1e-103"
misc-feature	96980..97816	
gene	98096..99091	/gene="pfkA" /locus-tag="YE0089" /gene="pfkA" /locus-tag="YE0089" /codon-start=1 /transl-table=11 /product="6-phosphofructokinase" /protein-id="CAL10231.1" /db-xref="GI:122087450" /db-xref="GOA:AlJHZ3" /db-xref="InterPro:IPR000023" /db-xref="InterPro:IPR012003" /db-xref="InterPro:IPR012828" /db-xref="InterPro:IPR015912" /db-xref="UniProtKB/Swiss-Prot:AlJ HZ3" /translation="MVKKIGVLTSGGDAPGMNAA IRGVVRAALSEGLEVYGIEDGYLG LYHNRMKQLDRYSVSDMINRGGTFLGSRARFEFR DPEIRKIALQNMKERGIDGLVVG GDGSYAGADLLTKEGGIHCVGLPGTIDNDVAGTD YTIGFFTALETVVEAIDRLRDTSS SHQRISIVEVMGRFCGDLTLAAAIAGGCEFIAIP EVEFKREDLVKEIKAGIAKGGKHA IVAITEKLDNIDELAKYIEKETDRETRGTVLGHI QRGGAPVAYDRILASRMGAYAVDL LVNKKISPPPLNFSGGFCVGIQNEKMHVHLSVCI APENKKSKFKEDWYDTAKKLF"
CDS	98096..99091	
misc-feature	98102..98932	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:PFAM:PF00365" /note="Pfam match to entry PF00365 PFK, Phosphofructokinase, score 607.0, E-value 7.1e-180"
misc-feature	98627..98659	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:Prosites:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	98828..98884	/gene="pfkA" /locus-tag="YE0089" /inference="protein motif:Prosites:PS00433" /note="PS00433 Phosphofructokinase signature."
repeat-region	complement(99130..10055 6)	/note="label:IS1660; IS4-like insertion sequence element IS1660"
repeat-region	99130..99145	/note="Inverted repeat for

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IS4-like element IS1660"
/rpt-type=INVERTED

stem-loop      complement(99131..99162
)
gene            complement(99139..10047 /locus-tag="YE0090"
3)
CDS             complement(99139..10047 /locus-tag="YE0090"
3)
               /inference="similar to
               sequence:INSDC:X81894"
               /inference="similar to
               sequence:UniProtKB:P03835"
               /note="Highly similar to many
               transposases from the IS element
               IS4 including: Escherichia coli
               transposase InsG for insertion
               sequence element IS4
               SWALL:INSG-ECOLI (SWALL:P03835)
               (442 aa) fasta scores: E():
               9.8e-166,89.54 38d in 440 aa and
               to Pantoea agglomerans insertion
               element protein SWALL:P71168
               (EMBL:X81894) (440 aa) fasta
               scores: E(): 1.7e-86, 52.42 38d in
               433 aa"
               /codon-start=1
               /transl-table=11
               /product="transposase for
               insertion sequence element IS1660"
               /protein-id="CAL10232.1"
               /db-xref="GI:122087451"
               /db-xref="GOA:AJJH4"
               /db-xref="InterPro:IPR002559"
               /db-xref="UniProtKB/TrEMBL:AJJH4"
               /translation="MHIGQALDLVSRYSRLRNPL
               TTLGDYLDPQLISRCLAESGTVL
               RKRRPLEMMVWCIVGMALERKEPLHQIVNRLDI
               MLPGDRPFVAPSAVIQARQRLGSE
               AVRRVFSQTAQLWHGVSVTHPHWCGLTLLAVDGVV
               WRTPTDPENDTAFPRQTYAGQPGI
               YPOVKMVCQELTSHLLTAAFGTMKESEYTLAE
               QLIDQTADNTLTLMCKGYYSGLLL
               NAWSQAGEHRHNMIPKKGQAQYEEIRKLKGDHLL
               VKLKTSPQARKKWPELGAEMTARL
               LTIIRKGVYHLLTSMIDTMRYPGGEMADLYGHR
               WEIELGYREIKQTMQLSRLTLRSK
               KPVELVEQELWGVLLAYNLVRYQMIKMGALKGYW
               PNQLSFSESCGMVMRMLMTLQGAS
               PGRIPELMRDMESMAQMVKLPIRRERAFPRVVEK
               RPYKYKGARKNKASQLLN"
               /locus-tag="YE0090"

misc-feature    complement(99418..10009
5)
               /inference="protein
               motif:PFAM:PF01609"
               /note="Pfam match to entry PF01609
               Transposase-11, Transposase DDE
               domain, score 160.8, E-value
               1.5e-45"

repeat-region  complement(100541..1005
56)
               /note="Inverted repeat for
               IS4-like element IS1660"
               /rpt-type=INVERTED

gene            100712..101701
               /gene="sbp1"

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CDS	100712..101701	<pre> /locus-tag="YE0091" /gene="sbpl" /locus-tag="YE0091" /codon-start=1 /transl-table=11 /product="exported sulfate-binding protein" /protein-id="CAL10233.1" /db-xref="GI:122087452" /db-xref="GOA:AlJHZ5" /db-xref="InterPro:IPR000957" /db-xref="InterPro:IPR005669" /db-xref="InterPro:IPR006059" /db-xref="UniProtKB/TrEMBL:AlJHZ5" /translation="MRKWGVGLSLLLAGAMAK DIQLNVSYDPTREFFYQEYNQAFS KHWQEQTGDKVIVRQSHGSGGKQATSINGIEAD VVTLLALAYDVDAIAERGRIDKDWI KRLPDNSAPYTTSTIVFLVRKGNPKQIHDWSDLVK PGTSVITPNPKTSGGARWNYLAAW AYALEHNNNDQAKAQEFVKQLYKNVEVLDSGARG ATNTFIVERGIGDVLIAWENEALLA VNEVGKDQFDIITPSISILAETPSVVDKVVDKR GTREVDADYLYLSPGQTIAAK NYYRPRDPAVAAKFAKEFFQLKLITIDDFVGGWT KAQQVHFATGGVFDEISKR" </pre>
sig-peptide	100712..100768	<pre> /gene="sbpl" /locus-tag="YE0091" /note="Signal peptide predicted for YE0091 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 1.000 between residues 19 and 20" </pre>
misc-feature	100712..101698	<pre> /gene="sbpl" /locus-tag="YE0091" /inference="protein motif:PFAM:PF01100" /note="Pfam match to entry PF01100 Sulphate-binding, Prokaryotic sulphate- and thiosulphate-binding protein ,score 761.1, E-value 2.9e-226" </pre>
misc-feature	101144..101170	<pre> /gene="sbpl" /locus-tag="YE0091" /inference="protein motif:Prosite:PS00757" /note="PS00757 Prokaryotic sulfate-binding proteins signature 2." </pre>
gene	101902..102093	<pre> /locus-tag="YE0092" </pre>
CDS	101902..102093	<pre> /locus-tag="YE0092" /inference="similar to sequence:INSDC:U59485" /note="Poor database matches. Weakly similar to the N-terminal region of Agrobacterium tumefaciens hypothetical protein AttU SWALL:Q9WWC8 (EMBL:U59485) (78 aa) fasta scores: E(): 9.2, 32.55 38d in 43 aa. Doubtful CDS" /codon-start=1 /transl-table=11 </pre>

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        /product="hypothetical protein"
        /protein-id="CAL10234.1"
        /db-xref="GI:122087453"
        /db-xref="UniProtKB/TrEMBL:AlJHZ6"
        /translation="MANYAEKIIDIHGVSSAILI
        DNPGLDSPSPSLSGSLARSGSIESL
        HSNSSICEPIWHCHIKGGG"
gene      complement(102318..1030 /gene="tpiA"
85)

        /locus-tag="YE0093"
        /note="synonym: tpi"
CDS       complement(102318..1030 /gene="tpiA"
85)

        /locus-tag="YE0093"
        /codon-start=1
        /transl-table=11
        /product="triosephosphate
        isomerase"
        /protein-id="CAL10235.1"
        /db-xref="GI:122087454"
        /db-xref="GOA:AlJHZ7"
        /db-xref="InterPro:IPR000652"
        /db-xref="InterPro:IPR013785"
        /db-xref="UniProtKB/Swiss-Prot:AlJ
        HZ7"
        /translation="MRHPLVMGNWKLNGSTHMVN
        ELIANLRKELSTVEGCGVAIAPFA
        IYLNQAKHELSGSRIALGAQNVDVNLGSAFTGET
        SAEMLKDIGAQYIIIGHSEERRYH
        KESDEFIAKKFGVLKEVGLTPVLCIGETEAENEA
        GQTEAVCAKQLDAVLNTLGAKAFE
        GAVIAYEPIWAI GTGKSATPAQAQAVHKFIRDHI
        AKQDAIAAQVYIIQYGGSVNDKNA
        AELETFQPDIDGALVGGASLKADAFVIVKAAAAA
        KKA"
misc-feature complement(102330..1030 /gene="tpiA"
82)

        /locus-tag="YE0093"
        /inference="protein
        motif:PFAM:PF00121"
        /note="Pfam match to entry PF00121
        TIM, Triosephosphate isomerase,
        score 523.6, E-value 9.4e-155"
misc-feature complement(102561..1025 /gene="tpiA"
93)

        /locus-tag="YE0093"
        /inference="protein
        motif:Prosite:PS00171"
        /note="PS00171 Triosephosphate
        isomerase active site."
gene      complement(103214..1037 /locus-tag="YE0094"
98)
CDS       complement(103214..1037 /locus-tag="YE0094"
98)

        /codon-start=1
        /transl-table=11
        /product="putative exported
        protein"
        /protein-id="CAL10236.1"
        /db-xref="GI:122087455"
        /db-xref="InterPro:IPR009918"
        /db-xref="UniProtKB/TrEMBL:AlJHZ8"

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/translation="MTILLIATVSRHADPDAGSYQAAEETQPTAPYLLSGAPTFDLTLVKFRERYNHANPTLPISEFHAITVKDDAPLTRAASKINENLYASTALERTGKIKTIQITYLPPIKGSEEKAARLVAVNYMAALMRQFEPPTLTLEQSSISNVQQLLTQGGKSPFFAHPVGAIRYVVDNGEKGTLTFAVEPIKLSLSEA"
sig-peptide      complement(103751..103798) /locus-tag="YE0094"
                  /note="Signal peptide predicted for YE0094 by SignalP 2.0 HMM (Signal peptide probability 0.988) with cleavage site probability 0.985 between residues 16 and 17"
gene             104103..104537 /locus-tag="YE0095"
CDS              104103..104537 /locus-tag="YE0095"
                  /codon-start=1
                  /transl-table=11
                  /product="conserved membrane protein"
                  /protein-id="CAL10237.1"
                  /db-xref="GI:122087456"
                  /db-xref="GOA:AJJH29"
                  /db-xref="InterPro:IPR008523"
                  /db-xref="UniProtKB/TrEMBL:AJJH29"
                  /translation="MTIQQWCFSLKGRIGRDFW
IWIGLWLLAMLIIFTLAGQNWLS
QTAAFAIVFLLWPTAAVMVKRLHNRNKGAWWALL
VVLAWMLMAGNWQLAPIWQWGVG
RFIPTLIMVMLIDCGAFLGTEGENRFGEAPVP
KFLAEKSQ"
sig-peptide      104103..104252 /locus-tag="YE0095"
                  /note="Signal peptide predicted for YE0095 by SignalP 2.0 HMM (Signal peptide probability 0.698) with cleavage site probability 0.268 between residues 50 and 51"
misc-feature      join(104160..104213, /locus-tag="YE0095"
104223..104291,
104316..104384,
104397..104465)
                  /inference="protein
motif:TMHMM:2.0"
                  /note="4 probable transmembrane helices predicted for YE0095 by TMHMM2.0 at aa 20-37, 41-63, 72-94 and 99-121"
gene             complement(104780..105526) /gene="fpr"
                  /locus-tag="YE0096"
                  /note="synonym: mvrA"
CDS              complement(104780..105526) /gene="fpr"
                  /locus-tag="YE0096"
                  /codon-start=1
                  /transl-table=11
                  /product="ferredoxin--NADP reductase"
                  /protein-id="CAL10238.1"
                  /db-xref="GI:122087457"
                  /db-xref="GOA:AJJI00"

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/db-xref="InterPro:IPR001433"
/db-xref="InterPro:IPR008333"
/db-xref="UniProtKB/TrEMBL:A1JI00"
/translation="MAEWSVGKITHIEHWTDTLF
SIRVNAPIDPFTAGQFAKLALDID
GERVQRAYSYVNAPSNNLEFYLVTVPEGKLSR
LDQLAVGGEVMVTQQAAGFFVLEE
IPDCDTLWMLATGTAIGPYLSILQEGRDLERFKN
LVLVHAARFARDLSYPLMQQLEQ
RYNGKLRIQTVVSREQSPGSLTGRVPALIENGSL
EAAVGLKIDAEDSHVMLCGNPQMV
RDTQMLKEQGRMKHLRRKPGHMTSEQYW"
/misc-feature complement(104855..1052
11) /gene="fpr"

/locus-tag="YE0096"
/inference="protein
motif:PFAM:PF00175"
/note="Pfam match to entry PF00175
NAD-binding-1,Oxidoreductase
NAD-binding domain, score 82.4,
E-value 6.1e-22"
/misc-feature complement(105227..1055
11) /gene="fpr"

/locus-tag="YE0096"
/inference="protein
motif:PFAM:PF00970"
/note="Pfam match to entry PF00970
FAD-binding-6,Oxidoreductase
FAD-binding domain, score 25.6,
E-value 3.3e-06"
gene 105845..107029 /gene="emrD"
CDS 105845..107029 /locus-tag="YE0097"
/gene="emrD"

/locus-tag="YE0097"
/inference="similar to
sequence:INSDC:AL627280"
/inference="similar to
sequence:UniProtKB:P31442"
/note="Similar to Escherichia coli
multidrug resistance protein D
EmrD SWALL:EMRD-ECOLI
(SWALL:P31442) (394 aa) fasta
scores: E(): 6.1e-104, 71.28 38d
in 390 aa, and to Salmonella typhi
multidrug resistance protein D
STY3981 SWALL:Q8Z2L0
(EMBL:AL627280) (394 aa) fasta
scores: E(): 2.3e-106, 72.33 38d
in 394 aa"
/codon-start=1
/transl-table=11
/product="multidrug resistance
protein D"
/protein-id="CAL10239.1"
/db-xref="GI:122087458"
/db-xref="GOA:A1JI01"
/db-xref="InterPro:IPR004812"
/db-xref="InterPro:IPR007114"
/db-xref="InterPro:IPR011701"
/db-xref="UniProtKB/TrEMBL:A1JI01"
/translation="MRKIENFHLVMLILLVAVG
QMAQTIYVPVVADIARDLSVRSGT

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		VQRVMAAYLLTYGFSQLIYGPLSDRVGRRPVILA GMMIFMLGALGAWLANSLSLVAA SALQMG TG VAGVMARTMPRDLYAGTALRYANSM LNMGILVSPLMAPVIGGVLASLFG WRACYAFLLFLCGGVAFCMFRWLPETRPQQTEKR RMLASFRLLLSDRAFSCYLVMLIG ALAGIAVFASAGVLMGGVLGLSGVTVSILFILP IPAAFFGAWYAGRDGKTFHNLMMH SVISCLLAGLMMWIPGWFGVMNIWTLVIPAALFF FGAGMLFFPLATTGAMEPPFYLAGA AGALVGGQLQNVGSLATWLSAMPLPQTGQFSLGLL MFAMAVLILLCWWPLSHRMOPQEH RV" /gene="emrD" /locus-tag="YE0097" /note="Signal peptide predicted for YE0097 by SignalP 2.0 HMM (Signal peptide probability 0.998) with cleavage site probability 0.934 between residues 23 and 24" 
sig-peptide	105845..105913	
misc-feature	105881..107017	/gene="emrD" /locus-tag="YE0097" /inference="protein motif:PFAM:PF00083" /note="Pfam match to entry PF00083 sugar-tr, Sugar (and other) transporter, score -92.8, E-value 0.00014" 
misc-feature	join(105986..106045, 106064..106123, 106136..106195, 106253..106321, 106334..106393, 106451..106519, 106562..106630, 106667..106735, 106745..106813, 106832..106900, 106928..106996)	/gene="emrD"  /locus-tag="YE0097" /inference="protein motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0097 by TMHMM2.0 at aa 7-28, 48-67, 74-93, 98-117,137-159, 164-183, 203-225, 240-262, 275-297, 301-323,330-352 and 362-384" 
gene	complement(107115..1081 25)	/gene="glpX"
CDS	complement(107115..1081 25)	/locus-tag="YE0098" /gene="glpX"  /locus-tag="YE0098" /inference="similar to sequence:UniProtKB:P28860" /inference="similar to sequence:UniProtKB:P28900" /note="Similar to Escherichia coli putative fructose 1,6-bisphosphatase GlpX SWALL:GLPX-ECOLI (SWALL:P28860) (336 aa) fasta scores: E(): 

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6.2e-107, 86.01 38d in 336 aa, and
to Shigella flexneri putative
fructose 1, 6-bisphosphatase GlpX
SWALL:GLPX-SHIFL (SWALL:P28900)
(336 aa) fasta scores: E():
2.2e-106, 85.71 38d in 336 aa"
/codon-start=1
/transl-table=11
/product="putative fructose 1,
6-bisphosphatase"
/protein-id="CAL10240.1"
/db-xref="GI:122087459"
/db-xref="GOA:ALJI02"
/db-xref="InterPro:IPR004464"
/db-xref="UniProtKB/TrEMBL:ALJI02"
/translation="MKRELAIEFSRVTEAALAG
YKWLGRGDKNAADGAAVKAMRIML
NQVNIDGQIVIGEGEIDEAPMLYIGENVGTGQGD
AVDIAVDPIEGTRMTAMGQANALA
VLAVGDKGTFLHAPDMYMEKLVVGPAGKAIDLN
LPLELNLNRNVAIKLNKPLTDLTVI
TLAKPRHDGIIAEMQQLGVKVFAlPDGDVAASIL
TCMPESEVDVMYCIGGAPEGVISA
AVIRALDGMQGRLLPRHVKGDNDNRRIGEEE
LVRCKSMGIEAGKVLLLGDMARND
NVIFSATGITKGDLLLEGYIRKGNMATTETLLIRG
KSRITRRIRSTHFLDRKDPALHEF LL"
/misc-feature complement(107160..1081
22) /gene="glpX"

/locus-tag="YE0098"
/inference="protein
motif:PFAM:PF03320"
/notes="Pfam match to entry PF03320
FBPase-glpX, Bacterial
fructose-1,6-bisphosphatase,
glpX-encoded, score 788.7,E-value
1.4e-234"
/gene="glpK"
/gene complement(108307..1098
30)

/locus-tag="YE0099"
/gene="glpK"
/gene complement(108307..1098
30)

/locus-tag="YE0099"
/EC-number="2.7.1.30"
/inference="similar to
sequence:INSDC:AL627279"
/inference="similar to
sequence:UniProtKB:P08859"
/notes="Similar to Escherichia coli
glycerol kinase GlpK
SWALL:GLPK-ECOLI (SWALL:P08859)
(501 aa) fasta scores: E():
2e-178, 85.23 38d in 501 aa, and
to Salmonella typhi glycerol
kinase STY3784 SWALL:Q8Z2Y6
(EMBL:AL627279) (501 aa) fasta
scores: E(): 1.6e-177, 85.17 38d
in 499 aa"
/codon-start=1
/transl-table=11
/product="glycerol kinase"
/protein-id="CAL10241.1"

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/db-xref="GI:122087460"
/db-xref="GOA:AlJI03"
/db-xref="InterPro:IPR000577"
/db-xref="InterPro:IPR005999"
/db-xref="UniProtKB/TrEMBL:AlJI03"
/translation="MTTENTTQKKYIVALDQGT
SSRAVLDHDANIVSISQREFEQI
YPKAGWVEHDPMEIWATQSSILVEVLAKAGISSD
EIAIGITNQRETTIVWDKTTGKP
VYNAIVWQCRRTADICEKLKKEGLEEYIRHNTGL
VVDPYFSGTKVKWILDNVEGARDR
AERGELLFGTVDTWLVNMTQGRVHVTDYTNASR
TMMFNIRTKEWDERMLKALNIPRS
MLPEVRPSSEVYQQTNIIGGKGGTRIPIAGIAGDQ
QAALFGQLCVQPGMAKNITYGTGCF
LLMNTGTEAVQSNHGLLTTIACGPRGEVNYALEG
AVFIGGASIQWLRDELKLISSDADD
SEYFATKVKKDSNGVYVPAFTGLGAPYWDPYARG
AIFGLTRGVNSNHIIRATLESIAI
QTRDVLDMQADSGERLKSRLRVGGAVANNFLMQ
FQADILGTRVERPEVRESTALGAA
FLAGLATGFWNLDLDEVKSKATIEREFRPGIETTE
RDFRYKGGWKKAVARAQAWEEHEE"
misc-feature complement(108373..1090
50) /gene="glpK"
/locus-tag="YE0099"
/inference="protein
motif:PFAM:PF02782"
/note="Pfam match to entry PF02782
FGGY-C, FGGY family of
carbohydrate kinases, C-terminal
domain, score 353.3,E-value
1.7e-103"
misc-feature complement(108667..1087
29) /gene="glpK"
/locus-tag="YE0099"
/inference="protein
motif:Prosite:PS00445"
/note="PS00445 FGGY family of
carbohydrate kinases signature 2."
misc-feature complement(109057..1098
00) /gene="glpK"
/locus-tag="YE0099"
/inference="protein
motif:PFAM:PF00370"
/note="Pfam match to entry PF00370
FGGY, FGGY family of carbohydrate
kinases, N-terminal domain, score
452.8,E-value 1.9e-133"
misc-feature complement(109372..1094
10) /gene="glpK"
/locus-tag="YE0099"
/inference="protein
motif:Prosite:PS00933"
/note="PS00933 FGGY family of
carbohydrate kinases signature 1."
gene complement(109907..1107
55) /gene="glpF"
/locus-tag="YE0100"
CDS complement(109907..1107
55) /gene="glpF"
/locus-tag="YE0100"

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facilitator protein"
/protein-id="CAL10242.1"
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/db-xref="InterPro:IPR012269"
/db-xref="UniProtKB/TrEMBL:A1JI04"
/translation="MSQTASSTLKGQCIAEFLGT
ALLIFFGVGCVAALKLAGASFGQW
EISIIWGLGVAMAIYLTAAISGAHLNPAVTIALW
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AALVFGLYYNLFIDFEQTHQIARGSVESLNLAGI
FSTYPNPHISVFQAFVLVETVITAI
LMCLILALIDDDNGIPRGPLAPLLIGILIAVIGG
SMGPLTGFALNFARDFGPKLFAYF
AGWGEVAFVTGGRDIPYFLVPIFGPIVGLVGAFG
YRALIGRHLPCDVCVADDEETTVT TTERKA"
/misc-feature complement(join(109985..
110053,110150..110218,
110255..110323,
110423..110491,
110549..110617,
110660..110719))
/gene="glpF"

/locus-tag="YE0100"
/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted for YE0100 by
TMHMM2.0 at aa 13-32, 47-69,
89-111, 145-167,180-202 and
235-257"
/misc-feature complement(109997..1107
55)
/gene="glpF"

/locus-tag="YE0100"
/inference="protein
motif:PFAM:PF00230"
/note="Pfam match to entry PF00230
MIP, Major intrinsic protein,
score 420.9, E-value 7.8e-124"
/misc-feature complement(110510..1105
42)
/gene="glpF"

/locus-tag="YE0100"
/inference="protein
motif:Prosite:PS00013"
/note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
/misc-feature complement(110528..1105
54)
/gene="glpF"

/locus-tag="YE0100"
/inference="protein
motif:Prosite:PS00221"
/note="PS00221 MIP family
signature."
/misc-feature complement(110666..1106
98)
/gene="glpF"

/locus-tag="YE0100"
/inference="protein
motif:Prosite:PS00013"

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		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /locus-tag="YE0101" /locus-tag="YE0101" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10243.1" /db-xref="GI:122087462" /db-xref="InterPro:IPR009252" /db-xref="UniProtKB/Swiss-Prot:A1J I05" /translation="MSFEVFEKLEVKVQQAIDTI TLLQMETELKEKNNTLSQEVQEA AGGREALVRENEQLKQEQHVWQDRLRALLGKME V"
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CDS	111350..111589	
		/locus-tag="YE0102" /gene="menG" /locus-tag="YE0102" /codon-start=1 /transl-table=11 /product="S-adenosylmethionine:2-d emethylmenaquinone methyltransferase" /protein-id="CAL10244.1" /db-xref="GI:122087463" /db-xref="GOA:A1JI06" /db-xref="InterPro:IPR005493" /db-xref="InterPro:IPR010203" /db-xref="InterPro:IPR014339" /db-xref="UniProtKB/Swiss-Prot:A1J I06" /translation="MKYDTS DLCDIYHEEVNVVE PLFSNFGGRTSFGGKITTVKCFED NGLLFDLLEENGLGRVLVVDGGSVRRALINAE LADLALKNEWEGIVVYGAVRQVDEL AELDIGIQAMAAIPVGADEGIGESDIRVNFVGGV TFFSGDHLYADNTGIILSEEPLDI E"
gene	complement(111726..112211)	
CDS	complement(111726..112211)	
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misc-feature	complement(111753..112211)	
gene	complement(112342..113196)	
CDS	complement(112342..113196)	

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sig-peptide	complement(113152..113196)	/locus-tag="YE0103" /note="Signal peptide predicted for YE0103 by SignalP 2.0 HMM (Signal peptide probability 0.814) with cleavage site probability 0.628 between residues 15 and 16" /gene="menA"
misc-feature	complement(112345..113196)	/locus-tag="YE0103" /inference="protein" motif:PFAM:PF01040" /note="Pfam match to entry PF01040 UbiA, UbiA prenyltransferase family, score 121.0, E-value 1.5e-33" /gene="menA"
misc-feature	complement(join(112348..112416,112450..112509,112522..112590,112651..112719,112732..112791,112828..112887,112900..112968,113068..113127))	/locus-tag="YE0103" /inference="protein" motif:TMHMM:2.0" /note="8 probable transmembrane helices predicted for YE0103 by TMHMM2.0 at aa 24-43, 77-99, 104-123, 136-155,160-182, 203-225, 230-249 and 261-283" /gene="menA"
misc-feature	complement(112903..112935)	/locus-tag="YE0103" /inference="protein" motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /gene="hslU"
gene	complement(113424..114755)	/locus-tag="YE0104" /gene="hslU"
CDS	complement(113424..114755)	/locus-tag="YE0104" /gene="hslU"



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/db-xref="InterPro:IPR013093"
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I08"
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LTDAAVKVMVRHQSIKEMRYRAEELAEERILDVLI
PPAKNNWGQPEETQEPSPTRQAFR
KKLREGQLDDKEIIDLAAAPVGVEIMAPPGMEE
MTNQLQSMFQNIAGQKQKPRKIKI
KEAFKLLIEEEAAKLVNPEELKQQAIDAVEQHGI
VFIDEIDKICKRGQTSFGPDVSREG
VQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAF
QVSSPSDLIPELQGRLPPIRVELQA
LITDDFERILTEPSASLIEQYKALMATEGVTVEF
TREGIRKIAEAAQVNERTENIGA
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02)               /gene="hslU"

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motif:PFAM:PF00004"
/notes="Pfam match to entry PF00004
AAA, ATPase family associated with
various cellular activities (AAA),
score 27.3, E-value 5.6e-07"
misc-feature      complement(114564..1145
87)               /gene="hslU"

/locus-tag="YE0104"
/inference="protein
motif:Prosite:PS00017"
/notes="PS00017 ATP/GTP-binding
site motif A (P-loop). "
gene              complement(114810..1153
34)               /gene="hslV"

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CDS               complement(114810..1153
34)

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/db-xref="UniProtKB/Swiss-Prot:A1J
I09"
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misc-feature	complement(115164..11523)	/gene="hslV"  /locus-tag="YE0105" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0105 by TMHMM2.0 at aa 38-57"
gene	complement(115434..116297)	/gene="ftsN"  /locus-tag="YE0106" /note="synonym: msgA"
CDS	complement(115434..116297)	/gene="ftsN"  /locus-tag="YE0106" /codon-start=1 /transl-table=11 /product="cell division protein" /protein-id="CAL10248.1" /db-xref="GI:122087467" /db-xref="GOA:AlJI10" /db-xref="InterPro:IPR007730" /db-xref="InterPro:IPR011930" /db-xref="UniProtKB/TrEMBL:AlJI10" /translation="MAQRDYVSRGRSGARRKSTS RKKRSAPAVSKTVMALAVALLVVF VGGLYFITHNKPGLPLLP SHDPR TGNGLPPKPE ERWR YIKEL ENR QIGVPTPTESA GGEVNSKTQLTNEQRQLLEQM QADMRQQPTQLSE VPYNEGMPVFRSAVIKPPVINMQ QPLTPPRQIVAPVPAPQTQVQPPVTPPTTQQPT APVTQAATPPKPEKEKEKAQRWV QCGSFKAVDQAESIRAQLAFEGIESRITAGGGWN RVVLGPYSTKAAADKALQRLKGAG QSGCIPLAVGG"
sig-peptide	complement(116136..116297)	/gene="ftsN"  /locus-tag="YE0106" /note="Signal peptide predicted for YE0106 by SignalP 2.0 HMM (Signal peptide probability 0.661) with cleavage site probability 0.196 between residues 54 and 55"
misc-feature	complement(116145..116213)	/gene="ftsN"  /locus-tag="YE0106" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0106 by TMHMM2.0 at aa 29-51"
gene	complement(116363..117391)	/gene="cylR"  /locus-tag="YE0107"
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/db-xref="UniProtKB/TrEMBL:A1J11"
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GDCAQQPQQERSFVNLIITKQIDGMLLGSNLFP
DASKEEQRNLPMPVMANFAFELE
LPTVHIDNLTAAYEAVEYLIRLGHQRIACVAGPE
NFFLCQYRLQGYIQALRRNGIEVD
SNYIIRGDFS YEAGVDTFIKLMDLPEPPTAIFCH
NDVMAIGAMWQAKMGLRIPQDVS
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93) /gene="cytR"
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/inference="protein
motif:PFAM:PF00532"
/note="Pfam match to entry PF00532
Peripla-BP-like, Periplasmic
binding proteins and sugar binding
domain of the LacI family, score
116.6, E-value 3.1e-32"
misc-feature complement(117287..1173
70) /gene="cytR"
/locus-tag="YE0107"
/inference="protein
motif:PFAM:PF00356"
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lacI, Bacterial regulatory
proteins, lacI family, score 53.4,
E-value 3.2e-13"
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64) /gene="cytR"
/locus-tag="YE0107"
/note="Predicted helix-turn-helix
motif with score 1874.000, SD 5.57
at aa 10-31, sequence
ATMKDVAEMAGVSTATVSRALM"
misc-feature complement(117302..1173
58) /gene="cytR"
/locus-tag="YE0107"
/inference="protein
motif:Prosite:PS00356"
/note="PS00356 Bacterial
regulatory proteins, lacI family
signature."
gene complement(117622..1198
20) /gene="priA"
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CDS complement(117622..1198
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/db-xref="InterPro:IPR011545"
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DSATACPVVGARVSVFPFKRNAIG
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KQQQALAAALLQKPVYRHQVNMAL
TESALQTLRSKGLIDLRAQVAATDWRNGFSVLG
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HSGLNDSERLSVWLRARNGEAAIVIGTRSALFTP
FSRLGVIIIDEEHDSYKQQEGWR
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DLKGLPLKVGLSQPLLRKMKAHLQADNQVILFLN
RRGYAPALLCHECGWIAECQRCDH
YYTLHQNRHLRCHHCDSQRPVFPQCPKCGSTHM
VSVGVGTEQLENELAPLFPDPTIT
RIDRDTTSRKGSLEQHLADVHGGGARILIGTQML
AKGHHFPDVTLVALLDVGALFSA
DFRSAERFAQLYTVQVSGRAGRAGKQGEVILQTHH
PEHPLLQILLQQGYDAFAKQALAE
RKSVMFLPPYTSHIIVRSEHDNQQSALFLQQLRN
LLEASPLKDEALWIMGPVFPALQAK
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11)                /gene="priA"
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                    /note="Pfam match to entry PF00271
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                    C-terminal domain, score 27.9,
                    E-value 1.6e-05"
misc-feature      complement(119128..1191
51)                /gene="priA"
                    /locus-tag="YE0108"
                    /inference="protein
motif;Prosite:PS00017"
                    /note="PS00017 ATP/GTP-binding
                    site motif A (P-loop)."
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CDS 120213..120431 /locus-tag="YE0109"

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/locus-tag="YE0109"

/codon-start=1

/transl-table=11

/product="50S ribosomal protein L31"

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misc-feature	120213..120413	
misc-feature	120321..120338	
misc-feature	120333..120389	
gene	complement(120521..120838)	/locus-tag="YE0110" /gene="metJ"
CDS	complement(120521..120838)	/locus-tag="YE0110" /codon-start=1 /transl-table=11 /product="transcriptional repressor protein" /protein-id="CAL10252.1" /db-xref="GI:122087471" /db-xref="GOA:AlJI14" /db-xref="InterPro:IPR002084" /db-xref="UniProtKB/Swiss-Prot:AlJ114" /translation="MAEWNGEYVSPYAHEHGKKSE QVKKITVSIPLKVLKILTDERTRR QVNNLRHATNSSELLCEAFLEHAFTGQPLPNDEDLR KERSDEIPEAAKILMRELGVDPDT WEY" /gene="metJ"
misc-feature	complement(120524..120835)	/locus-tag="YE0110" /inference="protein motif:PFAM:PF01340" /note="Pfam match to entry PF01340 MetJ, Met Apo-repressor, MetJ, score 292.2, E-value 4.2e-85" /gene="metB"
gene	121214..122371	/locus-tag="YE0111" /gene="metB"
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AVELAWWANNIGVTGAAFDSYLLRGLRTLSPRM
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HPSLLQHPGHEIACRQQSGFGAMLSFELDGDEQV
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motif:PFAM:PF01053"
/note="Pfam match to entry PF01053
Cys-Met-Meta-PP,Cys/Met metabolism
PLP-dependent enzyme, score
708.0,E-value 2.9e-210"
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motif:Prosite:PS00868"
/note="PS00868 Cys/Met metabolism
enzymes pyridoxal-phosphate
attachment site."
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misc-feature	122412..123242	
misc-feature	122421..122447	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:Prosites:PS00324" /note="PS00324 Aspartokinase signature."
misc-feature	123795..124199	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:PFAM:PF03447" /note="Pfam match to entry PF03447 NAD-binding-3, Homoserine dehydrogenase, NAD binding domain, score 167.0, E-value 2.1e-47"
misc-feature	124203..124793	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:PFAM:PF00742" /note="Pfam match to entry PF00742 Homoserine-dh, Homoserine dehydrogenase, score 344.9, E-value 5.8e-101"
misc-feature	124341..124409	/gene="metL" /locus-tag="YE0112" /inference="protein" motif:Prosites:PS01042" /note="PS01042 Homoserine dehydrogenase signature."
gene	complement(124892..1270	/locus-tag="YE0113"

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/inference="similar to
sequence:INSDC:AE007704"
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sequence:UniProtKB:P57414"
/note="Similar to several
including: Clostridium
acetobutylicum predicted permease
Cac2003 SWALL:Q9/HK8
(EMBL:AE007704) (832 aa) fasta
scores: E(): 0.072, 24.67 id in
535 aa and Buchnera aphidicola
OmpA-like protein precursor or
bu332 SWALL:OMPA-BCAI
(SWALL:P57414) (349 aa) fasta
scores: E(): 6.6, 24.17 38d in 273
aa. Note that this CDS lies within
a localised low G+C region."
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ADEYALLLTIIATTTTSKVLDRDNI
INSVDSDISTDGSAGSSAGSYSENRRDELTTWINKH
VKPEHKS KVDLLSAPDRHAELKD
KVYLS DMLLFSGKKTIPFKLKEIILNNTVVVKFN
NTSLRLSHSRIDKINNASDKKTAL
QMGLFKKIYICMNGKRLSDLYDFTHDHKNGEK
LFIQSNGRIQEKLTSVINKKMPRL
KTVEIDNSETVAKELQKILKEKAINLQDNIFTKI
VYFEDKEDTTGKTYIYISKNFPPVY
KPNIPYVHPENEQGASKYVVS KDDNFVALAPT KK
EKFSTKNNFHD LKGLNSIKTGLVV
APDLMISHNAGICLDHLNNA PLQSVFKIAVN
ELKKLHEIQGYLRDIK PANMAYDG
KQVNFIDVDDRIKAHEITKISAPVFKIYGEV IY
TPKYITQGLVNNIYESNPGNPGKK
TLKQTDITHDLQIADEYAF LMTMITATTKDNALK
SSIKNAKVDIIGVRIINRIKNEID
QCSDRQKDKLTDKLIETQKEYNN TGIMNKS NKT
YFTPW LKENIKPKHHKSVKLLTD
PAKYADTAPKTHLADMLLFK"
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folate reductase"
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/db-xref="GI:122087475"
/db-xref="GOA:A1J118"

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gene 127374..128258

CDS 127374..128258



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/misc-feature 127404..128246 /gene="metF"
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/inference="protein
motif:PFAM:PF02219"
/notes="Pfam match to entry PF02219
MTHFR, Methylene tetrahydrofolate
reductase, score 555.3, E-value
2.6e-164"
/gene 128578..129780 /locus-tag="YE0115"
CDS 128578..129780 /locus-tag="YE0115"
/inference="similar to
sequence:INSDC:AL139076"
/inference="similar to
sequence:UniProtKB:Q9Z9E3"
/notes="Similar in parts to
Campylobacter jejuni hypothetical
protein Cj0849C SWALL:Q9PF74
(EMBL:AL139076) (719 aa) fasta
scores: E(): 0.19, 22.86 38d in
258 aa and to Chlamydia pneumoniae
phosphoenolpyruvate-protein
phosphotransferase PtsI or Cpn0038
SWALL:PT1-CHLPN (SWALL:Q9Z9E3)
(571 aa) fasta scores: E(): 3.5,
19.57 38d in 332 aa"
/codon-start=1
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/db-xref="GI:122087476"
/db-xref="UniProtKB/TrEMBL:AJJI19"
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LGAVDQQIETFNKAKIAADKADNNKALCNFMS
IYQSNAGCKAINAEARHQFGNANQ
SAKLNGNQVIAEYVKTHGDNVSGGNAPVKSIAIQ
SHCSNLP TLVKDVAKAWYSPTDIT
TTSHRQGQMTQDGDIKLMSQFSDRAGSVYKLGQ
FFSTSKENVNAKAFADRTGDSVKI
MFEVKGNSGRGIVVSGGLKFDNNEREVLSPYPLAK
FAVTDIKGSAKGYTIKLENEVDQ TKAKLLPY"
/gene="ppc"
/gene 129861..132500 /locus-tag="YE0116"

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CDS	complement(129861..132500)	/note="synonym: glu" /gene="ppc"  /locus-tag="YE0116" /codon-start=1 /transl-table=11 /product="phosphoenolpyruvate carboxylase" /protein-id="CAL10258.1" /db-xref="GI:122087477" /db-xref="GOA:A1J120" /db-xref="InterPro:IPR001449" /db-xref="InterPro:IPR015813" /db-xref="UniProtKB/Swiss-Prot:A1J120" /translation="MNEQYSAMRSNVSMGLTLLG DTIKEALGEHILEKVEITIRKLSKS SRAGNEASRQELTTTLQNLNDELTPVARAFSQF LNLINTAEQYHSISPHGEAASNPE ALAQLFTRLKDKKLSQEDMSRAVDLSIELVLTA HPTETIRRTLIIHKLVEVNTCLSQL DHNDLADYERNKIMRRLRQLVAQSWHTDEIRKIR PSPVDEAKWGFVAVENSLWEGVPA FLREFNEQLQNSLDYRLPVEAVPIRFTSWMGGRD DGNPNVTAEITRHVLLSRNKATD LFLRDIQVLVSELSMSECTPELRELAGEEVLEP YRELMKRVRTQLTNTQAYLEARLK GERVLPTDLLVSNQDLWDPLYACYQSLKACGME IANGQLDLTLRRVRCFQVPLVRI DVRQESTRHTDAIAELTRYLGLGDYESWSEADKQ AFLIRELNSKRPLVPLKWEPSADT QEVLETCTRVIAEAPQGSIAAYVISMAKVPSDVLA VHLLLEKAGCPFTLPVAPLFETLD DLNNADDVMTQLLNIDWYRGLIQGQMVMIGYS SAKDAGVMAASNAQYRAQDALIKT CEKAGISLTLFHGRGGSIGRGGAPAHAAALLSQPP GSLKGLRVTEQGEMIRFKFGLPE VTISSLALYASAVLEANLLPPPEPKKEWNEVMDI LSDASCEMYRGYVRENPFQVYFR AATPELELGLPLGSRPAKRRPNNGVESLRAIPW IFAWTQNRMLMLPAWLGAAGLQKA IDAGKKEVLATMCRDWPFFSTRIGLMLEMFAKAD LWLAEYYDQRLVDKSLNPLGQQLR DQLEADIKVVLAIANDDHLMADLPWIAESIALRN VYTDPLNLVQAELLHRSRQQENAA DACVEQALMVTIAGVAAGMRNTG"
misc-feature	complement(129864..132500)	/gene="ppc"  /locus-tag="YE0116" /inference="protein motif:PFAM:PF00311" /note="Pfam match to entry PF00311 PEPcase, Phosphoenolpyruvate carboxylase, score 763.6, E-value 5.3e-227"
misc-feature	complement(130857..130895)	/gene="ppc"  /locus-tag="YE0116" /inference="protein motif:Prosite:PS00393" /note="PS00393 Phosphoenolpyruvate carboxylase active site 2."

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misc-feature    complement(132069..1321 /gene="ppc"
04)
                /locus-tag="YE0116"
                /inference="protein
                motif:Prosite:PS00781"
                /note="PS00781 Phosphoenolpyruvate
                carboxylase active site 1."
gene            complement(132848..1340 /gene="argE"
32)
                /locus-tag="YE0117"
CDS             complement(132848..1340 /gene="argE"
32)
                /locus-tag="YE0117"
                /codon-start=1
                /transl-table=11
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                deacetylase"
                /protein-id="CAL10259.1"
                /db-xref="GI:122087478"
                /db-xref="GOA:AlJI21"
                /db-xref="InterPro:IPR001261"
                /db-xref="InterPro:IPR002933"
                /db-xref="InterPro:IPR010169"
                /db-xref="InterPro:IPR011650"
                /db-xref="UniProtKB/TrEMBL:AlJI21"
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                RDPFTLTETHDNKLYGLGTADMGFFAFILDAVRD
                IDASTLSKPLYILATADEETTMAG
                ARYFAASTQLRPDAIIGEPTSLQPVRAHKGHIS
                NAIRITQSGHSSDPARGVNAIDL
                MHESITELMKLRTTLQERYNNPFAIPYPTMNF
                HINGGDAANRICACCELHMDIRPL
                EGLILSDLDELMTEALAPVSARWPGRLSIDQLHP
                PIPGYECPDHHMVGVIIEELLGER
                TAVVNYCTEAPFIQICPTLVLGPGSINQAHQPD
                EFIDMAFIEPTRELIGQLVDHFCQ QK"
misc-feature    complement(133004..1339 /gene="argE"
99)
                /locus-tag="YE0117"
                /inference="protein
                motif:PFAM:PF01546"
                /note="Pfam match to entry PF01546
                Peptidase-M20,Peptidase family
                M20/M25/M40, score 236.5, E-value
                2.5e-68"
misc-feature    complement(133562..1336 /gene="argE"
75)
                /locus-tag="YE0117"
                /inference="protein
                motif:Prosite:PS00759"
                /note="PS00759 ArgE / dapE / ACY1
                / CPG2 / yscS family signature 2."
misc-feature    complement(133751..1337 /gene="argE"
80)
                /locus-tag="YE0117"
                /inference="protein
                motif:Prosite:PS00758"
                /note="PS00758 ArgE / dapE / ACY1
                / CPG2 / yscS family signature 1."

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CDS	134395..135399	/gene="argC"
		/locus-tag="YE0119"
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		/transl-table=11
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		/protein-id="CAL10260.1"
		/db-xref="GI:122087479"
		/db-xref="GOA:A1JI22"
		/db-xref="InterPro:IPR000534"
		/db-xref="InterPro:IPR000706"
		/db-xref="InterPro:IPR006025"
		/db-xref="InterPro:IPR012280"
		/db-xref="UniProtKB/TrEMBL:A1JI22"
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misc-feature	134395..134844	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:PFAM:PF01118"
		/note="Pfam match to entry PF01118 Semi aldehyde-dh, Semi aldehyde dehydrogenase, NAD binding domain, score 174.7, E-value 1e-49"
misc-feature	134629..134658	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:Prosite:PS00142"
		/note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature."
misc-feature	134839..134889	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:Prosite:PS01224"
		/note="PS01224 N-acetyl-gamma-glutamyl-phosphate reductase active site."
misc-feature	134869..135327	/gene="argC"
		/locus-tag="YE0119"
		/inference="protein"
		motif:PFAM:PF02774"
		/note="Pfam match to entry PF02774 Semi aldehyde-dhC, Semi aldehyde dehydrogenase, dimerisation domain, score 103.9, E-value 2e-28"
gene	135487..136251	/gene="argB"
		/locus-tag="YE0120"
CDS	135487..136251	/gene="argB"

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/locus-tag="YE0120"
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/transl-table=11
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/db-xref="GOA:A1JI23"
/db-xref="InterPro:IPR001048"
/db-xref="InterPro:IPR004662"
/db-xref="InterPro:IPR011148"
/db-xref="UniProtKB/Swiss-Prot:A1J
123"
/translation="MVIKLGVLDDSEALERLF
TALVTYREKHERPLVIMHGGGCLV
DDLKKKLLALPVVKKNGLRVTPADQIDIITGALAG
TANKTLLAMAVKHDINAVGLCLGD
GNTVSVTPLDAALGHVGKAEAGSPALVQTLAAN
YMPIISSIGITKDGSLMNVNADQA
ATALAATLGADLILLSVSGIILDGKGQRIAEMTA
QKAEQLIAQGIIIDGMVVKVNAAL
DAARSLGRPVDIASWRHADQLPALFNGVPIGTRI
LA"
/misc-feature 135487..136182
/gene="argB"
/locus-tag="YE0120"
/inference="protein
motif:PFAM:PF00696"
/note="Pfam match to entry PF00696
aakinase, Amino acid kinase
family, score 120.0, E-value
2.8e-33"
gene 136489..137862
/gene="argH"
CDS 136489..137862
/locus-tag="YE0121"
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/locus-tag="YE0121"
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/transl-table=11
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/protein-id="CAL10262.1"
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/db-xref="InterPro:IPR000362"
/db-xref="InterPro:IPR003031"
/db-xref="InterPro:IPR009049"
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124"
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DSLRFDYRLAEQDIIGSVANSKAL
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LHTGRSRNDQVATDLKLWCKFQITELKTAVQQQLQ
QALVITAEANQDAVMPGYTHLQRA
QPVTFAHWCLAYAEMLARDESRLQDTLKRLDVSP
LGSGALAGTAYAI DREQLAGWLGF
ASATRNSLDSVSDRDHVLLELSDASIGMVHLSRF
AEDLIFFNSGEAAFVLDLSDRVTS
SSLMPOKKNPDAL ELIRGKGRVQGALTGMMMTL
KGLPLAYNKDMQEDKEGLFDALDT
WLDCLHMAALVLDG IQVKRPRCKEAAEQGYANAT
ELADYLVAKGVFPFEAAHII VGEAV
VEATRQKKALEALS LSLDQKFS AVIGDDVYPILA
LQSCLDKRVAKGGVSPQQVASAIA EAKARLF"

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misc-feature	136504..137784	/gene="argH" /locus-tag="YE0121" /inference="protein" motif:PFAM:PF00206" /note="Pfam match to entry PF00206 lyase-1, Lyase, score 606.8, E-value 8.1e-180"
misc-feature	137314..137343	/gene="argH" /locus-tag="YE0121" /inference="protein" motif:Prosite:PS00163" /note="PS00163 Fumarate lyases signature."
gene	138584..140911	/locus-tag="YE0122"
CDS	138584..140911	/locus-tag="YE0122" /codon-start=1 /transl-table=11 /product="putative TonB dependent receptor protein" /protein-id="CAL10263.1" /db-xref="GI:122087482" /db-xref="GOA:AlJ125" /db-xref="InterPro:IPR000531" /db-xref="InterPro:IPR010949" /db-xref="InterPro:IPR011276" /db-xref="InterPro:IPR012910" /db-xref="UniProtKB/TrEMBL:AlJ125" /translation="MEGTSNAHEGDWVYDELHSV SEISREQLDSRPARHAADILEQTS GVYSSVSQQDPALSVNIRGMQDYGRVNMNIDGMR QNFMKSGHGQRNGVMYIDPEILNN VVIEKGVTSGIGGAGVIGGIATFNTINASNFLEP GKEIGGQIRVLTDGNGTINFIGSAA LALGNEYGDILIAASERNLSDYWPGNKGNMGDIR FGTAAERFNYDLKNNKVEYTRYKM RSQLTKLGNLPAQRMLLSYLQTQINSPNASML TQIVDKADPYRIIKMGWKNSSVSD VLNRRNIGLDYSLKPEHIAWLDVAVKVYYVDIDDE TNTLCSDAIYCKKFWTQTRLTRG LQLQNTSFFTYADHHQFHINYGLEWFSDRSRGNS THETILGLTPPGKRTITSTFAQLN YDYDNWLRLEGGRLYDQFRILQGNTHMHSKNFRGN YTRENPCNQKTHEQYIINEGRCS FNWPSKMTWEVDRREQQLSPTLAIGIKPGVQWLE FFGNYGKSWRPPIATEVLATGSAH GHSWTLFPNPIAAEHSKAWAGMNIQHSNLFIAE DRLVAKLAYFDTRVTDYINLELSK TKPLHGSGDFTNATYINNLLATHFRGLEYQLSYD AGVFYTNLNYTRMIGVNTICSRA WLGGVNGIASKNKYEIYSIDRDDINNIVDCFAAN NLFSSAYLPGRDGSLLTGGRIFD KKLDLGTIVIRYKNKGRQDKSVLNNKGHVNTAYVAD WPKYITIFDLYASYKMTNNLLIRSS IENITNRAYLISYGDSLSFAPNRGRITIQGFYEYK E"
misc-feature	140567..140908	/locus-tag="YE0122" /inference="protein" motif:PFAM:PF00593" /note="Pfam match to entry PF00593 TonB-boxC, TonB dependent receptor C-terminal region, score 31.5, E-value 1.3e-06"

gene	141014..141649	/locus-tag="YE0123"
CDS	141014..141649	/locus-tag="YE0123"
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		/transl-table=11
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		/protein-id="CAL10264.1"
		/db-xref="GI:122087483"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:AJ126"
		/translation="MLLTIRKFIIMVTITKYQGQF SNDILTSYTKQWATTHGDIKDTEA EGYSKDFGQFAGGGWFDGTOYSIGSSHSSTGM IIEGDLTYNFAQHTLHGKVDLSLEL GKNLSINSNGIGKQLDQLKMSDLDLITGEFDPG KTMAENHQGDMHKSIIYGLMRGNAD PLLEVLTAKGIDVNTPLKDMAIASQFEAMVSDMP MIDTVGVVESSDMLLAA"
misc-feature	141404..141427	/locus-tag="YE0123"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
gene	141797..142450	/locus-tag="YE0124"
CDS	141797..142450	/locus-tag="YE0124"
		/inference="similar to
		sequence:INSDC:AJ414159"
		/note="Similar to Yersinia pestis
		hemophore HasA or Ypo3922
		SWALL:Q8ZA90 (EMBL:AJ414159) (205
		aa) fasta scores: E(): 1.5e-05,
		28.05 38d in 221 aa. Note the
		product of this CDS is also
		significantly similar to the CDS
		directly upstream and downstream,
		YE0123, YE0125 and YE0126."
		/codon-start=1
		/transl-table=11
		/product="probable hemophore"
		/protein-id="CAL10265.1"
		/db-xref="GI:122087484"
		/db-xref="InterPro:IPR010495"
		/db-xref="UniProtKB/TrEMBL:AJ127"
		/translation="MTITIKYHEKIANETITSYS QQWATNFGNMLWTMGVDYTLNASG YPIPPADSIKYVAASTHHNQSESNAAIVIALKKV AIENDQSIITDLRVSLFEGEALVP IANDGTSKHPHQLLLQQVQLDISGLDIRADVESS MPTLDYALWQDIYYQGGQNLGIYN LLKGANANPLLDILKAQGDIVNTPVKDMTIASQFE VPTDELLIETVGITDGGNTLLAA"
gene	142509..143150	/locus-tag="YE0125"
CDS	142509..143150	/locus-tag="YE0125"
		/inference="similar to
		sequence:INSDC:AJ414159"
		/inference="similar to
		sequence:UniProtKB:Q54450"
		/note="Similar to Yersinia pestis
		hemophore HasA or Ypo3922
		SWALL:Q8ZA90 (EMBL:AJ414159) (205
		aa) fasta scores: E(): 1.8e-08,
		33.48 38d in 218 aa and Serratia
		marcescens hemophore HasA

gene 143211..143819  
CDS 143211..143819

SWALL:HASA-SERMA (SWALL:Q54450)  
(188 aa) fasta scores: E(): 0.051,  
23.38 38d in 201 aa. Note the  
product of this CDS is also  
significantly similar to the CDS  
directly upstream and downstream,  
YE0123, YE0124 and YE0126."  
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/db-xref="UniProtKB/TrEMBL:ALJI28"  
/translation="MTITIKYHSQFAEYSVSSYI  
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NADNTGKQLQLKLDGLNIEDDFYPSLCSISQ  
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/locus-tag="YE0126"  
/inference="similar to  
sequence:INSDC:AJ414159"  
/note="Similar to Yersinia pestis  
hemophore HasA or Ypo3922  
SWALL:Q8ZA90 (EMBL:AJ414159) (205  
aa) fasta scores: E(): 2.1e-13,  
28.23 38d in 209 aa. Note the  
product of this CDS is also  
significantly similar to the CDS  
directly upstream, YE0123, YE0124  
and YE0125."  
/codon-start=1  
/transl-table=11  
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/protein-id="CAL10267.1"  
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/db-xref="UniProtKB/TrEMBL:ALJI29"  
/translation="MTVTIIFNGNIKDETIYSY  
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NDVHQMGFNLKAGNADVLEILIS  
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GGGILLAA"  
/locus-tag="YE0127"  
/locus-tag="YE0127"  
/codon-start=1  
/transl-table=11  
/product="ABC transporter protein"  
/protein-id="CAL10268.1"  
/db-xref="GI:122087487"  
/db-xref="GOA:ALJI30"  
/db-xref="InterPro:IPR003439"  
/db-xref="InterPro:IPR003593"  
/db-xref="InterPro:IPR010128"  
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gene 144005..145786  
CDS 144005..145786



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/db-xref="UniProtKB/TrEMBL:A1JI30"
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GRHKILWGIGLFTAVINLLMLAP
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GLLEWVRSAIVIRLGRIDMQLNQ
QVFNAAFASNLNGQKVOAAQALNDLTTLRQFATG
NALFAFFDAPWFFFYLLVIFILHP
WLGALAALGAVFLIFLAWLNHWICRKPLKEASHI
TSQATQANANLRNADAIQAMGML
KALRDRLWKQHSFLYQONIASDKSSRVTALS KS
SRQALQSMMLGLGALLVIDGAITA
GVMIAGSILVGRVLGPIDQLIAVWKQWSHTRLAY
QRLSSLLAQHSOPTTGMVLPPPKG
KLSVTQLTVCKPGTHIPVLQSFELQPGGVLG V
LGPSSGSGKSTLAKLLVASQPAFSG
SVRLDSADLARWDKSHLGEFIGYLPQDIQLFRGS
IAENIARFGLIDHAKVIAAAQLAD
VHDLIHLFPQGYDTSLGDEGEGLSGGQRQRIALA
RAMYGVPRLIVLDEPNASLDKVG E
QALLASISQLKQGGCTIVMVTHKPELLSGSDYLL
FLQNGQIELFDRDTQITILQDGGQKN
KATTGRNSWGSMSYGVAPIRRTASQKS"
/locus-tag="YE0127"

misc-feature      join(144080..144148,
144191..144259,
144410..144478,
144488..144556,
144794..144862)

/inference="protein
motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted for YE0127 by
TMHMM2.0 at aa 26-48, 63-85,
136-158, 162-184 and 264-286"

misc-feature      144083..144883
/locus-tag="YE0127"
/inference="protein
motif:PFAM:PF00664"
/note="Pfam match to entry PF00664
ABC-membrane, ABC transporter
transmembrane region, score 19.6,
E-value 4.6e-05"

misc-feature      145091..145645
/locus-tag="YE0127"
/inference="protein
motif:PFAM:PF00005"
/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
204.6, E-value 1e-58"

misc-feature      145112..145135
/locus-tag="YE0127"
/inference="protein
motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
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misc-feature 145421..145465

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motif:Prosite:PS00211"
/note="PS00211 ABC transporters
family signature."
/locus-tag="YE0128"
/locus-tag="YE0128"
/codon-start=1
/transl-table=11
/product="HlyD family secretion
protein"
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gene 145917..147149

CDS 145917..147149

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CDS 147226..148026
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Salmonella typhi IS 10 transposase
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aa) fasta scores: E(): 2e-43,
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QERDGRSSAKTPWLLTSSDDFRP
REVIKIYSRRMQIEQNFRDEKSERFGLRASRS
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nucleotide-disulphide
oxidoreductase, dimerisation
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150.3, E-value 2.2e-42"
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misc-feature	complement(151319..151786)	/locus-tag="YE0132" /inference="protein motif:PFAM:PF00578" /note="Pfam match to entry PF00578 AhpC-TSA, AhpC/TSA family, score 159.1, E-value 4.8e-45"
gene	151949..152881	/gene="oxyR" /locus-tag="YE0133"
CDS	151949..152881	/gene="oxyR" /locus-tag="YE0133" /codon-start=1 /transl-table=11 /product="oxidative stress transcriptional regulatory protein" /protein-id="CAL10274.1" /db-xref="GI:122087493" /db-xref="GOA:AlJI36" /db-xref="InterPro:IPR000847" /db-xref="InterPro:IPR005119" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:AlJI36" /translation="MNIRDLEYLVALAEFRHFRR AADSCHVSQPTLSGQIRKLEDELG VMLLERTSRKVLFTQAGLLLVQARTVLREVKVL KEMASLQGESMSGPLHIGLIPTVG PYLLPQIIPMLHQTFPKLEMYLHEAQTQNLALQ DSGKLDCAILALVKETEAFIEVPL FDEPMQLAIYADHPWADRDKVQMHELAGEKLLML EDGHCLRDQAMGFCFQAGADETDH FRATSLLETLRNMVAAGSGITLLPSLAVPNERKRD GVCYLECYKPVKRTIALVVRPGS PLRGRYEQLAEEAIREHMQPRMNSDVINQKEQAV "
misc-feature	151955..152134	/gene="oxyR" /locus-tag="YE0133" /inference="protein motif:PFAM:PF00126" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.2, E-value 2.1e-26"
misc-feature	151994..152059	/gene="oxyR" /locus-tag="YE0133" /note="Predicted helix-turn-helix motif with score 1674.000, SD 4.89 at aa 16-37, sequence

misc-feature	151997..152089	RHFRRAADSCHVSQPTLSGQIR" /gene="oxyR" /locus-tag="YE0133" /inference="protein motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature."
misc-feature	152204..152830	/gene="oxyR" /locus-tag="YE0133" /inference="protein motif:PFAM:PF03466" /note="Pfam match to entry PF03466 LysR-substrate, LysR substrate binding domain, score 202.6, E-value 3.9e-58"
gene	complement(152864..154264)	/gene="sthA" /locus-tag="YE0134" /note="synonyms: sth, udhA"
CDS	complement(152864..154264)	/gene="sthA" /locus-tag="YE0134" /codon-start=1 /transl-table=11 /product="soluble pyridine nucleotide transhydrogenase" /protein-id="CAL10275.1" /db-xref="GI:122087494" /db-xref="GOA:AlJ137" /db-xref="InterPro:IPR000815" /db-xref="InterPro:IPR001100" /db-xref="InterPro:IPR001327" /db-xref="InterPro:IPR004099" /db-xref="InterPro:IPR013027" /db-xref="UniProtKB/Swiss-Prot:AlJ137" /translation="MQQHFFHDAIVIGSGPGGEG AAMGLVKQGARVAVIERNNVGGG CTHWGTIPSKALRHAVSRIIEFNQNPFLYSNART ISSSFSDILNHADRVINQOTRMRO GFYDRNHCOMQFSGDASFIDANTINVRADGINDT LRADNIVIATGSRPYRPAVDFTH ERIYDSDTILQLSHEPQHVIYIGAGVIGCEYASI FRGLSVKVDLINTRDLLAFLDQE MSDALSYHFNNNGVVIRHNEEFQIEGTVDGVIV HLKSGKKVKADCLLYANGRTGNTS GLGLEKIGLEADSRGLKVNMSYQTALSHVYAVG DVIGYPSLASAAYDQGRIAAQAMI KGEANTHLIEDIPTGIYTIPEISSVGKTEQDLTA MKVPYEVGQAQFKHLARAQIVGMD TGSIKILFHRETQKILGIHCFGERAAEIIHIGQA IMEQKGEGNTIEYFVNTTFNYPTM AEAYRVAALNGLNRLF" /gene="sthA"
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		oxidoreductase, dimerisation domain, score 134.6, E-value 1.2e-37
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		motif:PFAM:PF00070"
		/note="Pfam match to entry PF00070 pyr-redox, Pyridine nucleotide-disulphide oxidoreductase, score 251.7, E-value 6.7e-73"
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		/locus-tag="YE0134"
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		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
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		FVPSILSVVLVFWILFKLKARKSA
		QTDINADTDTDDIDNQPPQ"
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		/locus-tag="YE0136"
		/inference="protein
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		/note="3 probable transmembrane
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		72-94"
misc-feature	155380..155412	/gene="yijD"
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		/inference="protein
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		/db-xref="UniProtKB/TrEMBL:ALJI40"
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		HKLFQIDYLSLTSGLLATLLYHRPLDEEWQOKA
		RELRLDQLREQGFDLQLIGRASKTK
		IMLDHDYIDEVLVPVAGRDMYRQVENSFTQPNA
		VNIHMLEWAIQVTHASGDLLELY
		CGNGNFSALARNFDRVLATEIAKPSVAAAQYNI
		AANHIDNVQIIRMSAEFTQAMQG
		VREFNRLKGIDLTSYNCETIFVDPPRSGLDDET
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misc-RNA	157085..157301	/note="Cobalamin riboswitch (RF00174) as predicted by Rfam, score 104.18, positions 1 to 190" /gene="btuB" /locus-tag="YE0139" /gene="btuB"
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CDS	157369..159267	/locus-tag="YE0139" /gene="btuB" /locus-tag="YE0139" /inference="similar to sequence:INSDC:AJ414159" /inference="similar to sequence:UniProtKB:P06129" /note="Similar to Escherichia coli vitamin B12 receptor precursor Btub or Bfe or Cer or DcrC or B3966 SWALL:BTUB-ECOLI (SWALL:P06129) (614 aa) fasta scores: E(): 2.3e-123, 52.7 38d in 628 aa, and to Yersinia pestis putative vitamin B12 receptor protein Ypo3910 SWALL:Q8ZAA1 (EMBL:AJ414159) (625 aa) fasta scores: E(): 5.4e-144, 58.45 38d in 633 aa" /codon-start=1 /transl-table=11 /product="exported vitamin B12 receptor protein" /protein-id="CAL10279.1" /db-xref="GI:122087498" /db-xref="GOA:AlJI41" /db-xref="InterPro:IPR000531" /db-xref="InterPro:IPR010101" /db-xref="InterPro:IPR010917" /db-xref="InterPro:IPR012910" /db-xref="UniProtKB/TrEMBL:AlJI41" /translation="MTTKNTITIKKYTLTALS VTAFTSGWAQGNATATGNKDEMMVTAS RFKQPVSTVLAPADVTRDDIDRWQAKSLNEVMR RLPQVDIAQFGGVGGQSSMYIRGT EARHVLILIDGIPLARTGIVNSVNLDDQIPISLVQ RVXEYIRGPRSAVYGSAGIGVINV ITQTDQEGAQINAGISGKGYQQYDGSVRQRFGDT LATLAGGYQTSNGYNIKPDSFNEI DNRDRGFRNKNFWAGLEHQFSQEISGFIRGYGYT NNSDYDIGLSLSPAYSGDEERLYN HTYDAGLRYASGAYSSQLIGSYQKYKDYNFSSQY GRYGVATTLDNMDQRNVQWGNITYS FESGTLISAGLDWQQQRLTSSSTQISDITYKRDNTG LYLSSGQQKIGNVTLEASGRGDKDE QFGNHETWQTAAGWEFVPDYRVLTLYSGTGFLAPS LGQQYGSQRFDIISNDLKPEESR QWEAGLEGVTGLDWRSLAYHNKIENLIDYSFON

		<p>SIFKGHYNVNSATIKGVEWTGNL  TTGIFTHGVTLQYIDPRNDLNNEVLARRSKQQAQ  YQLDWTMFNLDDIDISYQYYGKRYD  NSTSAYSSTQRELSSYSTVDVSAGYPVTSHLTVR  GRIANLFDKEYETAYGYKTAGREY YLTGSYNF"  /gene="btuB"  /locus-tag="YE0139"  /inference="protein  motif:PFAM:PF00593"  /note="Pfam match to entry PF00593  TonB-boxC, TonB dependent receptor  C-terminal region, score 71.2,  E-value 1.4e-18"</p>
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CDS	159212..160075	
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misc-feature	159821..159853	

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gene	160552..162040	/gene="16S rRNA"
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gene	162169..162245	/gene="tRNA-Ile (GAT)"
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rRNA	162741..165734	/gene="23S rRNA"
		/product="23S ribosomal RNA"
		/note="match to 23S-rRNA 1..2994
		(Y. enterocolitica 23S
		EMBL:U77925, Y.pestis KIM 98
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gene	165734..165970	/gene="5S rRNA"
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		Y.enterocolitica"
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		/db-xref="UniProtKB/TrEMBL:A1JI43"
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		AKIPVFLDRMIEVNDPSLYTAAVASDSVYEGKV
		AGEWLLKDVAGKPCNVVELQGTVG
		SSVA INRKKGFADG IASAPNVKI IRSQSGDFTRS
		KGKEVMESFIKAEQNGKNICAVYA
		HNDDMAIGAIQAIKEAGLKPGEIKIVSIDGVDP
		IFKAMSSGEANATVELTPNMAGPA
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		ESKKS LGY"
sig-peptide	166814..166876	/locus-tag="YE0141"

		/note="Signal peptide predicted for YE0141 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.998 between residues 21 and 22" /locus-tag="YE0141" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0141 by TMHMM2.0 at aa 5-27" /locus-tag="YE0141" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 2.7, E-value 1e-05" /locus-tag="YE0142" /locus-tag="YE0142" /codon-start=1 /transl-table=11 /product="putative sugar transport system ATP-binding protein" /protein-id="CAL10282.1" /db-xref="GI:122087501" /db-xref="GOA:AlJ144" /db-xref="InterPro:IPR003439" /db-xref="InterPro:IPR003593" /db-xref="UniProtKB/TrEMBL:AlJ144" /translation="METLLLEVRLGSVEFPVGVKAL DSVDFSLQRGEVVALLGENGAGKS TLIKALTGVYKRAAGEVYLDVAICPIDTADAQK MGIGTVYQEVNLLPNISIAANLFI GREPLRWGLIDHRAMNQATKLLKGYGLELDVQR PLADFSIAIQQIVAIARAVDLAK VLILDEPTASLDAKEVSMLLDLRLQRLDQIGMV FVTHFLDQVYRISDRITVLRNGKL VGTKNTTELPRIELVQMMLGHSFDEQLLKRGHEHN IAVSNPLVEFKNYSRRGVVENFDL SVSPGEIVGLAGLLSGRGTETAQLIFGVITPDGT EAKIQGKPVKIRTPRKASRYGFY CPEDRKTDGIVGAATVRENIILALQAQRGWLRI SIREQTQIAEDFIQQLGIRTPGPE QQIQYLSGGNQKVLRLARWLATKPRFLILDEPTR GIDVGAAHEIIRLIEKLCNEGLAL LIISSELELAGYADRVIVLRDRRHIAQLGHDEI SVPAINQAIQAVQ" /locus-tag="YE0142" /inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 196.8, E-value 2.1e-56" /locus-tag="YE0142" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0142" /inference="protein
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misc-feature	166880..167743	
gene	167855..169345	
CDS	167855..169345	
misc-feature	167942..168502	
misc-feature	167963..167986	
misc-feature	168695..169273	

		motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 101.9, E-value 8.2e-28" /locus-tag="YE0142" /inference="protein motif:Prosite:PS00211" /note="PS00211 ABC transporters family signature." /locus-tag="YE0143" /locus-tag="YE0143" /codon-start=1 /transl-table=11 /product="putative sugar transport system permease" /protein-id="CAL10283.1" /db-xref="GI:122087502" /db-xref="GOA:AlJI45" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:AlJI45" /translation="MGNRSLSMFQRPKRVKVL KGATQFGALIVILLIDSLVAPHFF SIHIQDGRLFSGVIDILNRGAPVALLALGMLTVI ATGGIDLSVGAVMAIAGATAATLT SAGHPFFTIVLVAALAVGALCGLWNGFLVAVLQIQ FIVATLMLMVAGRGIAQLITEGQI VTFDSGGLAELGSSSTLMYMPMSVVIASFMLIIVW LLTRKTALGLFIESVGINLRSARN AGVSTRRLVLISVYVIGCVCAAVAGIIVTADIRGA DANNAGLWLELDAILAVVIGGASL MGGFRNLLLSVIGALIIQGMNTGILLSGYQPEFN LVLKAIIVLAVLVQSPMISLSHI FRRRK" /locus-tag="YE0143"
misc-feature	169046..169090	
gene	169357..170376	
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gene	170376..171344	
CDS	170376..171344	

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sig-peptide	170376..170465	
misc-feature	170466..171329	
misc-feature	170946..170993	
gene	complement(171355..1722 36)	
CDS	complement(171355..1722 36)	
misc-feature	complement(171376..1719 87)	

		LysR-substrate, LysR substrate binding domain, score 56.9, E-value 3e-14"
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		/inference="protein motif:PFAM:PF00126"
		/note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.3, E-value 2e-26"
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		/inference="protein motif:Prosites:PS00044"
		/note="PS00044 Bacterial regulatory proteins, lysR family signature."
misc-feature	complement(172126..172191)	/locus-tag="YE0145"
		/note="Predicted helix-turn-helix motif with score 1285.000, SD 3.56 at aa 16-37, sequence RHFGRAAESLYLTQSAVSFRIR"
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gene	complement(172798..174321)	/locus-tag="YE0147"
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motif with score 1104.000, SD 2.95
at aa 446-467, sequence
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                  /note="Pfam match to entry PF01078
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subunit ChlI, score 299.4, E-value
2.8e-87"
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misc-feature	175435..175896	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:PFAM:PF00205" /note="Pfam match to entry PF00205 TPP-enzymes, Thiamine pyrophosphate enzyme, central domain, score 229.7,E-value 2.7e-66"
misc-feature	175933..176457	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:PFAM:PF02775" /note="Pfam match to entry PF02775 TPP-enzymes-C, Thiamine pyrophosphate enzyme, C-terminal TPP binding domain ,score 300.1, E-value 1.7e-87"
misc-feature	176122..176181	/gene="ilvG" /locus-tag="YE0148" /inference="protein" motif:Prosite:PS00187" /note="PS00187 Thiamine pyrophosphate enzymes signature."
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gene	176815..177741	/gene="ilvE"

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FNISGNLHQEKIINYKNKGLRAM
VQSNYDNGQSLKDSKSTYYINGEVDVVVEYSA
DGKVIVGRIEKAYNITNAILKET
ESSYSMDGKIIIGRINKEYSALDGRLEKITSNR
SDSGQLKREVESYLDINGQESKRI
SQYYSNGVTKCFERSFSAGKMTGKVMFEFDNNGN
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LRNLVPMVNYASRQ"
/misc-feature      181457..181525    /locus-tag="YE0153"
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motif:TMHMM:2.0"
                                     /note="1 probable transmembrane
helix predicted for YE0153 by
TMHMM2.0 at aa 7-29"
gene               complement(182937..1838
18)                /gene="ilvY"
CDS                complement(182937..1838
18)                /locus-tag="YE0154"
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                                     /locus-tag="YE0154"
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                                     /transl-table=11
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transcriptional regulatory
protein"
                                     /protein-id="CAL10294.1"
                                     /db-xref="GI:122087513"
                                     /db-xref="GOA:A1JI56"
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                                     /db-xref="InterPro:IPR005119"
                                     /db-xref="InterPro:IPR011991"
                                     /db-xref="UniProtKB/TrEMBL:A1JI56"
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RHALGQHGPSLSGELRLFCSVTAA
YSHLPPIILDRFRARHPVEIKLITGDAADAVDKV
QSNEDLGIAGRPEVLPTSVAFTQ
IGEIPVLVLIAPALPCAVRSQVSDQPDWATIPFI
LPEHGPSRKRIDLWFRQRITNPL
IYATVSGHEAIVSMVALGCGVALIPSVVVDNSPE
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QKKRLNEPLIEAFWGLL"
/misc-feature      complement(182940..1835
63)                /gene="ilvY"

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		/locus-tag="YE0154" /inference="protein motif:PFAM:PF03466" /note="Pfam match to entry PF03466 LysR-substrate, LysR substrate binding domain, score 118.2, E-value 9.9e-33" /gene="ilvY"
misc-feature	complement(183633..183812)	/locus-tag="YE0154" /inference="protein motif:PFAM:PF00126" /note="Pfam match to entry PF00126 HTH-1, Bacterial regulatory helix-turn-helix protein, lysR family, score 97.4, E-value 1.8e-26" /gene="ilvY"
misc-feature	complement(183678..183770)	/locus-tag="YE0154" /inference="protein motif:Prosite:PS00044" /note="PS00044 Bacterial regulatory proteins, lysR family signature." /gene="ilvY"
misc-feature	complement(183708..183773)	/locus-tag="YE0154" /note="Predicted helix-turn-helix motif with score 1928.000, SD 5.75 at aa 16-37, sequence RHFGRSAKAMHVSPSTLSRQIQ" /gene="ilvC"
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CDS	184071..185549	/locus-tag="YE0155" /codon-start=1 /transl-table=11 /product="ketol-acid reductoisomerase" /protein-id="CAL10295.1" /db-xref="GI:122087514" /db-xref="GOA:AlJI57" /db-xref="InterPro:IPR000506" /db-xref="InterPro:IPR013023" /db-xref="InterPro:IPR013116" /db-xref="InterPro:IPR014359" /db-xref="InterPro:IPR016040" /db-xref="UniProtKB/Swiss-Prot:A1J157" /translation="MANYFNTLNLRQQLAQLGKC RFMARDEFADAEAYLGKKVIVIG CGAQQLNQGLNMRDGLDVAYALRKEAIAEKRAS WRKATENGFKVGYEELIPQADLV VNLPDKQHSVAVVQAVQPLMKDGAALGYSHGFNI VEVGEQVRKIDITVMVAPKCPGTE VREYKRGFGVPTLIAVHPENDPKGEGMAIAKAW AAAATGGHRAGVLESSFVAEVKSDL MGEQTILCGMLQAGSLLCFDKLVSEGTDAAYAEK LIQFWETITEALKQGGITLMMDR LSNPAKLRAYALSEQLEIMAPLFQKHMDDIISG EFGSGMMADWANDDKLLNWREET

GKTAFENAPQFEGKISEQEYFDHGVLMIAMVKAG  
 VELAFETMVDSGIIEESAYYESLH  
 ELPLIANTIAKRRLYEMNVVISDTAEYGNLYFAN  
 AAVPLLKGKFMDSLQAGDLGKSWA  
 GTAVDNAQLRDVNEAIRNHPIEAVGHKLRGYMTD  
 MKRIAVAG"  
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 /locus-tag="YE0155"  
 /inference="protein  
 motif:PFAM:PF01450"  
 /note="Pfam match to entry PF01450  
 IlvC, Acetohydroxy acid  
 isomeroreductase, catalytic  
 domain, score 463.0, E-value  
 1.6e-136"  
 gene complement(185847..1865 /locus-tag="YE0157"  
 24)  
 CDS complement(185847..1865 /locus-tag="YE0157"  
 24)  
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 /transl-table=11  
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 protein"  
 /protein-id="CAL10296.1"  
 /db-xref="GI:122087515"  
 /db-xref="GOA:A1JI58"  
 /db-xref="InterPro:IPR001829"  
 /db-xref="InterPro:IPR008962"  
 /db-xref="InterPro:IPR016147"  
 /db-xref="InterPro:IPR016148"  
 /db-xref="UniProtKB/TrEMBL:A1JI58"  
 /translation="MACSVPMASVVAEKTRIIF  
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 IPPKATTKVDDSESVTLALRMQYKVFYRPKSLPA  
 PADTVSKALTFVLERNGNTASVRV  
 DNPITYYASLASLTLGLAEGLPDMVAPFSKLDFF  
 LNRVPIADSKTVNFVLIDDLGNRK PFSRELK"  
 misc-feature complement(185859..1861 /locus-tag="YE0157"  
 10)  
 /inference="protein  
 motif:PFAM:PF02753"  
 /note="Pfam match to entry PF02753  
 pili-assembly-C, Gram-negative pili  
 assembly chaperone, C-terminal  
 domain, score 28.6, E-value  
 9.5e-06"  
 misc-feature complement(186120..1864 /locus-tag="YE0157"  
 97)  
 /inference="protein  
 motif:PFAM:PF00345"  
 /note="Pfam match to entry PF00345  
 pili-assembly, Gram-negative pili  
 assembly chaperone, N-terminal  
 domain, score 141.8, E-value  
 8.2e-40"  
 misc-feature complement(186210..1862 /locus-tag="YE0157"  
 63)  
 /inference="protein  
 motif:Prosites:PS00635"  
 /note="PS00635 Gram-negative pili

gene complement(186571..187938) /locus-tag="YE0158" assembly chaperone signature."

CDS complement(186571..187938) /locus-tag="YE0158"

/codon-start=1  
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/product="putative exported protein"  
/protein-id="CAL10297.1"  
/db-xref="GI:122087516"  
/db-xref="InterPro:IPR011228"  
/db-xref="UniProtKB/TrEMBL:A1JI59"  
/translation="MLRPTEQLISCEVSRPTMPV  
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ACTRITAQSQLGAGDGTASAWSGLDYNNGSLGL  
PGVIDLSTAANFQPDGILLAAATS  
DFTTFLANTSYDPDRVLFRCAAADVDQLFEMYAT  
NGDNDYGGKNEGAIAGNVPSGFA  
TYVRNVVIRLTNLSTGEYYSLRWKGRRLTGLDTD  
STGRILVKAKNFSNLYTELFRIDY  
VRAGTNNAAASYTYAYTQPNAYIAFKGPGISGPVE  
GTDVSNWPGWYSTWPASIGLYNY  
VTFRRITICAVINFTPTVILPRISVAELNSGSSS  
SAEFSVDQCQTGITSGVNAGAVA  
MGFLVPAANAAKAQALGLMNGSGGISHLVSDNYG  
AAGMANGVGIRIYRNNNPFMYLLSK  
NVTQTGNNGGWYGFQGAQTIITGTVSGNSYTEN  
FRAELSKISQGTVTAGAVNNAHOV VIRVQ"

misc-feature complement(187801..187833) /locus-tag="YE0158"

/inference="protein  
motif:Prosite:PS00013"  
/note="PS00013 Prokaryotic  
membrane lipoprotein lipid  
attachment site."

gene complement(187956..190175) /locus-tag="YE0159"

CDS complement(187956..190175) /locus-tag="YE0159"

/codon-start=1  
/transl-table=11  
/product="putative outer membrane usher protein"  
/protein-id="CAL10298.1"  
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/db-xref="GOA:A1JI60"  
/db-xref="InterPro:IPR000015"  
/db-xref="UniProtKB/TrEMBL:A1JI60"  
/translation="MAERVKGASFHFDQAKLRLE  
LSIPQALLQORPRGYIERSEWEEG  
EKLAIFYNSANFYRSDTQTQONSTSDYGFVGLKS  
GLNLGLWQLRQQSNLSYSSNNNS  
DTQWNNIRTYVQRPISQLDSELTGETFTDSTLF  
GTMSFRGVKMATDQRMWPEMRGF  
APEVRGVATSNARV IISQNGREIYETNVAPGPFV  
INDLYSTTSQGDNLNVEVIEANGSR  
STFTVPFSAVPDSMRPGVSRYNNAVVGESRDFTNI  
DSYFTDFTYERGLTNQLTANSGR  
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NQTDGWRMQATYSQTFNETGTGF  
SLAGRYSTKGYRDLNDVFGVRSVQKNGGTWDSS



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TYKQRSQFTTTINQTLAGYGQLSA
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TTRYGNTENIASLTVSIPNLIGSGNQYLSMSANR
NPKSGNNYQTSLSGTAGERNTLNY
SVNAGYDDSDNVSGSSNNWGANVQKQFPNATVNGS
YSRGNNYTQYGAGARGAAVIHSGK
VILGPYLGDTFGLIEADGAQGATVRNAQGARIDK
NGFALVPSLTPYNYNTVGLDTKGI
NRNTELKENQGRVVPYAGAAVRVKFETILTGYAVL
IQTQTADGEGPLPGSDVYNNKDEL
VGMVGGQGNQIYARVKENKGSLYVRWGENSNEQCE
LPYDFASQDTEQDIHILTGSCRR"

misc-feature      complement(188010..1901
72)              /locus-tag="YE0159"

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motif:PFAM:PF00577"
                  /note="Pfam match to entry PF00577
Usher, Fimbrial Usher protein,
score 734.3, E-value 3.4e-218"

misc-feature      complement(189582..1896
14)              /locus-tag="YE0159"

                  /inference="protein
motif:Prosite:PS01151"
                  /note="PS01151 Fimbrial biogenesis
outer membrane usher protein
signature."

gene              complement(190653..1913
30)              /locus-tag="YE0160"

CDS               complement(190653..1913
30)              /locus-tag="YE0160"

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chaperone"
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                  /db-xref="GOA:AlJI61"
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                  /db-xref="InterPro:IPR008962"
                  /db-xref="InterPro:IPR016147"
                  /db-xref="InterPro:IPR016148"
                  /db-xref="UniProtKB/TrEMBL:AlJI61"
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PVNKAENKNNKMLVLMNRNIKVFYRPENIAGRVDQ
VSSALTFNVRQGGKDVVVTKNPT
GFYATIASGEVVGGGKKLKMKSEMIPPMQQAQWV
IPNSSVPSNAIVNFFLLVNDFGGQD TGSYKIQ"

misc-feature      complement(190665..1909
28)              /locus-tag="YE0160"

                  /inference="protein
motif:PFAM:PF02753"
                  /note="Pfam match to entry PF02753
pili-assembly-C, Gram-negative pili
assembly chaperone, C-terminal
domain ,score 33.8, E-value
2.6e-07"

misc-feature      complement(190938..1913
06)              /locus-tag="YE0160"

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gene	complement(191517..192047)	/locus-tag="YE0161"
CDS	complement(191517..192047)	/locus-tag="YE0161"  /codon-start=1 /transl-table=11 /product="putative fimbrial protein" /protein-id="CAL10300.1" /db-xref="GI:122087519" /db-xref="GOA:AlJI62" /db-xref="InterPro:IPR000259" /db-xref="InterPro:IPR014779" /db-xref="UniProtKB/TrEMBL:AlJI62" /translation="MNKILITLALFAASTTVAMA ASNNTITFOGEVTAQTCSVTVNGL DANPMVLLPTVSSGDLASGKTAGKITFTLGVS CATGAADIDIKTVFVGNQVITAGN LKNITGTASNVDLQLLKDATTTTGIDLNSSVGQDG IVLKAGDTSAEHDFAVQYFATGQA GPGSVIASVQYAVSYL"
sig-peptide	complement(191988..192047)	/locus-tag="YE0161"  /note="Signal peptide predicted for YE0161 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.991 between residues 20 and 21"
misc-feature	complement(191520..191978)	/locus-tag="YE0161"  /inference="protein motif:PFAM:PF00419" /note="Pfam match to entry PF00419 Fimbrial, Fimbrial protein, score 26.4, E-value 3.4e-08"
gene	complement(192664..192945)	/gene="ppiC"
CDS	complement(192664..192945)	/locus-tag="YE0162" /gene="ppiC"  /locus-tag="YE0162" /codon-start=1 /transl-table=11 /product="peptidyl-prolyl cis-trans isomerase C" /protein-id="CAL10301.1" /db-xref="GI:122087520" /db-xref="GOA:AlJI63" /db-xref="InterPro:IPR000297" /db-xref="UniProtKB/TrEMBL:AlJI63" /translation="MANKASALHILVDDKQAND ILAQLNNGANFQELAKKFSNCPSK RNGGDLGEFNKGDMPAFDKA VSCCELLQPYG PVTQFGYHIIKVLRYN"
misc-feature	complement(192673..192945)	/gene="ppiC"

42)

gene 193159..195183

CDS 193159..195183

misc-feature 193165..194610

misc-feature 193222..193245

gene complement(195239..197065)

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 motif:PFAM:PF00639"  
 /note="Pfam match to entry PF00639  
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 score 132.4, E-value 5.3e-37"  
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 /transl-table=11  
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 /protein-id="CAL10302.1"  
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 /db-xref="GOA:AlJi64"  
 /db-xref="InterPro:IPR000212"  
 /db-xref="InterPro:IPR005752"  
 /db-xref="InterPro:IPR014016"  
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 SQISNWKNDLLDPAAAAALARSER  
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 ELKVITANNEDHEAERVVGELIAH  
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 YRISGGDSFFSRPEIKDLLAYLRV  
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 /gene="rep"  
 /locus-tag="YE0163"  
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 motif:PFAM:PF00580"  
 /note="Pfam match to entry PF00580  
 UvrD-helicase, UvrD/REP helicase,  
 score 718.8, E-value 1.6e-213"  
 /gene="rep"  
 /locus-tag="YE0163"  
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 motif:Prosites:PS00017"  
 /note="PS00017 ATP/GTP-binding  
 site motif A (P-loop)."  
 /gene="pehX"

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CDS      complement(195239..197065)      /locus-tag="YE0164"
                                              /gene="pehX"

                                              /locus-tag="YE0164"
                                              /EC-number="3.2.1.82"
                                              /inference="similar to
sequence:INSDC:AF059505"
                                              /inference="similar to
sequence:UniProtKB:P15922"
                                              /note="Highly similar to the plant
pathogenic Erwinia chrysanthemi
exo-poly-alpha-D-galacturonosidase
PehX SWALL:P15922) (602 aa) fasta
scores: E(): 3.6e-145, 61.23 38d
in 601 aa. This CDS was previously
sequenced as: Yersinia
enterocolitica
exopolygalacturonase SWALL:O68975
(EMBL:AF059505) (601 aa) fasta
scores: E(): 0, 98.83 38d in 600
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                                              /transl-table=11
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ronosidase precursor"
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                                              /db-xref="UniProtKB/TrEMBL:AlJI65"
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TYKSGALWLKSDMTLNLQAGAILL
GSENPNDYPAGYRLPYSTIERPASLINAIDPNN
SKPGTFNRNIRITGSGVIDNGWLR
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ILAENNVMYLTDIGLRAKSTSTIGGGARNVIFRN
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                                              /gene="pehX"

sig-peptide complement(196979..197065)
                                              /locus-tag="YE0164"
                                              /note="Signal peptide predicted
for YE0164 by SignalP 2.0 HMM
(Signal peptide probability 1.000)

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		with cleavage site probability 0.985 between residues 29 and 30"
misc-feature	complement(195356..196519)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:PFAM:PF00295" /note="Pfam match to entry PF00295 Glyco-hydro-28, Polygalacturonase (pectinase), score -27.9, E-value 7.2e-09"
misc-feature	complement(196556..196579)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	complement(196637..196963)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:PFAM:PF00041" /note="Pfam match to entry PF00041 fn3, Fibronectin type III domain, score 28.4, E-value 1.1e-05"
misc-feature	complement(196979..197032)	/gene="pehX"  /locus-tag="YE0164" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0164 by TMHMM2.0 at aa 12-29"
gene	complement(197407..198903)	/gene="gppA"
CDS	complement(197407..198903)	/locus-tag="YE0165" /gene="gppA"  /locus-tag="YE0165" /EC-number="3.6.1.40" /codon-start=1 /transl-table=11 /product="guanosine-5'-triphosphat e, 3'-diphosphate pyrophosphatase" /protein-id="CAL10304.1" /db-xref="GI:122087523" /db-xref="GOA:AlJI66" /db-xref="InterPro:IPR003695" /db-xref="UniProtKB/Swiss-Prot:AlJ I66" /translation="MMLSSTSLYAAIDLGSNSFH MLVREVAGSIQTLARIKRKVR LA AGLDTQNHLSQEAMERGQCLKF SERLQDIPLD QIRVVATATLRLASNAEELQ TAT EILGCP IQVISGEEEARLIYH GVAHTTGPEQRL VVDIGGGSTELVTGNGAQANIL VLS LPMGCVTLWERYFSDRNLAKD NFDRSESAAREML KPVAQRFRHEGWQICVGASGT VQA LQEIIMVAQGMDELITLAKLQ LQRAIQCGKLEE LEIPGLTLERALVFP SGLSILIAI FQELAIESMTLAGGALREG LVGYMLHLPVEQDIR

		SRTVRNIQRRYLLDTEQAKRVSKL ADNFLQVEKEWRLDSRCRELLQNACLIHEIGLS IDFKRAPQHAAYLIRNLDLPGFTP AQKLLLAALLQNSDITLDSLNLQONALPVDMAQ HLCRLRLAIIFSSRRRDDTLPAV RLRANGETLYVLLPHGWLQHPYRAEALEQESHW QSYVQWPLLEEEN"
misc-feature	complement(197992..198840)	/gene="gppA"  /locus-tag="YE0165" /inference="protein motif:PFAM:PF02541" /note="Pfam match to entry PF02541 Ppx-GppA, Ppx/GppA phosphatase family, score 427.6, E-value 7.2e-126"
gene	complement(198907..199983)	/gene="rhlB"  /locus-tag="YE0166" /note="synonym: mmrA"
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		score 94.6, E-value 1.3e-25"
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		motif:PFAM:PF00085"
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		E-value 8.7e-48"
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misc-feature	201724..201798	/gene="rho" /locus-tag="YE0168" /inference="protein motif:Prosites:PS00464" /note="PS00464 Ribosomal protein L22 signature." 
misc-feature	201826..201849	/gene="rho" /locus-tag="YE0168" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." 
gene	202836..203933	/gene="rfe" /locus-tag="YE0169" /note="synonym: b3784" 
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misc-feature join(202848..202907,  
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203139..203198,  
203226..203294,  
203313..203372,  
203385..203453,  
203472..203540,  
203568..203624,  
203715..203768,  
203796..203849)

misc-feature 203052..203543

gene 203969..205030

CDS 203969..205030

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IPLMDMIAIMYRRLRKGMSPFSPD  
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/note="11 probable transmembrane  
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/note="Pfam match to entry PF00953  
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DEIEGAWAARTQSMKAQVKRQEA  
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misc-feature	join(204059..204127, 204947..205006)	/locus-tag="YE0170" /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0170 by TMHMM2.0 at aa 31-53 and 327-346" /gene="rffe" /locus-tag="YE0171" /note="synonyms: nfrC, wecB" /gene="rffe" /locus-tag="YE0171" /codon-start=1 /transl-table=11 /product="UDP-N-acetylglucosamine 2-epimerase" /protein-id="CAL10310.1" /db-xref="GI:122087529" /db-xref="GOA:ALJI72" /db-xref="InterPro:IPR003331" /db-xref="UniProtKB/TrEMBL:ALJI72" /translation="MKVLTVFGTRPEAIKMAPLV HALAQDEAFESRVCVTAQHREMLD QVLRLEFIQPDYDLNIMKPGQGLTEITCRILEGL KPVLAEFKPDVILVHGDTITTLST SLAAFYHRIPVGHVEAGLRTGNLYSPWPPEANRQ LTGHLAMYHFAPTENSQNLLREM VPDNRIFVTGNTVIDALFWVRDRVMNNPQLRASL AERYPFIDTNKKMILVTGHRRESF GGGFERICSALAEIALKHPEVQVVPVHLNPNVS EPVNRILKGIDNIIILIDPQDYLPF VYLMNHAYLILTDSGGIQEEAPSLGKPVLMRDT TERPEAVDSGTVLLVGTININKIVD AVTRLITDETAYHQMTRAHPYGDGHACQRILEA LKNHQVTL" /gene="rffe" /locus-tag="YE0171" /inference="protein motif:PFAM:PF02350" /note="Pfam match to entry PF02350 Epimerase-2, UDP-N-acetylglucosamin e 2-epimerase, score 723.5, E-value 6e-215" /gene="rffd" /locus-tag="YE0172" /note="synonyms: b3787, wecC" /gene="rffd" /locus-tag="YE0172" /codon-start=1 /transl-table=11 /product="putative"
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gene	206237..207499	
CDS	206237..207499	

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sig-peptide	206237..206305	
misc-feature	206246..206827	
misc-feature	206849..207127	
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gene	208794..209675	<pre> /gene="rffH" </pre>
CDS	208794..209675	<pre> /locus-tag="YE0174" /gene="rffH" /locus-tag="YE0174" /codon-start=1 /transl-table=11 /product="glucose-1-phosphate thymidyltransferase" /protein-id="CAL10313.1" /db-xref="GI:122087532" /db-xref="GOA:AlJI75" /db-xref="InterPro:IPR005835" /db-xref="InterPro:IPR005907" /db-xref="UniProtKB/TrEMBL:AlJI75" /translation="MKGILAGSGTRLHPITRG VSKQLLPVYDKPMIYYPLSVLMLA GIRDILIIISTPEDLPSPQRLLGNGDEFGINLSYA AQSPDGLAQAFIIGEEFIGNEPC CLVLGDNIFYGQGFSPKLKAVAREHGATVFGYQ VMDPERFGVVEFDDDFRALSIEEK PTQPKSNWAVTGLYFYDNQVVDFAKKVKPSSRGE LEITSINQMYLDRGELTVELLGRG FAWLDTGTHDSLIEASTFVQTEKRQGFKIACLE EISWRNGWLDDDGVRRAATALAKT GYGKYLLDLLHARPRQY" </pre>
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gene	209764..210390	
CDS	209764..210390	
misc-feature	210115..210354	/gene="rffC" /locus-tag="YE0175" /inference="protein motif:PFAM:PF00583" /note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 73.5, E-value 2.9e-19"
gene	210392..211522	/gene="rffA" /locus-tag="YE0176" /note="synonyms: b3791, wecE"
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		TIMALAKKHNLFVVEDAAQGVWMT YKGKALGTIGHIGCFSPHETKNYTAGGEGGATLI NDPSLIDRAEIIREKGTNRSQFFR GQVDKYTWDRDIGSSYLSMDLQAAYLWGQLEAADQ INQRRLLAWHTYYDAFKPLADAGR IDLPVIFPNLAQNAHMFYIKLRDIEDRSKFISFL KEAEIMAVFHYIPLHACPAGEEFG RMDGEDRFTTKESERLVRLPIFYNLTDVNQSTVI NTVLSFFA" /gene="rffa" /locus-tag="YE0176" /inference="protein" motif:PFAM:PF01041" /note="Pfam match to entry PF01041 DegT-DnrJ-EryC1, DegT/DnrJ/EryC1/St rS aminotransferase family, score 291.1, E-value 9.2e-85"
misc-feature	210410..211507	
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gene	211524..212780	
CDS	211524..212780	
misc-feature	211530..212375	

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VRGWITLWMLAAAGVFGIVGMFWLALKRYGLDWN
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LLQNYDKIDFQGLAPIIRDYFVFIPISSLWPARP
LVLNTANYFTWDVLDNHSGLAISP
TLIGSLVVMGGVFLIPLGAIVVGLIHKWFDWLYE
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213996..214064,
214092..214151,
214212..214280,
214338..214406,
214425..214484,
214494..214553,
214557..214616,
214893..214961,
215022..215075,
215103..215171)

/locus-tag="YE0179"
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motif:TMHMM:2.0"
/note="11 probable transmembrane
helices predicted for YE0179 by
TMHMM2.0 at aa 6-25, 38-60, 70-89,
110-132,152-174, 181-200, 204-223,
225-244, 337-359, 380-397 and
407-429"
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and gamma 'Greek key' motif
signature."
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/note="PS00013 Prokaryotic
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misc-feature	215465..215980	
gene	216379..217770	
CDS	216379..217770	
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	216661..216729, 216757..216825, 216844..216912, 216955..217023, 217099..217167, 217195..217263, 217375..217443, 217456..217524, 217585..217653, 217663..217731)	/inference="protein motif:TMHMM:2.0" /note="12 probable transmembrane helices predicted for YE0181 by TMHMM2.0 at aa 21-38, 42-61, 95-117, 127-149, 156-178, 193-215, 241-263, 273-295, 333-355, 360-382, 403-425 and 429-451" /locus-tag="YE0181" /inference="protein motif:Prosites:PS00218" /note="PS00218 Amino acid permeases signature." /locus-tag="YE0181" /inference="protein motif:Prosites:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /locus-tag="YE0181" /inference="protein motif:Prosites:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /gene="tRNA-Arg (CCG)" /gene="tRNA-Arg (CCG)" /product="tRNA-Arg" /note="codon recognized: CGG" /gene="tRNA-His (GTG)" /gene="tRNA-His (GTG)" /product="tRNA-His" /note="codon recognized: CAC" /gene="tRNA-Leu (CAG)" /gene="tRNA-Leu (CAG)" /product="tRNA-Leu" /note="codon recognized: CUG" /gene="tRNA-Pro (TGG)" /gene="tRNA-Pro (TGG)" /product="tRNA-Pro" /note="codon recognized: CCA" /gene="hemY" /locus-tag="YE0184" /gene="hemY" /locus-tag="YE0184" /codon-start=1 /transl-table=11 /product="putative protoheme IX biogenesis protein" /protein-id="CAL10321.1"
misc-feature	216505..216597	
misc-feature	217249..217281	
misc-feature	217684..217716	
gene	217919..217995	
tRNA	217919..217995	
gene	218079..218154	
tRNA	218079..218154	
gene	218170..218256	
tRNA	218170..218256	
gene	218332..218408	
tRNA	218332..218408	
gene	complement(219361..2205 60)	
CDS	complement(219361..2205 60)	

		/db-xref="GI:122087540" /db-xref="GOA:AlJI83" /db-xref="InterPro:IPR005254" /db-xref="InterPro:IPR010817" /db-xref="InterPro:IPR011990" /db-xref="InterPro:IPR013026" /db-xref="InterPro:IPR013105" /db-xref="UniProtKB/TrEMBL:AlJI83" /translation="MLRVLLFLILTAGIVLGPMLAGHQGYVLIQTDNYNVETSVTGLVIMLVLVLVAFILVIEWILRRIFGTARTRGWFLGRKRLTRARKQTKAALIKLAEGDFKQVEKLLTRNADHAEQPMVNYLLAAEAAQQRGDEFRTNQYLERAAEVAADTDQLPVDITRVRIQLAQGHVHAARHGVDRLDQAPRHPEVLRRLAEQAYLRSGAYSSLLEILPAMSKVQVHTAEETIAALEQQAYIGMMNQMAEEGSDGLKRWKDKQSRKVRNEIPLQVALAEHLIECDSDVAQQIILDGLKROYDERLVLLIPRLKSGNPEPIEKSLRQHIKQHGAFTPLNSTLQQLMLKHGEWEKASEAFKAALAQRPDGYDYANLADALDKLHRPEDAAQARREGLLLTL RQNGESL"
sig-peptide	complement(220492..220560)	/gene="hemY" /locus-tag="YE0184" /note="Signal peptide predicted for YE0184 by SignalP 2.0 HMM (Signal peptide probability 0.919) with cleavage site probability 0.457 between residues 23 and 24"
misc-feature	complement(220072..220101)	/gene="hemY" /locus-tag="YE0184" /inference="protein motif:Prosites:PS00215" /note="PS00215 Mitochondrial energy transfer proteins signature."
misc-feature	complement(join(220375..220443, 220480..220548))	/gene="hemY" /locus-tag="YE0184" /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted for YE0184 by TMHMM2.0 at aa 5-27 and 40-62"
gene	complement(220563..221687)	/gene="hemX" /locus-tag="YE0185" /gene="hemX"
CDS	complement(220563..221687)	/locus-tag="YE0185" /codon-start=1 /transl-table=11 /product="putative uroporphyrin-III C-methyltransferase" /protein-id="CAL10322.1" /db-xref="GI:122087541" /db-xref="GOA:AlJI84" /db-xref="InterPro:IPR007470"

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ADFLVKMAGRKLWSDQDVTTAATL
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misc-feature complement(221517..2215
85) /gene="hemX"

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motif:TMHMM:2.0"
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TMHMM2.0 at aa 35-57"

gene complement(221720..2224
66) /gene="hemD"

CDS complement(221720..2224
66) /locus-tag="YE0186"
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synthase"
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GRELLGESLRERGATVTFCECYQR
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misc-feature complement(221735..2224
39) /gene="hemD"

/locus-tag="YE0186"
/inference="protein
motif:PFAM:PF02602"
/note="Pfam match to entry PF02602
HEM4, Uroporphyrinogen-III synthase
HemD, score 165.6, E-value
5.5e-47"

gene complement(222463..2224
04) /gene="hemC"

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CDS complement(222463..2224
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I86"
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DPRDAFVSINYAHLDELPAQSVGTSSSLRRQCQL
RERRPDLIIRDLRGNVGTIRLAKLD
KGEYHAILAVAGLKRLGLETRIRYAMPAAESLP
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L
DGDTLWLRALVGAPDGSEIIRGER
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PPL"
misc-feature      complement(222511..222732) /gene="hemC"
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/inference="protein
motif:PFAM:PF03900"
/note="Pfam match to entry PF03900
Porphobil-deamC, Porphobilinogen
deaminase, C-terminal domain,
score 117.1, E-value 2.1e-32"
misc-feature      complement(222664..222714) /gene="hemC"
/locus-tag="YE0187"
/inference="protein
motif:Prosite:PS00533"
/note="PS00533 Porphobilinogen
deaminase cofactor-binding site."
misc-feature      complement(222754..222392) /gene="hemC"
/locus-tag="YE0187"
/inference="protein
motif:PFAM:PF01379"
/note="Pfam match to entry PF01379
Porphobil-deam, Porphobilinogen
deaminase, dipyrromethane cofactor
binding domain, score 471.6,
E-value 4.3e-139"
gene              223809..226355 /gene="cyaA"
/locus-tag="YE0189"
/note="synonym: cya"
CDS               223809..226355 /gene="cyaA"
/locus-tag="YE0189"
/codon-start=1
/transl-table=11
/product="adenylate cyclase"
/protein-id="CAL10325.1"
/db-xref="GI:122087544"
/db-xref="GOA:AlJI87"
/db-xref="InterPro:IPR000274"
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STSSIGQCHTSLDLIWWCHQAWLDAEERNLQKK
CSLLEKWAASMGVEVSFFLIDENR
FRHNAGSLGGEDCGSTQHILLLDEFYRSVRLA
GKRILWNMVPVEEENNYDDYVLSL
YAQVLTPTNEWLDLGGSLTSLSAEYFGASLWQLY
KSIDSPYKAVLKTVLLEAYSWEYP
NSQLLAMEIKQRLHAGEIVAFGLDAYCMMLDRVT
RYLTQINDTTRLNLVRRCFYLKVC
EKLRTPTASVGWRREILSQLVSEWGSDES LAVL
DNRANWKIERVREAHNELLDAMMQ
SYRNLIRFARRNNLSVSASPQDIGVLRKLYAAF
EALPGKVTILVNPQISPDLSSEHLT
FIHVPAGRANRPGWYLYNQAPSMETIVSHQPLEY
NRYLNKLVSWAYFNGLLTSKTHLH
IKSANLCDTVKLQELVTDISHHFPRLRPAPTPKA
LYSPCEIRHLAIIVNLEHDP TAAF
RNQVVHDFRKLDFVSFGEQQQCLVGSIDLLYRN
SWNEVRTLHFSGEQAVLEALKITIL
GKMHQDAAPPESDVDFCYSOHLRGLIRTRIQQVLV
SECIELRLSSTRQEPGRFKAVRVA
GQTWGLFFERLSVSQKLENAIEFYGAISNNKLH
GLSIQVETDQIHLFPVVDGFASEG
IIQFFEGTADKEGFNIYILDETNRVEVYHHCEG
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IADKETSAPAQQFQLH"
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/locus-tag="YE0189"
/inference="protein
motif:PFAM:PF01295"
/note="Pfam match to entry PF01295
Adenylate-cyclase, Adenylate cyclase,
class-I, score 2160.8, E-value 0"
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/gene="cyaA"
/locus-tag="YE0189"
/inference="protein
motif:Prosites:PS00343"
/note="PS00343 Gram-positive cocci
surface proteins 'anchoring'
hexapeptide."
/misc-feature 224532..224567
/gene="cyaA"
/locus-tag="YE0189"
/inference="protein
motif:Prosites:PS01092"
/note="PS01092 Adenylate cyclases
class-I signature 1."
/misc-feature 225600..225644
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class-I signature 2."
gene complement(226526..2268
46)
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CDS complement(226526..2268
46)
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misc-feature	complement(226529..226846)	<pre> /locus-tag="YE0190" /inference="protein motif:PFAM:PF01491" /notes="Pfam match to entry PF01491 Frataxin-Cyay,Frataxin-like domain, score 242.5, E-value 3.8e-70" </pre>
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sig-peptide	226960..227028	<pre> /locus-tag="YE0191" /notes="Signal peptide predicted for YE0191 by SignalP 2.0 HMM (Signal peptide probability 0.994) with cleavage site probability 0.378 between residues 23 and 24" </pre>
misc-feature	226972..227040	<pre> /locus-tag="YE0191" /inference="protein motif:TMHMM:2.0" /notes="1 probable transmembrane helix predicted for YE0191 by TMHMM2.0 at aa 5-27" </pre>
misc-feature	226987..227019	<pre> /locus-tag="YE0191" /inference="protein motif:Prosite:PS00013" /notes="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." </pre>
gene	227252..228076	<pre> /gene="dapF" </pre>
CDS	227252..228076	<pre> /locus-tag="YE0192" /gene="dapF" /locus-tag="YE0192" /codon-start=1 /transl-table=11 /product="diaminopimelate epimerase" /protein-id="CAL10328.1" /db-xref="GI:122087547" /db-xref="GOA:A1J190" /db-xref="InterPro:IPR001653" </pre>

		/db-xref="UniProtKB/Swiss-Prot:AlJ190" /translation="MQFSKMHLGNDFMVVDVAVTQNVYFSPELIRRLADRHGTGVGFDQMLVVPEPPYDPELDFHYRIFNADGSEVSCGNGARCFARFVRLKGLTKNRDISVSTQTGRMILSVTEDELVCVNMGEPNFEFQSVPFRAAKAEKTIYLRAAEHTVLCGVVSMGNPHCMQVQDDVSVANVALLGPVLESHERFFPERANIGFMQVVSREHIRLRVYERGAGETQACGSGACAAVAVGIQEELLGEEVHVLPGGSLHISWKGPGHPLYMTGPATHVYDGFIDL"
misc-feature	227258..227623	/gene="dapF" /locus-tag="YE0192" /inference="protein motif:PFAM:PF01678" /note="Pfam match to entry PF01678 DAP-epimerase, Diaminopimelate epimerase, score 179.5, E-value 3.5e-51"
misc-feature	227441..227485	/gene="dapF" /locus-tag="YE0192" /inference="protein motif:Prosite:PS01326" /note="PS01326 Diaminopimelate epimerase signature."
misc-feature	227702..228052	/gene="dapF" /locus-tag="YE0192" /inference="protein motif:PFAM:PF01678" /note="Pfam match to entry PF01678 DAP-epimerase, Diaminopimelate epimerase, score 182.3, E-value 5.2e-52"
gene	228170..228874	
CDS	228170..228874	/locus-tag="YE0193" /locus-tag="YE0193" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10329.1" /db-xref="GI:122087548" /db-xref="InterPro:IPR007435" /db-xref="UniProtKB/TrEMBL:AlJI91" /translation="MKSSEEQALAGIELDDDAVMQYLLQNPDDFFIRNARLVEQMHPHPVRGTVSLVWQLGRQRNIGQLLEEITLLMEQA GLNEVLFNRLQLQGNLAAASSLQDMLNRLQRWARDFLAGANVRLFTDRWQIGAPSD FTHLGLSRHAFEPMRIQRLGNARH YLGSGLNPPELLLLPQAKQVGSVALSLLGKEGDL GVIVFSSRDIQHYQQGMGTVMNLQ LSMLLPSLLERWIEPV"
gene	228871..229782	/gene="xerC"
CDS	228871..229782	/locus-tag="YE0194" /gene="xerC" /locus-tag="YE0194" /codon-start=1 /transl-table=11 /product="putative integrase/recombinase" /protein-id="CAL10330.1"



		/db-xref="GI:122087549" /db-xref="GOA:AlJI92" /db-xref="InterPro:IPR002104" /db-xref="InterPro:IPR004107" /db-xref="InterPro:IPR011931" /db-xref="InterPro:IPR013762" /db-xref="UniProtKB/TrEMBL:AlJI92" /translation="MTDFSTSLAPQVEAFLRYLK VERQLSPLTITSYRRQLQALMEMG EQMGLAHWQTLDAQVRSLSRSKRAGLHSSSLA LRLSALRSFLNWLVSQGVQLQANPA KGVSTPRSGRHLPKNIDVDEVAKLDDIDLNDPLA VRDRAMLEVMYGAGLRLSELVGMN CKHVDLASGEVWVMGKSGKRVPIGKTAVKWLD HWLELRELFEPQDDAIFLANTGKR ISARNVQKRFAEWGKQGVSSSHIHPHKLHRSFAT HMLESSGDLRAVQELLGHANLTTT QIYTHLDFQHLATVYDAAHPRAKRGKS" /gene="xerC" /locus-tag="YE0194" /inference="protein motif:PFAM:PF02899" /notes="Pfam match to entry PF02899 Phage-integr-N, Phage integrase, N-terminal SAM-like domain, score 104.1, E-value 1.8e-28"
misc-feature	228898..229158	
		/gene="xerC" /locus-tag="YE0194" /inference="protein motif:PFAM:PF00589" /notes="Pfam match to entry PF00589 Phage-integrase, Phage integrase family, score 208.0, E-value 9.4e-60"
misc-feature	229222..229737	
		/locus-tag="YE0195" /locus-tag="YE0195" /codon-start=1 /transl-table=11 /product="putative haloacid dehalogenase-like hydrolase" /protein-id="CAL10331.1" /db-xref="GI:122087550" /db-xref="GOA:AlJI93" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006439" /db-xref="UniProtKB/TrEMBL:AlJI93" /translation="MHFYRPLERISAITFDLDDT LYDNRPVISRTEQESVAFLOQYHP NLAQLQAADLHFRFRRELLEQDPDIYHDVTQWRWH AIELGLMRHGLSKSEAQCGADAAM ENFALWRSRIYVPPATHDTLSALAEHYPLVAITN GNADPKACGLDNYFQFVLRSGPHG RAKPFPRDMYHKAANHLDIPLKNILHVGGDLTTDV AGSLRCGMQACWVNDROQSLMTAS DSRLPHIEISQLASLTALL" /locus-tag="YE0195" /inference="protein motif:PFAM:PF00702" /notes="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 92.0, E-value 7.7e-25"
gene	229782..230498	
CDS	229782..230498	
misc-feature	229809..230411	

gene	230599..232761	/gene="uvrD" /locus-tag="YE0196" /note="synonyms: mutU, pdeB, rad, recl"
CDS	230599..232761	/gene="uvrD" /locus-tag="YE0196" /codon-start=1 /transl-table=11 /product="DNA helicase II" /protein-id="CAL10332.1" /db-xref="GI:122087551" /db-xref="GOA:AlJ194" /db-xref="InterPro:IPR000212" /db-xref="InterPro:IPR005753" /db-xref="InterPro:IPR014016" /db-xref="InterPro:IPR014017" /db-xref="UniProtKB/TrEMBL:AlJ194" /translation="MDVSDLLDLSLNEKQREAVAA PRCNLLVLGAGSGKTRVLVHRIA WLLSVENASPYSIIAVFTTNKAAAEMRHRIEHLI GTSQGGMWIGTFHGLAHRLLRAHH MDANLPQDFQILDSDQLRLKKLVKALNLDEKQ WPPRQAMWYINGKKDEGLRPQHIE SYGNPVEATWLRIFYAQEACDRAGLVDFAEALL RAHELWLNKPHILNHYRERFTNIL VDEFQDTNNIQAWIRLLAGDRSNVMIVGDDDDQS IYGWRGAQVENIQRFLKDFPGAET IRLEQNYRSTSNILTAANTLIANNDRMGKNLWT DGAQGEPISLYCAFNEDEARFVV NRIKAWQDNGGALNDCAILYRSNAQSRVLEEALL QTAMPYRIYGGQRFERQEIKDAL AYLRLISNRNDAAFERVVNTPTRGIGDRTLVDVI RQTARDRLTLWQSTRAMLOQEVK AGRAASALQRFVELVDSLAEHETADMLPHVQTDVR IRDSGLWSMYEQEKGEGKQARVEN LEELVNATRQYSYQDEDDQLMPLQAFLSHALEA GEGQADAYQDAVQLMTIHSAGLE FPQVFIWGMEEGMFPQSMSLDEGGRLEEERRLAY VGVTIRAMQKLTLCYAESRRLYGKE VNHRPSPRFIGELPQECVEEVLRLATVSRPVNHRH MGTPMNENDSGFSLGQVRVHPKFG EGTIVNLESGEHSRLQVAFPEGIKWLVAAYAR LEAV"
misc-feature	230626..232068	/gene="uvrD" /locus-tag="YE0196" /inference="protein motif:PFAM:PF00580" /note="Pfam match to entry PF00580 UvrD-helicase, UvrD/REP helicase, score 747.8, E-value 2.9e-222"
misc-feature	230683..230706	/gene="uvrD" /locus-tag="YE0196" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	232705..232734	/gene="uvrD" /locus-tag="YE0196" /inference="protein motif:Prosite:PS00215" /note="PS00215 Mitochondrial energy transfer proteins"

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signature."
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58)
CDS       complement(233186..2337 /locus-tag="YE0197"
58)
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          /db-xref="GOA:AlJI95"
          /db-xref="InterPro:IPR001647"
          /db-xref="UniProtKB/TrEMBL:AlJI95"
          /translation="MSMYEQGAFFPSIIEVANAAQ
          LSRATAYRYFPTQSALVSAMVDES
          LGPILAWQPTQPDAGORIAELLSFAYPRMLQHEG
          VLRaalHLSLQQWADNRSNPNNEE
          KLIRGNRRRLKLAVEPLEGKLTPEALQRVIHAF
          SLIYGSEVMVLKDIWHLDDAGIQ
          DVTQWMGKAILLQAEETDAKQAAQDESRMNK"

misc-feature complement(233639..2337 /locus-tag="YE0197"
19)
          /inference="protein
          motif:PFAM:PF00440"
          /note="Pfam match to entry PF00440
          tetR, Bacterial regulatory
          proteins, tetR family, score 22.2,
          E-value 3.4e-05"

misc-feature complement(233666..2337 /locus-tag="YE0197"
31)
          /note="Predicted helix-turn-helix
          motif with score 1464.000, SD 4.17
          at aa 10-31, sequence
          PSIIEVANAAQLSRATAYRYFP"

gene      234065..235297
CDS       234065..235297
          /locus-tag="YE0198"
          /locus-tag="YE0198"
          /codon-start=1
          /transl-table=11
          /product="conserved hypothetical
          protein"
          /protein-id="CAL10334.1"
          /db-xref="GI:122087553"
          /db-xref="InterPro:IPR003006"
          /db-xref="InterPro:IPR008322"
          /db-xref="InterPro:IPR010647"
          /db-xref="UniProtKB/TrEMBL:AlJI96"
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          GTALITPAMQSLPIGIPKLMVSTMASGDVSGYIG
          ASDIAMMYSVTDIAGLNIRISRRVL
          SNAHQIAGAVYFAKEVFAQAEALATDDKPALGLT
          MFGVTTPCIQAVSAALSAEYDCLV
          FHATGSGGKAMEKLAESGLLAGALDLTTTEVCDL
          LFDGVLACGPERFDAIAHSQIPYV
          GSCGALDMVNFGPSATIPVKYADRLFYEHNAQVT
          LMRTTKQENIEMARWIGEKLNRC
          GEVRFILPQGGFSALDAPGPWFDEKALQAFIHT
          LQETVIQTDKRLVHYPFNINDFQ
          FAQAAVENFKEIAKTPSH"

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misc-feature	234704..234724	/locus-tag="YE0198" /inference="protein motif:Prosite:PS00290" /note="PS00290 Immunoglobulins and major histocompatibility complex proteins signature." /locus-tag="YE0199" /locus-tag="YE0199" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10335.1" /db-xref="GI:122087554" /db-xref="InterPro:IPR009215" /db-xref="UniProtKB/TrEMBL:AJJI97" /translation="MPKFQQRQAILAKFREMIARR EPIIGGGAGTGLSAKCEEAGGIDL IVIYNSGRYRMAGRGS LAGLLAYGNANEIVVDMA KEVLPVVKHTPVLAVGVNGTDPFCQ FDQFLDQLKALGFSGVQNFPTVGLIDGNFRANLE ETGMGYGLEVDMIRLAHEKDLLTT PYVFS AEDAVAMTQAGADIIVPHMGLTTGGNIGA DTALKLADCVPLINKWAAA KAVR EDVIVLCHGGPISTFPQDAQYIMDNCFQC DGFYGA SSMERLPTEIALTDITTKQFKNIKR"
gene	235324..236154	
CDS	235324..236154	
gene	236657..237607	/gene="corA" /locus-tag="YE0200" /gene="corA" /locus-tag="YE0200" /codon-start=1 /transl-table=11 /product="magnesium and cobalt transport protein" /protein-id="CAL10336.1" /db-xref="GI:122087555" /db-xref="GOA:AJJI98" /db-xref="InterPro:IPR002523" /db-xref="InterPro:IPR004488" /db-xref="UniProtKB/TrEMBL:AJJI98" /translation="MLS AFKLNNRLSRLELDES DDLITSLWVDLVEPEGERERVQN ELGQSLATRP ELDDIEASARFFEDEDGLHIHSFF YYEDAEDHAGNSTVAFTIR DGRLY TLRERELPAFRLYRMARNQTLVDGNAYELLLDL FETKIEQLADEIENIYSDLEALS R VIMEGQQGDEYDAALSTLAEQEDIGWKVRLCLMD TQRALNFLVRKARLPSGQLEQARE VLRDIESLLPHNESLFQKVNFLMQAAMGFINIEQ NRIIKIFSVSVVFLPPTLVASSY GMNFEFMPELRWSFGYPAAIGLMIAGLAPLYLYF KRKNWL"
CDS	236657..237607	
misc-feature	236717..237604	/gene="corA" /locus-tag="YE0200" /inference="protein motif:PFAM:PF01544" /note="Pfam match to entry PF01544 CorA, CorA-like Mg <sup>2+</sup> transporter protein, score 394.8, E-value 5.5e-116"
misc-feature	join(237419..237475, 237518..237586)	/gene="corA"

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        /locus-tag="YE0200"
        /inference="protein
        motif:TMHMM:2.0"
        /note="2 probable transmembrane
        helices predicted for YE0200 by
        TMHMM2.0 at aa 255-273 and
        288-310"
gene      complement(237795..2386
85)       /gene="rard"

        /locus-tag="YE0201"
        /gene="rard"

        /locus-tag="YE0201"
        /codon-start=1
        /transl-table=11
        /product="putative membrane
        protein"
        /protein-id="CAL10337.1"
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        /db-xref="InterPro:IPR000620"
        /db-xref="InterPro:IPR004626"
        /db-xref="UniProtKB/TrEMBL:AJI99"
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        WSFFFMILLTVSRNWPQVRSIAIKNRKRLLLAV
        TAVLIASNWLLFIKAVNNHMHLEA
        SLGYFINPLNVNLFGLMFLGERFRMRQWVAVALA
        FGGVLQLWQFGSLFVIGLGLAIT
        FALYGLIRKKLGIDAQTGMLVETMWLLPIAAVYL
        FFIADSPSTSHMGANAWSLNVLLAA
        AGVITTIPLLFFTAAATRLRLSTLGFQYLGPTL
        MFILAVTFYGETIIGNDKMVFVFI
        WAALLFTLDALYTQKRLRG"
misc-feature complement(join(237819.
.237878,237891..237959,
237996..238064,
238092..238151,
238185..238238,
238251..238304,
238323..238391,
238401..238469,
238506..238574,
238602..238661)) /gene="rard"

        /locus-tag="YE0201"
        /inference="protein
        motif:TMHMM:2.0"
        /note="10 probable transmembrane
        helices predicted for YE0201 by
        TMHMM2.0 at aa 9-28, 38-60, 73-95,
        99-121,128-145, 150-167, 179-198,
        208-230, 243-265 and 270-289"
misc-feature complement(237831..2382
11)       /gene="rard"

        /locus-tag="YE0201"
        /inference="protein
        motif:PFAM:PF00892"
        /note="Pfam match to entry PF00892
        DUF6, Integral membrane protein
        DUF6, score 21.2, E-value 0.0016"
misc-feature complement(238251..2386
34)       /gene="rard"

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/locus-tag="YE0201"
/inference="protein
motif:PFAM:PF00892"
/note="Pfam match to entry PF00892
DUF6, Integral membrane protein
DUF6, score 53.9, E-value 2.3e-13"
gene      complement(238765..2392 /locus-tag="YE0202"
35)
CDS       complement(238765..2392 /locus-tag="YE0202"
35)
/locus-tag="YE0202"
/codon-start=1
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/db-xref="InterPro:IPR006683"
/db-xref="UniProtKB/TREMBL:ALJIA0"
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YHMPFNRELGLKLTREQDFAEIT
FDNNDKLVGNIAQRILHGGVIAAVLDVAAGLVCV
GNSLVRHEPLIQEQLOMKLAKMGT
IDLRVLDYLRPGRGEHFIASSCILRSGNKVSVARV
ELHNENQMHIASATATYLVG"
misc-feature complement(238765..2391 /locus-tag="YE0202"
81)
/inference="protein
motif:PFAM:PF02584"
/note="Pfam match to entry PF02584
DUF157, Uncharacterized protein
PaaI, COG2050, score -2.7, E-value
0.00013"
gene      239416..240294
/locus-tag="YE0203"
CDS       239416..240294
/locus-tag="YE0203"
/codon-start=1
/transl-table=11
/product="phospholipase A"
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/db-xref="GI:122087558"
/db-xref="GOA:ALJIA1"
/db-xref="InterPro:IPR003187"
/db-xref="UniProtKB/TREMBL:ALJIA1"
/translation="MGRFWQILIALLLVPTLVQA
EEATVEKIHDAPTVRGSIIAAMLQ
DHDNPFLLYPYETNYLLTYTSDINKDAISSYDW
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GDNSLLGASYTQRSWWQASNKDESSPFRETNYEP
QLFLAWATDYELAGWTFREVEFGY
NHQSNKGADPTSRSDRVYTRMAQRGNLEIDLK
PWYRLPESDSKDDNPDINKYMGYY
RLKVGVALGESVFLDGRYNWNTGYGAEMGWSY
PITKHVRFTYQVFSGYGESMIDYN
FRQTRVGVGIMLNDVL"
sig-peptide 239416..239475
/locus-tag="YE0203"
/note="Signal peptide predicted
for YE0203 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability

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misc-feature	239479..240282	0.998 between residues 20 and 21" /gene="pIdA" /locus-tag="YE0203" /inference="protein motif:PFAM:PF02253" /note="Pfam match to entry PF02253 PLA1, Phospholipase A1, score 651.6, E-value 2.7e-193"
gene	240371..242221	/gene="recQ" /locus-tag="YE0204" 
CDS	240371..242221	/gene="recQ" /locus-tag="YE0204" /codon-start=1 /transl-table=11 /product="ATP-dependent DNA helicase" /protein-id="CAL10340.1" /db-xref="GI:122087559" /db-xref="GOA:AlJIA2" /db-xref="InterPro:IPR001650" /db-xref="InterPro:IPR002121" /db-xref="InterPro:IPR004589" /db-xref="InterPro:IPR006293" /db-xref="InterPro:IPR011545" /db-xref="InterPro:IPR014001" /db-xref="InterPro:IPR014021" /db-xref="UniProtKB/TrEMBL:AlJIA2" /translation="MSTAAVINRELLAEQVLRDT FGYQQFRPQQEIIINATLSGQDCCL VVMPTGGGKSLCYQIPALVTDGLTLVVSPSLISM KDQVDQLLAYGVGAGCLNSQTRE QQLAVMDGCRSGQIKLLYIAPERLVMESFLDQLH QWRPALLAVDEAHCISQWGHDFRP EYRALGQLKQRFNLPVIALTATADEATRGDIVR LLNLDDQLIQVSSDFRPNIRYTLV EKFKPLDQLWRFVQDQRGKSGIYICNSRAKVEDT TARLQSRGLSVAAYHAGLDNERRA QVQEAQFRDDQLQVVVATVAFGMGINKPNVRFVHV FDIPRTIESYYQETGRAGRDLGFA EAMLLYDPADMAWLRRCLLEEKPAQAQDIERHKL NAMGAFAEAQTCRLVLLNLYFEGEG KQQSCGNCDICLDPKRYDGLADAQKALSCVYRV GQRFGLGYIVEVLRGANNQRIEF DHDKLSVYGIGREQSHEHWSVSLRQLIHLGLLSQ NIAMFSAQLTEAARPVLRALFL QLAVPRIQSLKVRSSANQKSYGGNYDRKLFALR KLKRSIADEGNIPYVVFNDATLL EMAEQMFITASELLSVNGVGQRKLERFAGPFMAM IRDHVDNIHVDNNVDD"
misc-feature	240416..241024	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00270" /note="Pfam match to entry PF00270 DEAD, DEAD/DEAH box helicase, score 152.1, E-value 6.2e-43"
misc-feature	240620..240652	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:Prosite:PS00013" /note="PS00013 Prokaryotic membrane lipoprotein lipid

misc-feature	241148..241363	attachment site." /gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00271" /note="Pfam match to entry PF00271 helicase-C, Helicase conserved C-terminal domain, score 103.7, E-value 2.4e-28"
misc-feature	241961..242203	/gene="recQ" /locus-tag="YE0204" /inference="protein motif:PFAM:PF00570" /note="Pfam match to entry PF00570 HRDC, HRDC domain ,score 116.3, E-value 3.7e-32"
gene	242284..242904	/gene="rhtC" /locus-tag="YE0205"
CDS	242284..242904	/gene="rhtC" /locus-tag="YE0205" /codon-start=1 /transl-table=11 /product="threonine efflux protein" /protein-id="CAL10341.1" /db-xref="GI:122087560" /db-xref="GOA:AlJIA3" /db-xref="InterPro:IPR001123" /db-xref="InterPro:IPR004778" /db-xref="UniProtKB/TrEMBL:AlJIA3" /translation="MLMLFLTVALVHLVALMSPG PDFFVVSQTAAASRSRREAMMGVTG ISLGIVVWAGVALMGLNLILHKMAWLHQIIMVGG GLYLCWGMWQLLSARSKRDTSEA EVQVALPARGRTFLRGFLTNLNSNPKAVIYFGSVF SLFVGDNVTAGARWGLFVLIVAET FVWFISIVACVFALPVMRRRGYQRLSKWIDGLAGVL FAGFGIHLILSR" /gene="rhtC" /locus-tag="YE0205" /note="Signal peptide predicted for YE0205 by SignalP 2.0 HMM (Signal peptide probability 0.709) with cleavage site probability 0.229 between residues 30 and 31" /gene="rhtC"
sig-peptide	242284..242373	
misc-feature	join(242293..242361, 242407..242475, 242485..242553, 242638..242706, 242734..242802, 242839..242898)	/locus-tag="YE0205" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0205 by TMHMM2.0 at aa 4-26, 42-64, 68-90, 119-141,151-173 and 186-205"
misc-feature	242485..242811	/gene="rhtC" /locus-tag="YE0205" /inference="protein motif:PFAM:PF01810"



		/note="Pfam match to entry PF01810 LysE, LysE type translocator, score 115.7, E-value 5.8e-32"
gene	complement(242954..243574)	/gene="rhtB"
CDS	complement(242954..243574)	/locus-tag="YE0206" /gene="rhtB"  /locus-tag="YE0206" /codon-start=1 /transl-table=11 /product="putative homoserine/homoserine lactone efflux protein" /protein-id="CAL10342.1" /db-xref="GI:122087561" /db-xref="GOA:AlJIA4" /db-xref="InterPro:IPR001123" /db-xref="InterPro:IPR004778" /db-xref="UniProtKB/TrEMBL:AlJIA4" /translation="MTLDWNLTYLLTTLILSLSP GSGAINTMSTAISHGTRGVASIC GLQLGLAVHIVLVGVGLGALISQSLAFELKWL GAAYLIWLGIQWRAAGALDLHAL ANSMPRRKLFKRAVEVNLTNPKSIVFLAALFPQF VLPHPQVQAQYLILGSTSVIVDII VMMGIATLATRIAGWIKSPQPMKLLNIRIFGGLFM LVGALLATARKV"
sig-peptide	complement(243503..243574)	/gene="rhtB"  /locus-tag="YE0206" /note="Signal peptide predicted for YE0206 by SignalP 2.0 HMM (Signal peptide probability 0.803) with cleavage site probability 0.440 between residues 24 and 25"
misc-feature	complement(join(242966..243025,243050..243118,243161..243229,243317..243385,243395..243463,243500..243562))	/gene="rhtB"
misc-feature	complement(243056..243364)	/locus-tag="YE0206" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0206 by TMHMM2.0 at aa 5-25, 38-60, 64-86, 116-138, 153-175 and 184-203"
gene	243778..244833	/gene="pIdB"
CDS	243778..244833	/locus-tag="YE0207" /gene="pIdB" /locus-tag="YE0207" /codon-start=1

		/transl-table=11 /product="putative lysophospholipase" /protein-id="CAL10343.1" /db-xref="GI:122087562" /db-xref="InterPro:IPR000073" /db-xref="UniProtKB/TrEMBL:A1JIA5" /translation="MPLDNHMNNWLTREEQFAAF VNGPLLDWFQQRDEDEFMGVDNIP IRYVRFCSPQHTRVVVVVPGRIESYVKYPEVAYD LFQQGYDVIVLDRHGQGRSGRILD DRNRGHVVKFDDYIEDFAQLVQREITGSHYQORF ALAHSMGGAII TRYLAAREPTVFNA VALCAPMFGIHLPMPGWLAHRIVDWTEKHQKLRD YYAIGTGQWRPLPYVNNMLTHSRE RYRRYLQRYADSPFIRVGGPTYHWVRESLLVGEQ IIAQADKITTVPVLLQASEDRVVH NPAHNFTQAMTLAGHPCEGEQFKLIKARHEIL FERDTLRAEALSAILRFFAQHHSS LQHKKPVGPQSDTTRG" /gene="pldB" /locus-tag="YE0207" /inference="protein motif:PFAM:PF00561" /note="Pfam match to entry PF00561 abhydrolase, alpha/beta hydrolase fold, score 94.9, E-value 1e-25"
misc-feature	244027..244752	
gene	244845..245654	
CDS	244845..245654	/locus-tag="YE0208" /locus-tag="YE0208" /codon-start=1 /transl-table=11 /product="putative haloacid dehalogenase-like hydrolase" /protein-id="CAL10344.1" /db-xref="GI:122087563" /db-xref="GOA:A1JIA6" /db-xref="InterPro:IPR000150" /db-xref="InterPro:IPR006379" /db-xref="InterPro:IPR013200" /db-xref="UniProtKB/TrEMBL:A1JIA6" /translation="MYHVVASDLDGTLSPDHIL TPYTKETLKLTLQRDVHVFATGR HHIDVAQIRDNLLEISAFMITSNGARVHNTAGELI FSHNLDADIARDLYNIEHHNPDIL TNVYLNDWEYMNRESPAQEEFFRESVFKYQVFEP ALLPTDGVCKVYFTCDHDKLLIL EEAINARWGDVRVNVSFSPFTCLEVMGGGVSKGHA LEQVAKIIGYSLKECIAFGDGMND LEMLSMSGKGCIMRDAHQRCLKDMLPNLEVIGSNA DDVAPHYLRKMFSGSK" /locus-tag="YE0208" /inference="protein motif:PFAM:PF00702" /note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 31.2, E-value 1.6e-06"
misc-feature	244848..245549	
misc-feature	244854..244889	/locus-tag="YE0208" /inference="protein motif:Prosites:PS01228" /note="PS01228 Hypothetical cof family signature 1."

gene complement(245866..2468 /gene="glpQ"  
64)  
/locus-tag="YE0209"

CDS complement(245866..2468 /gene="glpQ"  
64)  
/locus-tag="YE0209"  
/codon-start=1  
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/protein-id="CAL10345.1"  
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/db-xref="GOA:AlJIA7"  
/db-xref="InterPro:IPR004129"  
/db-xref="UniProtKB/TrEMBL:AlJIA7"  
/translation="MVIHRGASGYLPEHSLPAK  
AMAYAQADYLEQDLVMTKDNELV  
VLHDHYLDRVTDVAERFPDRARDGRYYAIDFTL  
PEIKSLKFTGEGFDIDKEGKKVQSY  
PGRFPMGKADFRVHTFQEEIEFVQGLNHSTGKNI  
GIYPEIKAPWFHKQEGKDISTKVL  
EVLKQYGYTTKADKVYLQCFDANELKRIKNELEP  
KMGMLNLKLVQLVAYTDWNETYEQK  
PDGKWNYSYDWMFKPGAMQVAQYADGIGPDYH  
MLVVTSTSPNNIKLTNMVKEAHAN  
NMVHPFTIRADKLPKYATDVNQLFDIIYNQAGV  
DGVFTDFPDKGQVFLKQKGQHQ"

misc-feature complement(245899..2468 /gene="glpQ"  
52)  
/locus-tag="YE0209"  
/inference="protein  
motif:PFAM:PF03009"  
/note="Pfam match to entry PF03009  
GDPD, Glycerophosphoryl diester  
phosphodiesterase family, score  
317.6, E-value 9.4e-93"

gene complement(247088..2484 /gene="glpT"  
52)  
/locus-tag="YE0210"

CDS complement(247088..2484 /gene="glpT"  
52)  
/locus-tag="YE0210"  
/inference="similar to  
sequence:INSDC:AE008802"  
/inference="similar to  
sequence:UniProtKB:P08194"  
/note="Highly similar to  
Escherichia coli  
glycerol-3-phosphate transporter  
glpT or b2240 SWALL:GLPT-ECOLI  
(SWALL:P08194) (452 aa) fasta  
scores: E(): 2.3e-165, 91.29 38d  
in 448 aa and to Salmonella  
typhimurium MFS family,  
Sn-glycerol-3-phosphate transport  
protein GlpT or stm2283  
SWALL:Q8ZNG6 (EMBL:AE008802) (452  
aa) fasta scores: E(): 2.8e-167,  
92.58 38d in 445 aa"  
/codon-start=1  
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transporter"
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/db-xref="GOA:AlJIA8"
/db-xref="InterPro:IPR000849"
/db-xref="InterPro:IPR005267"
/db-xref="InterPro:IPR007114"
/db-xref="InterPro:IPR011701"
/db-xref="UniProtKB/TrEMBL:AlJIA8"
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RKNFTLAMPYLIEQGFSGDGLGFALSGISIAYGF
SKFIMGSVSDRSNPRVFLSAGLIL
AAAVMLFMGFVPWATSSIAVMFVLLFLCGWFQGM
GWPPCGRTMVHWWSKKERGSIVSV
WNCANHNVGGGLPFLFLLGMAWFNDWKAALYMPA
FGAILVALIVFGLMRDIPQSVGLP
PIEEYKNDYDDYSEEAEEELTAKQIFMQYILPN
KLLWYIAIANVFVYLLRYGILDWS
PTYLKEVKHFALDKSSWAYFLYEYAGIPGTLCCG
WMSDKVFEKGNRGATGVFFMTLVTI
ATIVYWLNPVGNPFGIDMACMITIGFLIYGPVMLI
GLHALELAPKKAAGTAAGFTGLFG
YLGGSVAASAIVGYITVDYFGWDGGFMVMIGGSIL
AVLLLIIVVMFSEKKHHEELARQAE MDKK"
misc-feature      complement(247106..2483
68)                /gene="glpT"
                    /locus-tag="YE0210"
                    /inference="protein
motif:PFAM:PF00083"
                    /note="Pfam match to entry PF00083
sugar-tr, Sugar (and other)
transporter, score -109.0, E-value
0.00052"
misc-feature      complement(join(247142.
.247201,247229..247297,
247334..247402,
247430..247498,
247517..247576,
247634..247693,
247832..247891,
247904..247972,
248027..248095,
248105..248173,
248192..248260,
248318..248377))
                    /gene="glpT"
                    /locus-tag="YE0210"
                    /inference="protein
motif:TMHMM:2.0"
                    /note="12 probable transmembrane
helices predicted for YE0210 by
TMHMM2.0 at aa 26-45, 65-87,
94-116, 120-142,161-183, 188-207,
254-273, 293-312, 319-341,
351-373,386-408 and 418-437"
misc-feature      complement(247946..2479
96)                /gene="glpT"
                    /locus-tag="YE0210"
                    /inference="protein
motif:Prosites:PS00942"
                    /note="PS00942 glpT family of
transporters signature."

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gene	248974..250629	/gene="glpA" /locus-tag="YE0212"
CDS	248974..250629	/gene="glpA" /locus-tag="YE0212" /codon-start=1 /transl-table=11 /product="anaerobic glycerol-3-phosphate dehydrogenase subunit A" /protein-id="CAL10347.1" /db-xref="GI:122087566" /db-xref="GOA:AlJIA9" /db-xref="InterPro:IPR000447" /db-xref="InterPro:IPR006076" /db-xref="InterPro:IPR007419" /db-xref="InterPro:IPR017752" /db-xref="UniProtKB/TrEMBL:AlJIA9" /translation="MTNSSPYTETDVIIIGGGAT GAGIARDCARRGLACTLLERHDA TGATGRNHGLLHSGARYAVTDGESARECIEENRI LKRIARHCIEQTDGLFITLPEDSL EYQQQFIARCEAGIEAEADPKQALRLEPAANP TLIAAVRVDPDGTVDFFRLTAANML DAREHGANVLTIVEYIGLLRHGDRVSGVRVFDHK NQRQYDIHAQIVVNAAGINQGHIA EYADLRIRMFPAKGALLILGHRINNMVINRCRP ADADILVPGDITSLIGTTSSTHIEY DQIDNMVVTAQEVDTLIREGSKLSPQLAQTRILR AYAGVRPLVASDDDFSGRNVSRGI VLLDHASRDGLEFITITGGKLMTYRLMAEWATD KVCEKLGVTAACTTAQEPLPGSQQ SAEQTLISKVISLPASIRGSVYRHRGDRATQLLAG NRLDNLVCECAVTAQEVRYAIE SLSVNNLLDLRRRTRVGMTCQGLCACRAAGLL SRFKVITPQQSREQLRQFLNERWK GVRPIAWGDALRESEFTHWVYQGLCGLDDSPNTA NVQEKPEI"
misc-feature	249001..250074	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:PFAM:PF01266" /note="Pfam match to entry PF01266 DAO, FAD dependent oxidoreductase, score 408.8, E-value 3.2e-120"
misc-feature	249016..249069	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:Prosite:PS00977" /note="PS00977 FAD-dependent glycerol-3-phosphate dehydrogenase signature 1."
misc-feature	250030..250062	/gene="glpA" /locus-tag="YE0212" /inference="protein motif:Prosite:PS00978" /note="PS00978 FAD-dependent glycerol-3-phosphate dehydrogenase signature 2."
gene	250619..251893	/gene="glpB" /locus-tag="YE0213"
CDS	250619..251893	/gene="glpB" /locus-tag="YE0213"

		/codon-start=1 /transl-table=11 /product="putative anaerobic glycerol-3-phosphate dehydrogenase subunit B" /protein-id="CAL10348.1" /db-xref="GI:122087567" /db-xref="GOA:AlJIB0" /db-xref="InterPro:IPR003953" /db-xref="InterPro:IPR009158" /db-xref="UniProtKB/Swiss-Prot:AlJ IB0" /translation="MKFDVVIIGGGLAGLVCGIR LAEQGKYCAIVSAGQNALHFSSGS LDLLAKLPNGQAVSQPLSALETLAELAPEHPYSK MGQGTGVGELAQQAESLLSRCGLS LVGSAAKNHLRLTPLGNCRPTWLSPADIPVAPLE GFLPWQKVAVIGIEGFLDFQPMV ASALQEQGEVETSDYLLHLPALDRLRDNFSEFRAV NIARVLDLPENLOPLADELARLSS TAEMILLPACIGLDESAPLEALRAAVGKPIQLLP TLPPSLLGMRLHQALRHRFQQLGG IVMPGDVLRRAELVGNRITGLYSRNGHDIPLRAA QMVLASGSFFSNGLVATFEHVYEP ILDDLILSLPNRADWSNSNMFAQPYLQFGVNTD NLRALRGGVALDNLHVIGAVLGG YDPLQGGCGAGVSLTSALFVAEEQIVSAMEVTL" /gene="glpB" /locus-tag="YE0213" /note="Signal peptide predicted for YE0213 by SignalP 2.0 HMM (Signal peptide probability 0.893) with cleavage site probability 0.891 between residues 22 and 23" /gene="glpC" /locus-tag="YE0214" /gene="glpC" /locus-tag="YE0214" /codon-start=1 /transl-table=11 /product="anaerobic glycerol-3-phosphate dehydrogenase subunit C" /protein-id="CAL10349.1" /db-xref="GI:122087568" /db-xref="GOA:AlJIB1" /db-xref="InterPro:IPR001450" /db-xref="InterPro:IPR004017" /db-xref="InterPro:IPR012285" /db-xref="InterPro:IPR017753" /db-xref="UniProtKB/TrEMBL:AlJIB1" /translation="MARDKSFESCIKCTVCTTYC PVAKVNPYPGPKQAGPDGERLRL KDPALYDDALKYCTNCKRCEVACPSPDVKIGDIIQ RAKASYSSNKPRLRDAILSHDTLM GTLSTFPAPVINAVTGLKPVVRVLLDKALKIDHRR ELPKYSFGTFRRWYRKQAEKQQQY AEQVAFHGGCFVNYNHPQLGKDLVSVFNAMNIGV QLLKREKCCGVPLIANGFIEQAKK QARVNLESITDAVIDRDIPTVATSSSCTFTLRDE YPHLLDVDTAPVRDRVELATRYLY RLDDOGRLEPLKPLLSNOKPLRIAYHTPCHME
sig-peptide	250619..250684	
gene	251932..253155	
CDS	251932..253155	

		MGWTAYTLALLQRIPIGIELVVLDS QCCGIAGTYGFKSENYATSQIGASLFGQIEESG VDLVITDCETCKQIEMSTSKKCE HPITLLAQAALNPLCP"
misc-feature	251959..251994	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:Prosite:PS00198" /note="PS00198 4Fe-4S ferredoxins, iron-sulfur binding region signature."
misc-feature	252079..252150	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF00037" /note="Pfam match to entry PF00037 fer4, 4Fe-4S binding domain, score 13.2, E-value 0.0015"
misc-feature	252100..252135	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:Prosite:PS00198" /note="PS00198 4Fe-4S ferredoxins, iron-sulfur binding region signature."
misc-feature	252490..252681	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF02754" /note="Pfam match to entry PF02754 DUF224, Domain of unknown function (DUF224), score 35.2, E-value 9.6e-08"
misc-feature	252895..253083	/gene="glpC" /locus-tag="YE0214" /inference="protein motif:PFAM:PF02754" /note="Pfam match to entry PF02754 DUF224, Domain of unknown function (DUF224), score 61.2, E-value 1.5e-15"
gene	complement(253311..253754)	/gene="dcrB"
CDS	complement(253311..253754)	/locus-tag="YE0215" /gene="dcrB"  /locus-tag="YE0215" /codon-start=1 /transl-table=11 /product="putative lipoprotein" /protein-id="CAL10350.1" /db-xref="GI:122087569" /db-xref="UniProtKB/TrEMBL:A1JIB2" /translation="MGQPVSLLEGKVAFLPADL SDQSGKMGSQANNMHVYANKTGDK AVIVILGDDTNEALNVLTDRLAEQQQRARDANLQV VTNKAIKVDGHPFQQLDSIITSGG QKAYSSVLGMGQVDNHLMTIQITLPADNQQQAQTE AESIISTLKLK"
gene	complement(253896..254576)	/gene="yhhQ"  /locus-tag="YE0216"

CDS	complement(253896..254576)	/gene="yhhQ" /locus-tag="YE0216" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10351.1" /db-xref="GI:122087570" /db-xref="InterPro:IPR003744" /db-xref="UniProtKB/TrEMBL:A1JIB3" /translation="MFSFTAQQRM TALVWLSLFH IVIITSSNYLVQLPISIFGFHTTW GAFTFPFI FLATDLTVRIFGAPLARRIILSVMP ALLISYLISALFYQGSWQGFALS SFNLFVARIAAASFMA YVLGQILDVQVFNRLRQR SAWWVAPTAAAMFFGNISDTMAFFF IAFYRSSDPFMAANWVEIALVDYSFKLLICMLFF LPAYGMMLNLVLLKYFARKTEQQTL MQANTAEQ"
misc-feature	complement(253947..254564)	/gene="yhhQ" /locus-tag="YE0216" /inference="protein motif:PFAM:PF02592" /note="Pfam match to entry PF02592 DUF165, Uncharacterized ACR, YhhQ family COG1738, score 254.3, E-value 1.1e-73"
misc-feature	complement(join(253959..254027,254085..254153,254187..254255,254298..254366,254385..254444,254472..254540))	/gene="yhhQ" /locus-tag="YE0216" /inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted for YE0216 by TMHMM2.0 at aa 13-35, 45-64, 71-93, 108-130,142-164 and 184-206"
gene	254823..255077	/locus-tag="YE0217"
CDS	254823..255077	/locus-tag="YE0217" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10352.1" /db-xref="GI:122087571" /db-xref="GOA:A1JIB4" /db-xref="InterPro:IPR001455" /db-xref="UniProtKB/Swiss-Prot:A1JIB4" /translation="MTDIFANPDKTL DALGLRCP EPVMMVRKTVRHMEDGQTLIIAD DPATTRDIPGFCRFMDHQLLAQDTGTQTPYRYLVK KGAKAE"
misc-feature	254838..255059	/locus-tag="YE0217" /inference="protein motif:PFAM:PF01206" /note="Pfam match to entry PF01206"



UPF0033, Uncharacterized protein family UPF0033, score 136.2, E-value 3.8e-38"  
 /locus-tag="YE0217"  
 /inference="protein motif:Prosite:PS01148"  
 /note="PS01148 Uncharacterized protein family UPF0033 signature."  
 /locus-tag="YE0218"

misc-feature 254856..254894

gene complement(255099..2574 29)

CDS complement(255099..2574 29)

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 /protein-id="CAL10353.1"  
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 /db-xref="GOA:AlJIB5"  
 /db-xref="InterPro:IPR000150"  
 /db-xref="InterPro:IPR001366"  
 /db-xref="InterPro:IPR001757"  
 /db-xref="InterPro:IPR001969"  
 /db-xref="InterPro:IPR005834"  
 /db-xref="InterPro:IPR006121"  
 /db-xref="InterPro:IPR006404"  
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 /db-xref="UniProtKB/TrEMBL:AlJIB5"  
 /translation="MHSHSEHRHSTETQSHCGCG HDHAKKOTGCCSQPAANISHDSSN SVSEHSHQEGGCCQSSTDDGDEESDRLANATP AGSQHFSWQVKGMDPCSCARKIEN AVSNLVGIENVKVLFATEKLVVDARSDIRLQVQQ AVIQAGFSLIDIQSPGAGKNTSE SRFREYLPIALTLTLLSLWSGISLFSVELSELAF TVTTIVGLPIPVTKAWKLIRSGTP FAIETLMSVAAIGAMFIGATAEAMVLLFMVGE LLESYAANRARRGV TALMALVP EE ALLLKEGERRQVSASLRPGDIEVSPGGRLPAD AELMTPFASFDESALTGESVPVER VQGEKVAAGSLSVDRATEMRVISEPGNNAIDRIIL QLIELAEERRAPIERFIDRFRIY TPAIMFLSALVILVPPLAFAPWETWIRGLTLL LIGPCALVISTPAAITSAALAAAT RRGALIKGGAALQLGRIQTVAFDKGTGLTEGKP QVTDILPISGVSETRLLSLAAAVE AGSHHPLAVAIMQRAQONTMPLPLAEERRALAGI GVEGRVNGLVVRVSAPSKISPELL TAEWLAQFDELESSGKTAVAVLENEKFIGVVALR DTLRTDAKQAIADALKKLGIOGVML TGDNPRAAAAIA GELGIDYRAGLLPADKVQAVMA LNATHPTVMVGDGINDAPAMKAAS IGIAMSGTDVALETADAALHTNRLTGLAEIILL SRAANANIRQNIITIALGLKGIFLV TTLGLTGLWLAVLADSGALVTANALRLLRK DI"

misc-feature complement(255138..2551 73)

/locus-tag="YE0218"  
 /inference="protein motif:Prosite:PS00141"

		/note="PS00141 Eukaryotic and viral aspartyl proteases active site."
misc-feature	complement(join(255168..255236,256089..256157,256200..256268,256677..256745,256788..256856,256875..256934))	/locus-tag="YE0218"
		/inference="protein motif:TMHMM:2.0"
		/note="6 probable transmembrane helices predicted for YE0218 by TMHMM2.0 at aa 166-185, 192-214, 229-251,388-410, 425-447 and 732-754"
misc-feature	complement(255357..256028)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00702"
		/note="Pfam match to entry PF00702 Hydrolase, haloacid dehalogenase-like hydrolase, score 106.1, E-value 4.4e-29"
misc-feature	complement(255360..255428)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS01229"
		/note="PS01229 Hypothetical cof family signature 2."
misc-feature	complement(255990..256010)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS00154"
		/note="PS00154 E1-E2 ATPases phosphorylation site."
misc-feature	complement(256038..256703)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00122"
		/note="Pfam match to entry PF00122 E1-E2-ATPase, E1-E2 ATPase, score 295.6, E-value 4e-86"
misc-feature	complement(256989..257180)	/locus-tag="YE0218"
		/inference="protein motif:PFAM:PF00403"
		/note="Pfam match to entry PF00403 HMA,Heavy-metal-associated domain, score 53.8, E-value 2.5e-13"
misc-feature	complement(257079..257168)	/locus-tag="YE0218"
		/inference="protein motif:Prosite:PS01047"
		/note="PS01047 Heavy-metal-associated domain."
gene	complement(257713..258339)	/gene="yhhN"
		/locus-tag="YE0219"
CDS	complement(257713..258339)	/gene="yhhN"
		/locus-tag="YE0219"

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/transl-table=11
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/db-xref="UniProtKB/TrEMBL:A1JIB6"
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ALGAFFLSHLLYTSFASQMTFTL
FWPLPLVLIIVGALLLATIWRDLDEMWPVVAVF
GMTLLMVWMAGEQYFARSTDMFS
LLTGTVLLLVSHTIWLLNRYRFSFRASDAIVAGC
YFVGHFLIVRSLYL"
/misc-feature complement(join(257719..
.257775,257812..257871,
257899..257955,
257974..258042,
258055..258114,
258127..258186,
258199..258258))
/gene="yhhN"

/locus-tag="YE0219"
/inference="protein
motif:TMHMM:2.0"
/note="7 probable transmembrane
helices predicted for YE0219 by
TMHMM2.0 at aa 28-47, 52-71,
76-95, 100-122,129-147, 157-176
and 189-207"
/gene 258627..258947
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/protein-id="CAL10355.1"
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/db-xref="UniProtKB/TrEMBL:A1JIB7"
/translation="MANEQLLYRIQFINNGKNYQ
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AVTEKGSARISELGSNVMSFPYLP GNKP"
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CDS 258986..259369
/locus-tag="YE0222"
/codon-start=1
/transl-table=11
/product="putative membrane
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/protein-id="CAL10356.1"
/db-xref="GI:122087575"
/db-xref="UniProtKB/TrEMBL:A1JIB8"
/translation="MNKPPLLFIAVVVLIVVLAT
RQYWQKKRQDAENDRSPVRSQVVE
VIDKREVLAPNRRSRQREIEVAEEKRYEVYFQPL
LSGVEVKKSNEIKIVLPQQEYNRI
EQGAKGTLRLQGTRYISFVFNSSVAK"
/sig-peptide 258986..259042
/locus-tag="YE0222"
/note="Signal peptide predicted

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for YE0222 by SignalP 2.0 HMM  
 (Signal peptide probability 0.802)  
 with cleavage site probability  
 0.534 between residues 19 and 20"  
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 /codon-start=1  
 /transl-table=11  
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 /db-xref="GI:122087576"  
 /db-xref="InterPro:IPR009525"  
 /db-xref="UniProtKB/TrEMBL:A1JIB9"  
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 /locus-tag="YE0223"  
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 61-80"  
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 protein"  
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 /db-xref="InterPro:IPR002052"  
 /db-xref="InterPro:IPR004398"  
 /db-xref="InterPro:IPR016065"  
 /db-xref="UniProtKB/TrEMBL:A1JIC0"  
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 WLAPMIQGARCILDCEFAGSGALGLE  
 ALSRYAGFTVLLLEADRHVAKQLSNNLALLSADNG  
 QVVNTNSLQWLAPGQPPFDLVFLD  
 PPFKGLLAETVNLLEQFNWLTADAWIYVEAEAE  
 SAAADVPASWQLHREKIAGQVAYR  
 LYIRNKDVPQDRVSVVEEQEHHVD"  
 /locus-tag="YE0224"  
 /inference="protein

		motif:PFAM:PF03602" /note="Pfam match to entry PF03602 Cons-hypoth95,Conserved hypothetical protein 95, score 223.8, E-value 1.6e-64" /locus-tag="YE0224"
misc-feature	complement(259912..259932)	/inference="protein motif:Prosite:PS00092" /note="PS00092 N-6 Adenine-specific DNA methylases signature."
gene	260574..262097	/gene="ftsY"
CDS	260574..262097	/locus-tag="YE0225" /gene="ftsY" /locus-tag="YE0225" /codon-start=1 /transl-table=11 /product="cell division protein" /protein-id="CAL10359.1" /db-xref="GI:122087578" /db-xref="GOA:AlJIC1" /db-xref="InterPro:IPR000897" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR004390" /db-xref="InterPro:IPR013822" /db-xref="UniProtKB/TREMBL:AlJIC1" /translation="MAKEKKRGFFSWLGLGRQNE EHTAEPLATEKEETAQEVVNP EEQVLSEKQAEIAPDNTSVAAEARESVAEHSTLA PGWDSTAISEVAAETLPEVGAEP AAQSVVEEPINFAEDPQYLQHHFSQNHDDKDKVDS WDEGTVSAPELPLTEHHVVIDTPA PQAIVEESQAEVIEEPVVLLEEIEAEEVEVAVVA QEQRPTKEGFFARLKRSLIKTKQ NLGSGFMGLFSGKKIDDDLFEELEEQLLIADVGV ETTRKIIITSLTEHASRKQLKDAEA LYGLKEEMSEILSKVDKPLDVS GKNPFVILMVG VNGVGKTTTIGKLARQFQAEKSV MLAAGDTFRAAAVEQLQVWGDRNKIAVVAQHTGA DSASVIFDAIQAAKARGIDVLLAD TAGRLQNKAHLMEEKKIVRMKKLDGDAPHEVM LTLDTAGQNAVSQAKLFNEAVGL TGITLTKLDGTAKGVIFAIAQDFGIPIRYIGVG EGIEDLRPFKADDFIEALFARED"
misc-feature	261198..261443	/gene="ftsY" /locus-tag="YE0225" /inference="protein motif:PFAM:PF02881" /note="Pfam match to entry PF02881 SRP54-N, SRP54-type protein, helical bundle domain, score 81.0, E-value 1.6e-21"
misc-feature	261474..262088	/gene="ftsY" /locus-tag="YE0225" /inference="protein motif:PFAM:PF00448" /note="Pfam match to entry PF00448 SRP54, SRP54-type protein, GTPase domain, score 416.8, E-value 1.3e-122"
misc-feature	261501..261524	/gene="ftsY"

		/locus-tag="YE0225" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="ftsY" /locus-tag="YE0225" /inference="protein motif:Prosites:PS00300" /note="PS00300 SRP54-type proteins GTP-binding domain signature." /gene="ftsE" /locus-tag="YE0226" /gene="ftsE" /locus-tag="YE0226" /codon-start=1 /transl-table=11 /product="cell division ATP-binding protein" /protein-id="CAL10360.1" /db-xref="GI:122087579" /db-xref="GOA:AlJIC2" /db-xref="InterPro:IPR003439" /db-xref="InterPro:IPR003593" /db-xref="InterPro:IPR005286" /db-xref="InterPro:IPR013505" /db-xref="UniProtKB/TrEMBL:AlJIC2" /translation="MIRFEQVSKAYLGGRQALQG VDFHLRPAEMAFLTGHSAGKSTL LKLCIGIERPSAGHIWFGGHDISRLKNREVFFLR RQIGMIFQDHLLLDRTVYDNDVAM PLIIAGASTDIRRRVSAALDKVGLLDKAKNFPI QLSGGQQQRVGIARAVNKPALL ADEPTGNLDDALSEGILRLFEEFNRVGVTVLMAT HDTSLIARRRYPILTLSQGRMSG A HHGE" /gene="ftsE" /locus-tag="YE0226" /inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 239.0, E-value 4.5e-69" /gene="ftsE" /locus-tag="YE0226" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="ftsE" /locus-tag="YE0226" /inference="protein motif:Prosites:PS00211" /note="PS00211 ABC transporters family signature." /gene="ftsX" /locus-tag="YE0227" /note="synonym: ftsS" /gene="ftsX" /locus-tag="YE0227" /codon-start=1 /transl-table=11 /product="cell division protein"
misc-feature	262002..262043	
gene	262103..262771	
CDS	262103..262771	
misc-feature	262184..262741	
misc-feature	262205..262228	
misc-feature	262514..262558	
gene	262860..263720	
CDS	262860..263720	

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sig-peptide	262860..262964	
misc-feature	join(262878..262946, 263331..263399, 263460..263528, 263631..263690)	/locus-tag="YE0227" /inference="protein motif:TMHMM:2.0" /note="4 probable transmembrane helices predicted for YE0227 by TMHMM2.0 at aa 7-29, 158-180, 201-223 and 258-277" /gene="ftsX" /locus-tag="YE0227" /inference="protein motif:PFAM:PF02687" /note="Pfam match to entry PF02687 DUF214, Predicted permease, score 74.6, E-value 1.4e-19" /gene="rpoH" /locus-tag="YE0228" /note="synonyms: fam, hin, htpR" /gene="rpoH" /locus-tag="YE0228" /codon-start=1 /transl-table=11 /product="RNA polymerase sigma-32 factor" /protein-id="CAL10362.1" /db-xref="GI:122087581" /db-xref="GOA:AlJIC4" /db-xref="InterPro:IPR000943" /db-xref="InterPro:IPR007627" /db-xref="InterPro:IPR007630" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR012759" /db-xref="InterPro:IPR014284" /db-xref="UniProtKB/TrEMBL:AlJIC4" /translation="MTKEMQTLALVPQGSLEAYI
misc-feature	263310..263699	
gene	264131..264988	
CDS	264131..264988	

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misc-feature	264359..264400	
misc-feature	264884..264949	/gene="rpoH" /locus-tag="YE0228" /note="Predicted helix-turn-helix motif with score 2068.000, SD 6.23 at aa 252-273, sequence STLQELADQYGVSAERVRLQLEK"
misc-feature	264887..264967	/gene="rpoH" /locus-tag="YE0228" /inference="protein motif:Prosite:PS00716" /note="PS00716 Sigma-70 factors family signature 2."
gene	complement(265084..265476)	/gene="yhhK"
CDS	complement(265084..265476)	/locus-tag="YE0229" /gene="yhhK" /locus-tag="YE0229" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="CAL10363.1" /db-xref="GI:122087582" /db-xref="GOA:AlJIC5" /db-xref="InterPro:IPR000182" /db-xref="InterPro:IPR016181" /db-xref="UniProtKB/TrEMBL:AlJIC5" /translation="MKLTIERLTNLTHQDLIDLA KIWPEQQQTWQWINDGKPLFAA RFNERLLGAVKVMVDGQQALEDLYVREVTTRRRG VGLYLIEETLRQLPTIQWYLSDK QVVAANYEAMGSFMLACGFSRNKQGWQR"
misc-feature	complement(265111..265353)	/gene="yhhK" /locus-tag="YE0229" /inference="protein motif:PFAM:PF00583" /note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 23.4, E-value 0.00035"
gene	265898..267013	/gene="livK" /locus-tag="YE0230" /note="synonym: livJ"
CDS	265898..267013	/gene="livK"



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/codon-start=1
/transl-table=11
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acid-binding protein"
/protein-id="CAL10364.1"
/db-xref="GI:122087583"
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/db-xref="UniProtKB/TrEMBL:AlJIC6"
/translation="MKLTGKGVLLAGCIAMAMSH
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MEFTGARQAIADINAKGGIKGDKLVGVVEYDDACD
PKQAVAVANKVINDGIRYVIGHLC
SSSTQPASDIYEDEGVIMITPAATNADLTTRGYK
MIMRTTGLSDSQGPTAAKYILETI
KPKRIAVVHDKQQYGEGLARSVRDSLKKQGTPEPV
LFEGVTAGDKDFS TLVARLKKENV
DFVYFGGYYPEMQGILRQAKQAGLTARFMGPEGV
GNSSLNIAGDASEGMLVTLPKRY
DQVPANQPIVDALKAKKLDPTGPFVNTTYAALQS
LTTAMERSGSQEPADLVKDLKTGK
PVETVMGPLSWDEKGD LKGFEEGIFEWHADGSST
AVK"
sig-peptide      265898..265969
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/locus-tag="YE0230"
/note="Signal peptide predicted
for YE0230 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability
1.000 between residues 24 and 25"
misc-feature     265958..267007
/gene="livK"
/locus-tag="YE0230"
/inference="protein
motif:PFAM:PF01094"
/note="Pfam match to entry PF01094
ANF-receptor, Receptor family
ligand binding region, score
175.3, E-value 6.6e-50"
gene             267172..268098
/locus-tag="YE0231"
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/transl-table=11
/product="high-affinity
branched-chain amino acid
transport system, permease
protein"
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/db-xref="UniProtKB/TrEMBL:AlJIC7"
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VSVIASTYGSIERVAYKPVRS
KRLIALISAIGMSIFLQNYVSLNQGSRDALPSL
VTGQWTLAETNGFAATISTMQLTI
WIVTFLAMLALTLFIRYSRMGRACRACAEDLKMA

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		SLLGINTDRVISLTFVIGALMAAV AGVLLGQFYGVINPYIGFMAGMKAFATAAVLGGIG SIPGAMIGGLILGIAEALTSAYLS TEYKDAVSFALLIVVLLVMPGTGILGRPEVEKV" /gene="livH" /locus-tag="YE0231" /inference="protein" motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2,Branched-chain amino acid transport system / permease component, score 323.1, E-value 2e-94" /gene="livH"
misc-feature	267193..268083	
misc-feature	join(267214..267282, 267301..267369, 267379..267447, 267484..267543, 267628..267696, 267790..267858, 267901..267969, 268015..268074)	/locus-tag="YE0231" /inference="protein" motif:TMHMM:2.0" /note="8 probable transmembrane helices predicted for YE0231 by TMHMM2.0 at aa 15-37, 44-66, 70-92, 105-124,153-175, 207-229, 244-266 and 282-301" /gene="livM" /locus-tag="YE0232" /gene="livM" /locus-tag="YE0232" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid transport system, permease protein" /protein-id="CAL10366.1" /db-xref="GI:122087585" /db-xref="GOA:AlJIC8" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:AlJIC8" /translation="MKQLNFLNAIISSFVLLVLVA SFVMGLQLQLDGTLIVQGASEVR WLWIGAACIVVFFQVLVRPLIQQGIKKVSGPAWV LPSFDGTTTPRQKLLAAAI IIAAIA WPFVLVSRGSVDIATLTIYVMLGLGLNVVVVGLSG LLVLGYGGFYAIGAYTYALLNHYY GLGFWEESLPLAGIVAALSGFLLGFPVLRLRGDYL AIVTLGFGEIVRILLNNTEITGG PNGISQIPKPTILFGLFESRTAKDGGWDTFHNFFG LTYDPSDRIIIFLYMVALLLVILTL FVINRLRLMPLGRAWEALREDEIACRSI GLSPTK IKLTAFTISAAPFAGTAGTLFAARQ GFVSPESFTFVESAFVLAIVVLGGMGSGQFVILA AVLLVVSRELMRDLNAYSMLLLGA LMVLMMIWRPQGLLPMPKRPQLKLVADIKAKQGE QA" /gene="livM" /locus-tag="YE0232"
gene	268095..269381	
CDS	268095..269381	
sig-peptide	268095..268169	

		/note="Signal peptide predicted for YE0232 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.812 between residues 25 and 26" /gene="livM"
misc-feature	join(268113..268181, 268224..268277, 268365..268424, 268434..268502, 268506..268574, 268584..268652, 268671..268724, 268875..268943, 269037..269105, 269148..269216, 269235..269294)	
		/locus-tag="YE0232" /inference="protein motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0232 by TMHMM2.0 at aa 7-29, 44-61, 91-110, 114-136, 138-160, 164-186, 193-210, 261-283, 315-337, 352-374 and 381-400" /gene="livM"
misc-feature	268314..269351	/locus-tag="YE0232" /inference="protein motif:PFAM:PF02653" /note="Pfam match to entry PF02653 BPD-transp-2, Branched-chain amino acid transport system / permease component, score 357.7, E-value 8.3e-105" /gene="livG"
gene	269378..270145	/locus-tag="YE0233" /gene="livG"
CDS	269378..270145	/locus-tag="YE0233" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid transport, ATP-binding protein" /protein-id="CAL10367.1" /db-xref="GI:122087586" /db-xref="GOA:AJJIC9" /db-xref="InterPro:IPR003439" /db-xref="InterPro:IPR003593" /db-xref="UniProtKB/TrEMBL:AJJIC9" /translation="MSTQPLLAVEGLSMRFGGLL AVNNVGLNLNQGEIVSLIGPNGAG KTTIFNCLTGFYRPTGGTIKLDRHIEGLPGQVI ARMGVIRTFQHVRLFREMTVVENL LVAQHQLKSGVFAGLLKTPGFRRAEADALERAA TWLERVGLLELANRQAGNLAYGQQ RRLEIARCMVTRPELLMLDEPAAGLNPKETDELN QLIMELRDQHQVSVLLIEHDMKLV MGISDRIYVVNQGTPLAQGSPIERNPNPDVIRAY LGE"
misc-feature	269471..270070	/gene="livG" /locus-tag="YE0233" /inference="protein"

		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
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		230.2, E-value 1.9e-66"
misc-feature	269492..269515	/gene="livG"
		/locus-tag="YE0233"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
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misc-feature	269840..269884	/gene="livG"
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		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	270190..270891	/gene="livF"
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CDS	270190..270891	/gene="livF"
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		/transl-table=11
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		/db-xref="GOA:AlJID0"
		/db-xref="InterPro:IPR003439"
		/db-xref="InterPro:IPR003593"
		/db-xref="UniProtKB/TrEMBL:AlJID0"
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		FADRQQYQQRIERVYDLFPRLFERRAQRAGTMSG
		GEQQMLAIGRALMSQPKLLLLDEP
		SLGLAPIIILQIFDTIQQLREEGMTIFLVEQAN
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		ALLANEAVRSAYLGG"
misc-feature	270268..270816	/gene="livF"
		/locus-tag="YE0234"
		/inference="protein
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		200.5, E-value 1.7e-57"
misc-feature	270289..270312	/gene="livF"
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		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	270589..270633	/gene="livF"
		/locus-tag="YE0234"
		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	complement(270952..2720	/locus-tag="YE0235"
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22)

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PGTFSHTHYDVSFTIAANTLKNIR
IGATVGGVLNRGEQQYSLSSKGLSFGSTGKQCE
IFDPQAGVAPEAVKIDPKFRLSSA
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CIHYQSMGVRPVLHRIQANNLNG
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sig-peptide complement(271954..2720  
22)

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for YE0235 by SignalP 2.0 HMM
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misc-feature complement(271930..2719  
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/inference="protein
motif:TMHMM:2.0"
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helix predicted for YE0235 by
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gene complement(272084..2726  
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CDS complement(272084..2726  
02)

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EFSPANISWGTDHASLKLLSDNPQTFTVAKSTSS
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YQQLTLFFETNS"
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sig-peptide complement(272546..2726  
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/note="Signal peptide predicted
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CDS complement(272611..2732 /locus-tag="YE0237"  
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/db-xref="UniProtKB/TrEMBL:ALJID3"  
/translation="MASFLPVGTFAAIDIQPHVL  
EVQOKSAVVTVINHGTEYITVQ  
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gene complement(273233..2739 /locus-tag="YE0238"  
19)

CDS complement(273233..2739 /locus-tag="YE0238"  
19)  
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PLKAPAQETLYRLYINPIVDIKAIAGNSEDKSKIH  
APMTVSIYGVLVHHLPPHAEQIR  
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sig-peptide complement(273854..2739 /locus-tag="YE0238"  
19)  
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0.796 between residues 22 and 23"

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07)  
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motif:TMHMM:2.0"  
/note="1 probable transmembrane  
helix predicted for YE0238 by  
TMHMM2.0 at aa 5-27"

gene complement(273937..2762 /locus-tag="YE0239"  
49)

CDS complement(273937..2762 /locus-tag="YE0239"  
49)  
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/db-xref="GI:122087592"  
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IPYLQCCQNGCDYILSNHRITVDKVNHVVTIINN
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EQYRAVSARGGYLGLPYQSFAFAHWFYNAARIK
NNNSYAHQSGYQQQTQIGVGSWYL
QKNFQAHYLRAGRQNNLDSAGSIHTLVNPDQ
FVTLGSQSYLAIDKPSAGSLVLYA
TSDGDFEIIYRDNQLIRRIQAQLGRNEIDYSQLPG
GYITVEIRLVDRITGKVINQESQTI
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KSNVSGSFHRSGSRGDVSRAGVDNKIANGGIS
YNGMLAISPGQIALGRSSYSGTAL
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sig-peptide      complement(276163..2762
49)              /note="Signal peptide predicted
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51)              /inference="protein
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45)              /inference="protein
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gene              complement(276430..2769
06)              /locus-tag="YE0240"

CDS               complement(276430..2769
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gene	277469..278788	/gene="ugpB" /locus-tag="YE0241"
CDS	277469..278788	/gene="ugpB" /locus-tag="YE0241" /codon-start=1 /transl-table=11 /product="glycerol-3-phosphate-binding periplasmic protein" /protein-id="CAL10375.1" /db-xref="GI:122087594" /db-xref="GOA:A1JID7" /db-xref="InterPro:IPR006059" /db-xref="InterPro:IPR006061" /db-xref="UniProtKB/Swiss-Prot:A1JID7" /translation="MFNNAIRKTSICVALTLAFS ANAMAVTEIPFVHSMEGELGVEVN SLADRFNQSHSDYKIVPVYKNGYEQSLAAGIAAF RSGKAPAILQVYEVGTATMMASKA IKPVFQVKDANINFDESVPVPTVAGYYTDAKTG HLLSQPFNSSTPVLYYNKDAFKKA GLNPDQPPKTTQQLAEDTAKLRAAGSSCGYASGW QGWIQIENFSAWHGQPIASRNNGF DGTDAVLEFNKPLQVKHIQLLSDMNKKGDFTYFG RKDESTAKFYNGDCAITASSGSL ADIRHYAKFNYGVGMMFPYDADAKDAPQNAIIGGA SLWVMDGKDKDIYKGVAEFLQFLT QPEIAAEWHQKTGYLPITTAAYELTKQQGFYDKN PGADVATRQMLNKPPLPYTKGLRL GNMPQIRTVVDEELEGVNTGKKTPQQALDTAVSR GDVLLHRRFEQTNK"
sig-peptide	277469..277543	/gene="ugpB" /locus-tag="YE0241" /note="Signal peptide predicted for YE0241 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.966 between residues 25 and 26"
misc-feature	277571..278731	/gene="ugpB" /locus-tag="YE0241" /inference="protein motif:PFAM:PF01547" /note="Pfam match to entry PF01547 SBP-bac-1, Bacterial extracellular solute-binding protein, score 217.0, E-value 1.9e-62"
misc-feature	277892..277945	/gene="ugpB" /locus-tag="YE0241" /inference="protein motif:Prosite:PS01037" /note="PS01037 Bacterial extracellular solute-binding proteins, family 1 signature."



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                                         ID8"
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                                         GSRITYQTLMLPYAVAPAAVLWIFLFPNGLGL
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                                         LVVNLVYAFFDITFPVIDAATGGGPMQATTTLIYK
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                                         VIGLTVIQFRFVERKVRYQ"
misc-feature    join(278931..278999,
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279513..279581,
279693..279761)
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                                         /note="6 probable transmembrane
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GenBank ACC. NO. (GBN): AM236080
GenBank VERSION (VER): AM236080.1 GI:115254414
CAS REGISTRY NO. (RN): 906734-09-6
SEQUENCE LENGTH (SQL): 5057142
MOLECULE TYPE (CI): DNA; circular
DIVISION CODE (CI): Bacteria
DATE (DATE):      14 Nov 2006
DEFINITION (DEF): Rhizobium leguminosarum bv. viciae chromosome complete
genome, strain 3841.
KEYWORDS (ST):    complete genome
SOURCE:            Rhizobium leguminosarum bv. viciae 3841
ORGANISM (ORGN):  Rhizobium leguminosarum bv. viciae 3841
                  Bacteria; Proteobacteria; Alphaproteobacteria;
                  Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium
                  group; Rhizobium
REFERENCE:          1
AUTHOR (AU):       Young,J.W.; Crossman,L.C.; Johnston,A.W.B.;
                  Thomson,N.R.; Ghazoui,Z.F.; Hull,K.H.; Wexler,M.;

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Curson,A.R.J.; Todd,J.D.; Poole,P.S.; Mauchline,T.H.;  
 East,A.K.; Quail,M.A.; Churcher,C.; Arrowsmith,C.;  
 Cherevach,A.; Chillingworth,T.; Clarke,K.; Cronin,A.;  
 Davis,P.; Fraser,A.; Hance,Z.; Hauser,H.; Jagels,K.;  
 Moule,S.; Mungall,K.; Norbertczak,H.; Rabinowitsch,E.;  
 Sanders,M.; Simmonds,M.; Whitehead,S.; Parkhill,J.  
 The genome of *Rhizobium leguminosarum* has recognizable  
 core and accessory components  
 Genome Biol., 7, R4-R4 (2006)  
 CA 145:307927  
 2 (bases 1 to 5057142)  
 Crossman,L.C.  
 Direct Submission  
 Submitted (21-FEB-2006) Crossman L.C., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Hinxton, Cambridge, Cambridgeshire, CB10 1SA, UNITED  
 KINGDOM

TITLE (TI):

JOURNAL (SO):

OTHER SOURCE (OS):

REFERENCE:

AUTHOR (AU):

TITLE (TI):

JOURNAL (SO):

FEATURES (FEAT):

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CDS	complement(join(5056183 ..5057142,1..72))	/locus-tag="RL4742" /gene="hemE"  /locus-tag="RL4742" /EC-number="4.1.1.37" /inference="similar to sequence:INSDC:RC16796" /inference="similar to sequence:INSDC:SME591793" /note="similarity:fasta; with=UniProt:DCUP-RHOCA (EMBL:RC16796); Rhodobacter capsulatus (Rhodopseudomonas capsulata).; hemE; Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD). Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).; length=344; id 50.621; 322 aa overlap; query 1-318; subject 23-344 similarity:fasta; with=UniProt:Q92KV8-RHIME (EMBL:SME591793); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE UROPORPHYRINOGEN DECARBOXYLASE PROTEIN (EC 4.1.1.37).; length=319; id 81.073; 317 aa overlap; query 1-317; subject 1-317; uroporphyrinogen decarboxylase" /codon-start=1

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misc-feature 1999..2718

gene 2778..3389  
CDS 2778..3389

misc-feature 2781..3314

gene 3382..4104  
CDS 3382..4104

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AGGASRAI IQAVDRGFK EIHVVN  
RTVERARELADRF GPRVQAHPAGALVEVMKGAGL  
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kinase; coaE; length 197 aa; 192  
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subject 1-192 aa similarity:fasta;  
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Escherichia coli; DNA polymerase

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243 aa; 244 aa overlap; query
2-233 aa; subject 7-241 aa
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(EMBL:AL591782); Rhizobium
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CRRYGIDNSHRTKHGALLDSELLA
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151 aa overlap; query 1-151 aa;
subject 1-145 aa similarity:fasta;
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CDS	complement(4756..5271)	
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gene	5394..6098	
CDS	5394..6098	

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282 aa overlap; query 92-369 aa;
subject 112-360 aa
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meliloti; putative lytic murein
transglycosylase a protein; length
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8-371 aa; subject 3-365 aa"
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CDS	7772..8149	/locus-tag="RL0011" /locus-tag="RL0011" /inference="similar to sequence:INSDC:AE008975" /note="similarity:fasta; SWALL:Q8UJB7 (EMBL:AE008975);

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Agrobacterium tumefaciens;
transcriptional regulator; length
121 aa; 121 aa overlap; query
1-121 aa; subject 1-121 aa"
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/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="CAK05499.1"
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/translation="MTPFGEAVRRRLRARKGVSSQK
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TFDLLQRIAGYFNIIWDEAEELFLARSSDPRVV
IDTSGLPPEYTEFANRLARRIRNL
DSAEIGRLSALLENGKGDGKAS"
/misc-feature 7793..7960 /locus-tag="RL0011"
/inference="protein
motif:Pfam:PF01381.9"
/note="Pfam match to entry
PF01381.9 HTH-3"
/gene="gyrB"
/locus-tag="RL0012"
/gene="gyrB"
/locus-tag="RL0012"
/inference="similar to
sequence:INSDC:AE007943"
/inference="similar to
sequence:INSDC:CEK132C8R"
/note="similarity:fasta;
with=UniProt:GYRB-ECOLI
(EMBL:CEK132C8R); Shigella
flexneri.; gyrB; DNA gyrase
subunit B (EC 5.99.1.3).;
length=EC 5.99.1 ( 803; id 58.612;
807 aa overlap; query 12-811;
subject 1-803 similarity:fasta;
with=UniProt:Q8UJB6
(EMBL:AE007943); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; gyrB; DNA gyrase subunit
B (AGR-C-19p).; length=AGR-C-19p;
id 86.190; 811 aa overlap; query
1-811; subject 6-816"
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subunit B"
/protein-id="CAK05500.1"
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/db-xref="UniProtKB/TrEMBL:Q1MNE5"
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KVLKGLDAVRRKPGMYIGDIDDGS
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VIMTQLHAGGKFDQNSYKVSGLHGVGVSVVNAL
SVWLKLRIRRHDKIHEMSFTHGVA
DAPLKVTGDAPNETGTEVFSMPSTDTFTMTEDFY
GTLEHRLRELAFNLNSGVRILLTDK
RHSDIKQEELRYDGGLEAFVAYLDRAKKSLVDKP

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		VAIHGKDKGITVEVAMWVNDGYHE NVLCFTNNIPQRDGGTHMAGFRAALTQVVSYAD SSGITKREKVTLQGEDCREGLTAV LSVKVPDPKFSSTQDKLVSVSEVRPVVSELVNEA LNTWFEHPSEAKILVGKVVEAAA AREAARKARELTRRKALDIASLPGLADCSEKD PTKSEVFLVEGDSAGGSAKQGRSR ENQAILPLRGKILNVERARFDKMLSSSQEIGTLIT ALGTGIGKDEFNVKELRYHKIIM TDADVDAHIRTLLTLFFFRMPOLIERGHLYIA QPPLYKVSRGKSVQYLKDEKALEE YLISQGLEADSLRLGSGEVVRAGQDLREVILDALR MRALLDNLHSRYNRSASVEQAAIAG ALNAELASDPARALALANAVAGRLDIAEETERG WRGVDVTTDGLRLERMVRGREL VLDMALIGSSDARHIDQLTARLKEIYQTPPSLHR REGDIEISGPRALLDAIFASGRKG LTMQRYKGLGEMNAEQWLWETTLDPNVRSLLQVRV NDATDADGLFARLMGDEVPRREF IQDNALSVANLDI"
misc-feature	8405..8839	/gene="gyrB" /locus-tag="RL0012" /inference="protein motif:Pfam:PF02518.9" /note="Pfam match to entry PF02518.9 HATPase-c"
misc-feature	8981..9493	/gene="gyrB" /locus-tag="RL0012" /inference="protein motif:Pfam:PF00204.9" /note="Pfam match to entry PF00204.9 DNA-gyraseB"
misc-feature	9662..9910	/gene="gyrB" /locus-tag="RL0012" /inference="protein motif:Pfam:PF01751.7" /note="Pfam match to entry PF01751.7 Toprim"
misc-feature	10487..10684	/gene="gyrB" /locus-tag="RL0012" /inference="protein motif:Pfam:PF00986.8" /note="Pfam match to entry PF00986.8 DNA-gyraseB-C"
gene	complement(10828..11427)	/locus-tag="RL0013"
CDS	complement(10828..11427)	/inference="similar to sequence:INSDC:AE007944" /note="similarity:fasta; with=UniProt:Q8UJB5 (EMBL:AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; NAD(P)H-flavin oxidoreductase (AGR-C-21p).; length=P; id 60.204; 196 aa overlap; query 1-196; subject 1-195" /codon-start=1 /transl-table=11 /product="putative oxidoreductase"

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/protein-id="CAK05501.1"
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/db-xref="UniProtKB/TrEMBL:Q1MNE4"
/translation="MTKSNHRESYPIIDPMFLDR
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QEWARNASALIFVVSRAFTGAAGS
TEEKPSYTHSFDAAGAWGLAIQARLSGLYAHGM
GGIKHEEIRQAFIPEGYRVEAGV
AIGRLADKSVLSERNQAREFPSQRKPLSEVAFNG
RFVAN"

misc-feature    complement(10936..11379 /locus-tag="RL0013"
)

/inference="protein
motif:Pfam:PF00881.10"
/notes="Pfam match to entry
PF00881.10 Nitroreductase"

gene            complement(11473..11769 /locus-tag="RL0014"
)

CDS             complement(11473..11769 /locus-tag="RL0014"
)

/inference="similar to
sequence:INSDC:AP002994"
/notes="similarity:fasta;
SWALL:Q98NF3 (EMBL:AP002994);
Rhizobium loti; msl0164 protein;
length 97 aa; 92 aa overlap; query
5-96 aa; subject 1-92 aa"
/codon-start=1
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protein"
/protein-id="CAK05502.1"
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/db-xref="UniProtKB/TrEMBL:Q1MNE3"
/translation="MEFEMHLSKAVVRTEHASRY
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IDDLHKRFARFEEELDIVNTN"
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/inference="similar to
sequence:INSDC:SSD917"
/notes="similarity:fasta;
with=UniProt:P74752 (EMBL:SSD917);
Synechocystis sp. (strain PCC
6803).; Slr0605 protein.;
length=319; id 56.013; 316 aa
overlap; query 1-315; subject
1-314"
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/db-xref="UniProtKB/TrEMBL:Q1MNE2"
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TGEAGFAASAGRYHLYVAYICPWASRTLIGRKLK

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misc-feature	12531..12767	
gene	13031..13873	
CDS	13031..13873	
misc-feature	13286..13783	
gene	14079..15356	
CDS	14079..15356	

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sequence:INSDC:AF474374"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q71KW6
(EMBL:AF474374); Azospirillum
brasiliense.; phaZ; PHB
depolymerase.; length=603; id
57.471; 348 aa overlap; query
61-406; subject 257-602
similarity:fasta;
with=UniProt:Q92TD3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02770.; length=424; id 76.000;
425 aa overlap; query 1-424;
subject 1-423 Codons 60 to the
C-terminus are similar to codons
255 to the C-terminus of
Azospirillum brasiliense PHB
depolymerase phaZ UniProt:Q92TD3
(EMBL:SME591782) (603 aa), and
entire protein is similar to
Rhizobium meliloti (Sinorhizobium
meliloti) Hypothetical protein
SMc02770 UniProt:Q92TD3
(EMBL:SME591782) (424 aa)"
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depolymerase"
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EVVWSRPFPCNLLHFARNAPAAAGN
DPRILIVAPMSGHYATLLRGTV EALLPSADIYIT
DWIDARMVPMTEGTFDFDDYIDYV
IEMHLFHLGHDTHVVAVQCPSPVFLAAAAMVEEAR
DPLSPASMTLMGGPIDTRINPTAV
NKLAQERSLQWFSNDNVMVFPWPQPGFVRVPVPG
FLQLSGFMSMNLDRHLVAHKEFFM
HLVKNDGEPERHRDFYDEYLAVMDLTAEFYLTQTV
EEVF1KHS1PKGELMHRGRKVDPT
AIRNVALLTVEGENDDISGVGQTMAAQITICVNIP
EDMRMHYLPQDVGHYGVFNFSRFR
REIAPRIIDFVROHSRSVAVKPIQPRVIKGGRTG"
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/note="Pfam match to entry
PF06850.1 PHB-depo-C"
/locus-tag="RL0018"
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/inference="similar to
sequence:INSDC:AL591782"
/note="similarity:fasta;
SWALL:Q92TD2 (EMBL:AL591782);
Rhizobium meliloti; conserved

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misc-feature	14694..15299
gene	15502..15936
CDS	15502..15936

		hypothetical transmembrane protein; length 141 aa; 143 aa overlap; query 1-143 aa; subject 1-140 aa" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05506.1" /db-xref="GI:115254432" /db-xref="GOA:Q1MND9" /db-xref="UniProtKB/TrEMBL:Q1MND9" /translation="MNQSALLRPDWTPTATIALMI LGFMVFWPLGLAMLAYIIFGDRLR GFKRVDNEATDGFASCRPHGRHHPHFSTGNVA FDDWRKAELDRMEEERRKLDREME EFDSYLRELRAKDQEEFDRFMRDRRRAKRDNDG PVAEYQTP" /locus-tag="RL0018" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 15-37" /locus-tag="RL0019" /locus-tag="RL0019" /inference="similar to sequence:INSDC:HS360250" /note="similarity:fasta; with=UniProt:Q8UJB2 (EMBL:HS360250); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0016 (AGR-C-25p).; length=AGR-C ( 255; id 68.482; 257 aa overlap; query 1-252; subject 1-255" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05507.1" /db-xref="GI:115254433" /db-xref="UniProtKB/TrEMBL:Q1MND8" /translation="MFSLLKTRSKARKPAPPEMR TLDVAGRLMPLTIKQHDRATRIITL RIEPGGGALKMTVPKGLAAREVNAFLDRHQGWLL TKLAKFSTDTGLRDGGEILLRGVS HRIQHSGLSLRGLTEAVSIDGRPVLRVSGMPEHV GRRIAAFLKKEARADLARLATMHAA TIRAPIRSISMKDRSRWGSSEGNLSFSWRIV MAPSPVIDYLAHEVAHLKEMNHG PHFWALCRKLCPGMEAKSWLKRHGSQHLAIDFD "
misc-feature	15544..15612	
gene	16044..16802	
CDS	16044..16802	
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misc-feature	16131..16778	
gene	16969..17637	
CDS	16969..17637	

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sequence:UniProtKB:Q9X4E3"
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SWALL:TRPF-RHOSH (SWALL:Q9X4E3);
Rhodobacter sphaeroides;
n-(5'-phosphoribosyl)anthranilate;
trpF; length 212 aa; 206 aa
overlap; query 5-209 aa; subject
6-210 aa similarity:fasta;
SWALL:TRPF-AGRT5 (SWALL:Q8UJB1);
Agrobacterium tumefaciens;
n-(5'-phosphoribosyl)anthranilate;
trpF; length 220 aa; 210 aa
overlap; query 1-210 aa; subject
1-210 aa"
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N-(5'-phosphoribosyl)anthranilate"
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/db-xref="UniProtKB/TrEMBL:Q1MND7"
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VMKVFsvRTADDLKRVEAYIGIADRFDAKAPK
GSELPGGNGISFDWSLLSWLDGVS
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PGVKSVAKIDFEFFDAVEKANAPMM ASGS"
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/inference="protein
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/note="Pfam match to entry
PF00697.10 PRAI"
/gene 17640..18860
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/CDS 17640..18860
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sequence:UniProtKB:P56929"
/inference="similar to
sequence:UniProtKB:Q9X4E5"
/note="similarity:fasta;
SWALL:TRPB-RHOSH (SWALL:Q9X4E5);
Rhodobacter sphaeroides;
tryptophan synthase beta chain;
trpB; length 409 aa; 401 aa
overlap; query 8-406 aa; subject
7-407 aa similarity:fasta;
SWALL:TRPB-RHIET (SWALL:P56929);
Rhizobium etli; tryptophan
synthase beta chain; trpB; length
406 aa; 406 aa overlap; query
1-406 aa; subject 1-406 aa"
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/transl-table=11
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synthase beta chain"
/protein-id="CAK05509.1"
/db-xref="GI:115254435"

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misc-feature 17820..18809

gene 18864..19703

CDS 18864..19703

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ELGGAKIYFKREELNHTGSHKINN
CIGQILLAKRMGKTRIIAETGAGQHGVSATVAA
RFGLPCCVVYMGATDVERQAPNVFR
MKLLGAEVKPVTAGSGTLKDAMNEALRDWVTNVE
DTYYLIGTAAGPHYPPEMVRDFQS
VIGIEAKEQMLAAEGRPLDLVIAAVGGGSNAIGI
FHPFLDDPSVKIVGVEAGGKQLQG
DEHCASITAGSPGVLHGNRTYLLQSDSGQIKEGH
SISAGLDYPGIGPEHSWLNLTGRV
DYVPIMDHEALEAFQTLTRLEGIIPALEPSHAIA
EVIKRAFTMGKDEIILMNLSSGRGD
KDIFTVGKILGMGL"
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sequence:INSDC:AF107094"
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with=UniProt:TRPA-RHOSH
(EMBL:AF107094); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; trpA; Tryptophan
synthase alpha chain (EC
4.2.1.20).; length=263; id 62.214;
262 aa overlap; query 4-265;
subject 3-259 similarity:fasta;
with=UniProt:TRPA-AGRT5
(EMBL:AE007944); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; trpA; Tryptophan synthase
alpha chain (EC 4.2.1.20).;
length=279; id 84.229; 279 aa
overlap; query 1-279; subject
1-279; putative tryptophan
synthase, alpha subunit"
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/transl-table=11
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alpha chain."
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/db-xref="UniProtKB/TrEMBL:Q1MND5"
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YYNPIIYGVKFLDDALLAGIDGLIVVDLPPEM

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misc-feature 18888..19676

gene 19845..20750  
CDS 19845..20750

misc-feature 20172..20372

DDELCPAIRKGINFIRLATPTTD  
EKRLPKVLKNTSGFVYVSMNGITGSALPDPSLV  
SGAVERIKQHTKLPVCVGFVKTA  
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sequence:INSDC:SME591782"  
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with=UniProt:ACCD-ECOLI  
(EMBL:HS028244); Escherichia coli  
O157:H7.; accD; Acetyl-coenzyme A  
carboxylase carboxyl transferase  
subunit beta (EC 6.4.1.2) (ACCase  
beta chain).; length=304; id  
46.831; 284 aa overlap; query  
1-283; subject 1-281  
similarity:fasta;  
with=UniProt:Q92TC7  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PROBABLE  
ACETYL-COENZYME A CARBOXYLASE  
CARBOXYL TRANSFERASE SUBUNIT BETA  
PROTEIN (EC 6.4.1.2).; length=304;  
id 85.526; 304 aa overlap; query  
1-301; subject 1-304; putative  
acetyl-coenzyme A carboxylase  
carboxyl transferase subunit"  
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carboxylase carboxyl transferase  
subunit beta (ACCase beta chain)."  
/protein-id="CAK05511.1"  
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/db-xref="UniProtKB/TrEMBL:Q1MND4"  
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KTEQEDTILAGVKVQGLKLVAVVHEFNFIGGSL  
GMAAGEAIVKAFERATAEKCLVLM  
FPASGGARMQEGILSMLQLPRTTVAVDMLKESGQ  
FYIVLTNPTTGGVTASYAMLGDI  
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/note="Pfam match to entry

gene	20778..22130	PF01039.9 Carboxyl-trans"
CDS	20778..22130	/gene="folC" /locus-tag="RL0024" /gene="folC" /locus-tag="RL0024" /inference="similar to sequence:INSDC:ECD862" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:FOLC-ECOLI (EMBL:ECD862); Escherichia coli.; folC; FolC bifunctional protein [Includes: Folylpolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS); Dihydrofolate synthase (EC 6.3.2.12)].; length=422; id 31.757; 444 aa overlap; query 1-442; subject 2-411 similarity:fasta; with=UniProt:Q92TC6 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE FOLC BIFUNCTIONAL PROTEIN INCLUDES: FOLYLPOLYGLUTAMATE SYNTHASE AND DIHYDROFOLATE SYNTHASE (EC 6.3.2.17) (EC 6.3.2.12).; length=447; id 75.901; 444 aa overlap; query 7-450; subject 4-447" /codon-start=1 /transl-table=11 /product="putative FolC bifunctional protein [Includes: Folylpolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS); Dihydrofolate synthase]." /protein-id="CAK05512.1" /db-xref="GI:115254438" /db-xref="GOA:Q1MND3" /db-xref="UniProtKB/TrEMBL:Q1MND3" /translation="MIPRGQTAVSEAAQEIDKLM GLHPKGFDSLDRITRLDLVLGNP HRKLPPVIHVAGTNGKGSVTAFCRALLEAGGYS A HVHTSPHLVNWHERYIRIGVKGGRG QLVDDAVF AEAVRRVADANAGQHITVFEILTAVT FILFSEHPADAAIIEVGLGGRFDA TNVISDFAVSVIMPISLDHQPYLGDRELIAAEK AGIMKPGFPVVIGHQEYDAALDVL MSTAERLHCPSAVFGQDFMAHEEYGRLVYQDEF G LADLPLPRLPGRHQYANAAAAIRA VKAAGFTVTETMMEKAMSSVEWPGRLQRLSEGR L LSHAPAGAEIWDGHHNPGAGEVI AEAMANFEERQSRPLFLIIGMINTKDPVGYFKAF AGLVEKVFVCPVIRGSEAMIDPVIL SNAAYDAGLVAEPMS TVGDALEAIKAVADPEALP PRILVGGSLYLVGDVLADNGTPPK /gene="folC"
misc-feature	20877..21641	

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        /locus-tag="RL0024"
        /inference="protein
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        /note="Pfam match to entry
        PF01225.11 Mur-ligase"
gene      complement(22203..22523 /locus-tag="RL0025"
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CDS       complement(22203..22523 /locus-tag="RL0025"
)
        /inference="similar to
        sequence:INSDC:A35135"
        /inference="similar to
        sequence:INSDC:AE008976"
        /note="similarity:fasta;
        with=UniProt:THIO-RHOSH
        (EMBL:A35135); Rhodobacter
        sphaeroides (Rhodopseudomonas
        sphaeroides).; trxA; Thioredoxin
        (TRX).; length=TRX; id 57.692; 104
        aa overlap; query 2-105; subject
        1-104 similarity:fasta;
        with=UniProt:Q8UJA6
        (EMBL:AE008976); Agrobacterium
        tumefaciens (strain C58/ATCC
        33970).; trxA; Thioredoxin C-1.;
        length=133; id 91.509; 106 aa
        overlap; query 1-106; subject
        28-133 Similar to entire protein
        of Rhodobacter sphaeroides
        (Rhodopseudomonas sphaeroides)
        Thioredoxin (TRX) trxA (104 aa),
        and similar, but truncated at the
        N-terminus, to Agrobacterium
        tumefaciens (strain C58/ATCC
        33970) Thioredoxin C-1 trxA (133
        aa)"
        /codon-start=1
        /transl-table=11
        /product="putative thioredoxin"
        /protein-id="CAK05513.1"
        /db-xref="GI:115254439"
        /db-xref="GOA:Q1MND2"
        /db-xref="UniProtKB/TrEMBL:Q1MND2"
        /translation="MATVVKVDINNFQSEVLESSE
        FVVVDFWAEWCGPCKMIAPSLSEI
        AVEMEGKVVKVAKLNIDENPELAAQFGVRSIPTLA
        IFKGGEVADISVGAKPKTALSNNW SSAA"
misc-feature complement(22206..22520
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        /inference="protein
        motif:Pfam:PF00085.8"
        /note="Pfam match to entry
        PF00085.8 Thioredoxin"
gene      complement(22599..26150 /locus-tag="RL0026"
)
CDS       complement(22599..26150 /locus-tag="RL0026"
)
        /inference="similar to
        sequence:INSDC:AE008977"
        /note="similarity:fasta;
        with=UniProt:Q8UJA5
        (EMBL:AE008977); Agrobacterium

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tumefaciens (strain C58/ATCC 33970).; uvrD; ATP-dependant DNA helicase.; length=1185; id 62.203; 1180 aa overlap; query 6-1183; subject 8-1185"  
/codon-start=1  
/transl-table=11  
/product="putative ATP-dependent UvrD family DNA helicase"  
/protein-id="CAK05514.1"  
/db-xref="GI:115254440"  
/db-xref="GOA:Q1MND1"  
/db-xref="UniProtKB/TrEMBL:Q1MND1"  
/translation="MSDVTALPNDGPGAWIGWT  
TIQQAIASDPLRSAWVANAGSGK  
THVLTQRVIRLLSGARPSAILCLTYTKAAASEM  
SNRVFERLAEWVVLDDDELRRIT  
QIEGMAPDGLKLAERRLFKALETGPGGLKIQTI  
HAFCEALLHQFFLEANVAGHFSVL  
DDRAAVALLSDARRALLTATAPDEDSALAEAFAY  
VLNLGDESGLENLLGDIVANRNAI  
RRFTAAAEQQGGVEMVLRKRLGLAVGDTEDRIEA  
QYWPLPELSGSVLELYLSLADQKG  
GAKAQEVAYGLRLAGREDDARRAQFLEKIFLTV  
KGEPKADSQFFVKAMLAEPQLAE  
AIAIARAHVAASRDRLKLRMYGATHAALVLADR  
LNHDYEELKKQRSQDFEDLITKT  
ADLLTKSGVGPWIHYKLDRGIDHILVDEAQTSP  
IQWSVIQSLAEDFFSGESARPIVR  
TLFAVGDEKQSIYSFQGARPERFSEESDRTRRRV  
SDSQGSFSSVRLPLSFRSTADVLE  
AVDHIFKTPENARGLSALGEPVVHRSRIGHPGA  
VDLWEMIAPEAVVKEEDWTAPFDA  
TPESAPAILARRIAHSIGTLVGRETIVDKGKER  
LIEAGDILVLVRKRDAFVNALTRA  
LKRGRDIPVAGADRLVLTSHIAVQDLLALGRFLL  
LPEDDLSLA AVLKSPFLDLSDDI  
FAIAALRGDNESFWSHLRSFAADGTFLFRAVER  
LELFLRQSRSLSVHDFYARVLGSY  
GGRRLQFLARLGTVEVSDILDEFLTFTLDHESGLP  
GLQSFISTLELEAPVMKREQDKGR  
NEVRIMTVHASKGLEAPIFLVLDGGSKAFTHTHL  
PKRLRIETRPDEPPMPVWVPVSDL  
ANSLTQDDAARIQMLAEEERYRLLYVAMTRAADR  
LVVCGYRGVRVNNDTWHMMISTAL  
HDDHPHVEATTFSGSDGEWPGIKWRVPRVERSE  
RIDRSQERGSEETLPDGLRLPLFP  
QAEPLPRPLSPSGAGTIIIDEDEGGLLVVSPFGEK  
EHSRSLKGRILHRMLQALPEIP  
LAERPDAAASYAERAARFWPEVERRKLVDVSLKL  
LDEEGLQAVLGAQAQPEVSIIMGT  
LTEDRRYAVSGRIDRLAVLADRVVILDYKTRNRP  
PATEEAIPFAHRAQLAIYREILTP  
LYDPKCLIDCMLVYTENASLYLSEKALGLALAAV  
KTK"

misc-feature complement (23925..26096 /locus-tag="RL0026"  
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/inference="protein  
motif:Pfam:PF00580.8"  
/note="Pfam match to entry  
PF00580.8 UvrD-helicase"

gene complement (26143..29334 /locus-tag="RL0027"

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)
CDS complement(26143..29334 /locus-tag="RL0027"
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sequence:INSDC:HS361251"
/note="similarity:fasta;
with=UniProt:Q8UJA4
(EMBL:HS361251); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu0024 (AGR-C-40p).; length=1061;
id 64.745; 1058 aa overlap; query
8-1063; subject 9-1061"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05515.1"
/db-xref="GI:115254441"
/db-xref="UniProtKB/TrEMBL:Q1MND0"
/translation="MAERQQPRILTIIPAGLPFLK
MLATTLCDGRLTPLFRHEADPLS
LAKVTIYLPTRRAVRVLRSEFVDLLGGRSAILPV
IRPLGETDDDSGYFDEVLPATIDL
AQPLSNTARLLELARLILAWRNKLP EIVRHIHSD
SPLVAPASPADAIWLARNLAEID
SIETEDLDWSELKSLDTGDYAAWQOLTAEFQIA
SAFWPQRLSELGKSSPARHRNAIL
RAEASRLSATKPAGPIIIAGSTGSPATADLIAA
VAHLPPEGVIVLPGLDLSMPERHWQ
MVAPEPAPQGHANPASRSHPOYGLSVLLKRLKLT
RADVTLLDRPEADLERRAEILSRA
LAPAEATSDWGAWNKNDLPAGALTSAFSDISLIEA
ANEREATAIAIALRLALERPGQD
SESRAALITPDRNLARRVMAELSRFGILADDSAG
TPLSAMPQGTLQLLLEAALRPGD
PVAIVSLLKHP LARFGLER GALISATEALELLAL
RGGVAEVDISTLEPLLAHQ LAEQA
LDRHAPQWRKALSPEAADAAYDLARRVQAQTEPL
ASALMRHRPEDRGRTTRFTLSEWA
ERTGRSLEAVADVPQGNLADLWSNEAGDALAALL
GEVIDTDGQMEADGPQWIDIMAAAL
AAGHAVKPRALSHRPFIFGTLEARLQSVDTLIL
GGLNEGTVPGQTANNPFIPRMKT
EIGLEPPERRIGQLAHDFEMANGTRHLIYSRALR
QGSTPTVASRWLQRLLALGGEAFE
AELKGRGNRFLQWAALIDRGEAQAPQRPSKPPK
LALQPKSYSFSEVGRLLRDPYAIY
ARRILRLDPVDPFNRPDGAERGTLHYKIIDRFI
REAHIACTPDAAAAMEHVLSELD
MEKLPPIHIDAVWRPFRFAVARAFLEWEAGRRHGI
LKTILEVRGGMELEPINIRLTGVA
DRIDITGPHSADIIDYKTGYNPSPAQARVLLDPQ
LALAAAALAGAFRDAGSLVPQEL
LYVRLRPGSRFQVDTVNNESARS DKAKSAMDLA
AESIDQLVKFVGLLQSSERGFTSR
LIPAQQDFDFGGDYDHLARVSEWSTAETEESGDE"

gene complement(29338..30069 /locus-tag="RL0028"
)
CDS complement(29338..30069 /locus-tag="RL0028"
)

/inference="similar to

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sequence:INSDC:AF285636"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q9AI35
(EMBL:AF285636); Burkholderia
mallei (Pseudomonas mallei).;
wcbM; length=230; id 28.033; 239
aa overlap; query 3-236; subject
1-225 similarity:fasta;
with=UniProt:Q92TC3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE NUCLEOTIDYL
TRANSFERASE PROTEIN (EC 2.7.7.-).;
length=243; id 72.500; 240 aa
overlap; query 1-240; subject
1-240"
/codon-start=1
/transl-table=11
/product="putative
nucleotidyltransferase protein"
/protein-id="CAK05516.1"
/db-xref="GI:115254442"
/db-xref="GOA:Q1MNC9"
/db-xref="UniProtKB/TrEMBL:Q1MNC9"
/translation="MTIRQAMVLAAGLGTRMRPI
TDTIPLVKIDGKPMIDYALDSL
VAAGVERAVVNVHVFADQMLDLHGKYHGLDIVIS
DERDALMNSGGGLAKGLRLNLRDN
IFVMNADLFWIGEQQGRPTNLQRLAGGFNAERMD
MALLCVGIEDTTGHNGKNDFSLAA
DGQLTRYRDDPSNPVYAGAIVMNPSSLDDAPKD
AFNLNIYFDKAIARGRLFGMVLEG
HWLTVGTPEAIGEAETIRRLRAFA"
/locus-tag="RL0028"

misc-feature      complement(29353..30057
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/inference="protein
motif:Pfam:PF00483.9"
/note="Pfam match to entry
PF00483.9 NTP-transferase"

gene              complement(30083..31600
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/locus-tag="RL0029"

CDS               complement(30083..31600
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/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q92KV3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02757.; length=504; id 64.113;
496 aa overlap; query 10-505;
subject 7-501"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05517.1"
/db-xref="GI:115254443"
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/translation="MTTGDAISLFLKDEAATIRL
GEDLALALKAGDCLALSGDLGAGK
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AVSHFDLRLRGDPAELTELGFDEA
LQNGICLVEWPEMAQSELPARIALTLAHEGSGR
RATIEAAGAQNTRIRRVLAIRDFL
DTAGYPAAKRRFLTGDASLRAYEAIYPKAENQRI
ILMDWPPLAEGPPVLGDKPYPKVA
HLAENAYPFVAIADALRKDFGAAPYVYKVDYNKG
ILLIEDLGSEGVLDHAGQPVIERY
RESVACLARLHALKFPQHIFVGRHVHHIPDFDR
TAMKMEVRLVLDWHLPPWKROGAPA
TEVERTEYLAIWDALIDELATAEKNLLLRDFHSP
NIIWRERESGIRKIGLIDFQDAMI
GPTAYDLASIVQDARVTIEPGLFRQLMDDYLGLR
RAQGSFDEDDGFMRAWAIMSAQRNC
KLAGLWVRLLRDQDGKPGYLKHMPTLSYLNVALE
HETLAPLRDWCSTRAGIGQSES"
misc-feature    complement(31184..31552
)
/locus-tag="RL0029"
/inference="protein
motif:Pfam:PF02367.5"
/note="Pfam match to entry
PF02367.5 UPP0079"
gene            complement(31597..34182
)
/locus-tag="RL0030"
CDS             complement(31597..34182
)
/locus-tag="RL0030"
/inference="similar to
sequence:INSDC:B87681"
/inference="similar to
sequence:INSDC:C97362"
/note="similarity:fasta;
with=UniProt:DIVL-CAUCR
(EMBL:B87681); Caulobacter
crescentus.; divL; Sensor protein
divL (EC 2.7.3.-).; length=769; id
31.950; 795 aa overlap; query
81-861; subject 2-766
similarity:fasta;
with=UniProt:Q8UJA1 (EMBL:C97362);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Two component
sensor kinase (AGR-C-44p).;
length=881; id 70.905; 818 aa
overlap; query 46-861; subject
67-881 Similar, but truncated at
the N-terminus, to Caulobacter
crescentus Sensor protein divL
(769 aa), and entire protein is
similar to Agrobacterium
tumefaciens (strain C58/ATCC
33970) Two component sensor kinase
(AGR-C-44p) (881 aa)"
/codon-start=1
/transl-table=11
/product="putative two-component
sensor histidine kinase
transcriptional regulatory
protein"
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LARFLKSCAAGTALATLARPALAQAEQQAATAH
LFTSSQVGVSVVIGVISAAALLST
LWLVRQRGNLENSREIRSALSDAQQRISQYQAL
IADKNRRRIVWDGNARPELLGQLP
PETGAPQDGEFLAFGLWLKSRGASELEKAIDRLR
DEAQSFDMMVETIRDEILEAQGRV
SGGRAVFRFVALNNLRALAE LRIERDRLMTSIS
AFQTMLDAIDMPAWQRDPVGRLTW
VNQAYGEAVEARSPOQAINEGREMLTTVARERIR
ATTTPESPFHDKISTTVVRGNRTFF
DVVDVRVPGGSAGIAIDVSDIEAVRAELERTLKS
HAETLDHLATPVAIFDGDRLRQFY
NQAFVALWELDIAFLEGRPDNSELLERLRAAKKL
PDQLNWKSWKEAALSVYRALDTQS
DLWHLPNGQTLRVFATAHPQGGATVWFENLTEQV
DLETRYNTLVKVGQETIDHLSGV
AVFGPDGRIRLSNPAFRALWGITETEAKPGTHIR
ALGEACTPSYDRPDGKWTFAELIT
SFDDERRSGGTLELFSGLVDYAVIPLPNAQTM
LTFVNMITSVRAERALTEKNEALR
KADELKNDVQHVSYELRSPLTNIIGFTDLLRTP
GVGPLTERQAEYIDHISTSSSVLL
TLVNDILDLATVDAGIMRLNYADIDLNDLLDDVS
MQIADRLHESGVALEITAPAYLGS
IVADPQRLKQILLKLLSNAANFSPEGTSISLECH
REGTDFVFVAVSDRGFGISPDMIAT
VFDRFATGAKSGKRGAGLGLSIVDSFVSLHHGD
VTIDSEPGKGTTVVCRIPSVVDVPH SAAAE"

misc-feature    complement(31627..31956) /locus-tag="RL0030"
)
/inference="protein
motif:Pfam:PF02518.9"
/note="Pfam match to entry
PF02518.9 HATPase-c"

misc-feature    complement(32092..32298) /locus-tag="RL0030"
)
/inference="protein
motif:Pfam:PF00512.10"
/note="Pfam match to entry
PF00512.10 HisKA"

gene            complement(34386..35786) /locus-tag="RL0031"
)

CDS             complement(34386..35786) /locus-tag="RL0031"
)
/inference="similar to
sequence:INSDC:SME591782"
/inference="similar to
sequence:INSDC:U76671"
/note="similarity:fasta;
with=UniProt:SAHH-RHOSH
(EMBL:U76671); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; ahcY;
Adenosylhomocysteinase (EC
3.3.1.1)
(S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase).;
length=463; id 82.251; 462 aa

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overlap; query 6-466; subject
3-463 similarity:fasta;
with=UniProt:SAHH-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; ahcY;
Adenosylhomocysteinase (EC
3.3.1.1)
(S-adenosyl-L-homocysteine
hydrolase) (AdoHcyase).;
length=466; id 90.558; 466 aa
overlap; query 1-466; subject
1-466"
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S-adenosyl-L-homocysteine
hydrolase"
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/db-xref="UniProtKB/TrEMBL:Q1MNC6"
/translation="MSTEKDYVVADIGLADFGRK
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CNIFSTQDHA AAAAIAASGVPVFAI
KGESLEDYVVYTDKIFQWADGGLSNMILDDGGDA
TMYILLGARA EAGEDVLSHPHSEE
EEILFAQIKKRLAASPGWFTKQDAIKGVTEETT
TGVNRLYQLSQKGLLPFPAINVND
SVTKSKFDNKYGCKESLVDGIRRGTDVMMAGKVA
VVCYGVDVGKGSAA SLSGAGARVK
VTEADPICALQAAMDGYEVVLLLEDVSSADIFIT
TTGNKDVIRIDHMRAMKDMAIVGN
IGHFDNEIEVAALRNKWTNVKQPQVDLIEFPKGN
RIILLSEGRLLNLGNATGHPSFVM
SASFNTQTLAQIELFTKPDQYSNQVYILPKHLDE
KVARLHLDKLGKLT ELSSEEQAAY
IGVSPKGPFSKDHRYR"
misc-feature complement(34392..35774 /locus-tag="RL0031"
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/inference="protein
motif:Pfam:PF05221.5"
/notes="Pfam match to entry
PF05221.5 AdoHcyase"
misc-feature complement(34629..35108 /locus-tag="RL0031"
)
/inference="protein
motif:Pfam:PF00670.10"
/notes="Pfam match to entry
PF00670.10 AdoHcyase-NAD"
gene complement(35943..36218 /locus-tag="RL0032"
)
CDS complement(35943..36218 /locus-tag="RL0032"
)
/inference="similar to
sequence:INSDC:A38120"
/inference="similar to
sequence:INSDC:SME591782"
/notes="similarity:fasta;
with=UniProt:PTHP-ALCEU
(EMBL:A38120); Alcaligenes

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eutrophus (Ralstonia eutropha).;
phbH; Phosphocarrier protein HPr
(Histidine-containing protein)
(Protein H).; length=His ( 89; id
51.163; 86 aa overlap; query 4-89;
subject 2-87 similarity:fasta;
with=UniProt:Q92TC0
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
PHOSPHOCARRIER HPR TRANSMEMBRANE
PROTEIN.; length=96; id 83.333; 90
aa overlap; query 2-91; subject
7-96"
/codon-start=1
/transl-table=11
/product="putative phosphocarrier
protein HPr"
/protein-id="CAK05520.1"
/db-xref="GI:115254446"
/db-xref="GOA:Q1MNC5"
/db-xref="UniProtKB/TrEMBL:Q1MNC5"
/translation="MTSLSRRELLIINKRGLHARA
SAKFVQMVETFDAAITVSKDGMTV
GGTSIMGLMMLAASPGSSVVVSAGSQAEAELEA
LDQLIQNRFGEEM"
misc-feature complement(35961..36212 /locus-tag="RL0032"
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/inference="protein
motif:Pfam:PF00381.8"
/note="Pfam match to entry
PF00381.8 PTS-HPr"
gene complement(36228..36629 /locus-tag="RL0033"
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CDS complement(36228..36629 /locus-tag="RL0033"
)
/inference="similar to
sequence:INSDC:AE005404"
/inference="similar to
sequence:INSDC:AE007946"
/note="similarity:fasta;
with=UniProt:PTNA-ECOLI
(EMBL:AE005404); Escherichia
coli.; manX; PTS
system,mannose-specific IIB
component (EIIAB-Man)
(Mannose-permease IIB component)
(Phosphotransferase enzyme II, AB
component) (EC 2.7.1.69)
(EIII-Man).; length=322; id
30.645; 124 aa overlap; query
2-123; subject 2-125
similarity:fasta;
with=UniProt:Q8UJ97
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; PTS system, IIA component
(AGR-C-50p).; length=AGR-C-50 (
133; id 85.714; 133 aa overlap;
query 1-133; subject 1-133 Similar
to the N-terminus to codon 135 of
Escherichia coli mannose-specific

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IIAB component, manX,PTS system
(322 aa), and similar to entire
protein of Agrobacterium
tumefaciens (strain C58/ATCC 33970
PTS system, IIA component (133
aa); putative phosphotransferase
system component"
/codon-start=1
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mannose-specific IIAB component
(EIIAB-Man) (Mannose-permease IIAB
component) (Phosphotransferase
enzyme II, AB component)
(EIII-Man)."
/protein-id="CAK05521.1"
/db-xref="GI:115254447"
/db-xref="GOA:Q1MNC4"
/db-xref="UniProtKB/TrEMBL:Q1MNC4"
/translation="MIGLVLVTHGKLAEEFRHAV
EHVVGPKQFIETVCIGPEDDMDQR
RQDILEAVSGADGHHGVILTMFGGTPSNLAIS
VMSSGHTEVIAGVNLPLMLIKLAGV
RGENNMEKALVEASEAGRKYINVASRVLSGK"
misc-feature complement(36279..36626 /locus-tag="RL0033"
)
/inference="protein
motif: Pfam:PF03610.4"
/notes="Pfam match to entry
PF03610.4 EIIA-man"
gene complement(36780..37232 /locus-tag="RL0034"
)
CDS complement(36780..37232 /locus-tag="RL0034"
)
/inference="similar to
sequence:INSDC:SME591782"
/notes="similarity:fasta;
with=UniProt:Q92KV2
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02752.; length=148; id 48.951;
143 aa overlap; query 7-148;
subject 7-148"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05522.1"
/db-xref="GI:115254448"
/db-xref="UniProtKB/TrEMBL:Q1MNC3"
/translation="MTEAGFNHATAIVVGKTGL
LFGSPSGWGKSMLEAFTCMTEARRL
GLFTALVADDQVLLSAEAGAVIATCPPSITGLIE
LRGTGIVHQDHIKATMHYAVLPG
SATGENRIPPEGEMVSLAADFSLPALRLLTGVCS
PLAILMAKVPDIDGR"
gene complement(37229..39019 /locus-tag="RL0035"
)
CDS complement(37229..39019 /locus-tag="RL0035"
)
/inference="similar to

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sequence:INSDC:AF027298"
/inference="similar to
sequence:INSDC:HS362250"
/note="similarity:fasta;
with=UniProt:CHVG-RHIME
(EMBL:AF027298); Rhizobium
meliloti (Sinorhizobium
meliloti).; chvG; Sensor protein
chvG (EC 2.7.3.-) (Histidine
kinase sensory protein exoS).;
length=EC 2.7.3.- ( 577; id
82.087; 575 aa overlap; query
21-593; subject 1-574
similarity:fasta;
with=UniProt:CHVG-AGRT5
(EMBL:HS362250); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; chvG; Sensor protein chvG
(EC 2.7.3.-).; length=EC 2.7.3.- (
596; id 81.475; 583 aa overlap;
query 9-591; subject 11-589;
putative two-component regulator
sensor histidine kinase
transcriptional regulator"
/codon-start=1
/transl-table=11
/product="Sensor protein chvG
(Histidine kinase sensory protein
exoS)."
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/protein-id="CAK05523.1"
/db-xref="GI:115254449"
/db-xref="GOA:Q1MNC2"
/db-xref="UniProtKB/TrEMBL:Q1MNC2"
/translation="MAQLVQERDLDDAEGVSTRR
VRGRRWSHFPTLIRRIFGNAVFSS
LTRRILFFNLVALVVLVGGILYLNQFREGGLIDAR
AESLLTQGEIIAGAVSASASVDIN
SITIDPQKLELLQAGQSITPVPNDELEFPIDPE
KVAPVLRRLISPTRTRARIFDADA
NLLLDLRHLYSRQVLRFDLPVVEEEKQTWSEWF
ATLFNKALQPGNPLPLYKEAPGGDG
SIYPEVMNALTGVRGAVVRTEKGLIVSVAVPI
QRFRVILGVLLSTQAGDIDINIVH
AERLAIMRVFGVATLVNVLSSLVLSSTIANPLRR
LSAAAIRVRRGAKTREEIPDFSAR
QDEIGNLSIALREMTTALYDRIDAIESFAADVSH
ELKNPLTSLRSVETLPLARSDDS
KKRLMDVIQHDVRRDLRLISDISDASRLDAELAR
VDAGSDVMEVLLRDLIEVSRQVRS
TKKQVEIEYAIERKPNVKTRFVVNGHDLRIGQII
ANLIENARSFVPEKGKGITVRLVR
TRSRCVTITIEDNGPGIOAENIDRIFERFYTDRPE
AEGFGQNSGLGLSISRQIAEAHGG
SLRAENITDAESGHILGARFISLPIGIAAA"
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misc-feature complement(37241..37597
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/inference="protein
motif:Pfam:PF02518.9"
/note="Pfam match to entry
PF02518.9 HATPase-c"
/locus-tag="RL0035"
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misc-feature complement(37751..37948
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/inference="protein
motif:Pfam:PF00512.10"
/note="Pfam match to entry
PF00512.10 HisKA"
misc-feature complement(37958..38176 /locus-tag="RL0035"
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/inference="protein
motif:Pfam:PF00672.10"
/note="Pfam match to entry
PF00672.10 HAMP"
misc-feature complement(38816..38875 /locus-tag="RL0035"
)
/inference="protein
motif:TMHMM:2.0"
/note="1 probable transmembrane
helix predicted at aa 49-68"
gene complement(39204..39938 /locus-tag="RL0036"
)
CDS complement(39204..39938 /locus-tag="RL0036"
)
/inference="similar to
sequence:INSDC:B49902"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:CHVI-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; chvI; Transcriptional
regulatory protein chvI.;
length=240; id 90.574; 244 aa
overlap; query 1-244; subject
1-240 similarity:fasta;
with=UniProt:Q8UJ95 (EMBL:B49902);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; chvI; Two
component response regulator.;
length=265; id 91.393; 244 aa
overlap; query 1-244; subject
25-265"
/codon-start=1
/transl-table=11
/product="putative two-component
response regulator transcriptional
regulatory protein"
/protein-id="CAK05524.1"
/db-xref="GI:115254450"
/db-xref="GOA:Q1MNG3"
/db-xref="UniProtKB/TrEMBL:Q1MNG3"
/translation="MPTIALVDDDRNILTSVSIA
LEAGYKVEITYTDGASALDGLLAR
PPQLAIFDIKMPRMDGMELLRLRLQKSDIPVIFL
TSKDEEIDELFGLKMGADDFITKP
FSQRLIVERVRAVLRASSREAAAAGTSPTGAPK
NGAVQQARSLERGLVMDQERHTC
TWKGEAVTLTVTEFLILHSLAQRPVGVKSRDALM
DAAYDEQVYVDDRTIDSHIKRLRK
KFKMVDTDGDMITLYGVGVGFREAA"
misc-feature complement(39219..39449 /locus-tag="RL0036"
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/inference="protein
motif:Pfam:PF00486.11"

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misc-feature	complement (39579..39935)	/note="Pfam match to entry PF00486.11 Trans-reg-C" /locus-tag="RL0036"
gene	40276..41886	/inference="protein motif:Pfam:PF00072.9"
CDS	40276..41886	/note="Pfam match to entry PF00072.9 Response-reg" /gene="pckA" /locus-tag="RL0037" /gene="pckA" /locus-tag="RL0037" /EC-number="4.1.1.49" /inference="similar to sequence:INSDC:AE007946" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:PPCK-RHIME (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; pckA; Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).; length=536; id 80.224; 536 aa overlap; query 1-536; subject 1-536 similarity:fasta; with=UniProt:PPCK-AGRT5 (EMBL:AE007946); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pckA; Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK).; length=536; id 81.716; 536 aa overlap; query 1-536; subject 1-536; putative phosphoenolpyruvate carboxykinase" /codon-start=1 /transl-table=11 /product="Phosphoenolpyruvate carboxykinase [ATP] (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK)." /protein-id="CAK05525.1" /db-xref="GI:115254451" /db-xref="GOA:Q1MNG2" /db-xref="UniProtKB/TrEMBL:Q1MNG2" /translation="MEMFGVHNPAIELATVGLGG AASVRYNFSAAALYEEAIRRGEEAE LTAQALRAITGQHTGRSPRDKFVVRDINTDGEI WNDNNKPISPEHFVLRDDMLAHA AGKELFVQDLVGGAEEGHALPTRVVTEFAWHSLF IRLNLIREPTAALSSSFVKLIITD LPSFKADPARHGCRSETVIACDLTNGLVIGGTS YAGEMKKSVFTVLNLLPAKGVMP MHCSANVGPDGDAAVFGLSGTGKTTLSADPART LIGDDEHGWSENGIFNFEGGCYAK TIRLSAEAEPEIYATTORFGTVLNVNLSRESE

misc-feature 40339..41730

gene 41993..42436  
CDS 41993..42436

misc-feature 42011..42406

gene 42438..43049  
CDS 42438..43049

DFNDGSLTENTRCAYPMDFIPNAS  
KTGRAGHPKTIIMLTADAFVMPPIARLTPDQAM  
YHFLSGYTAKVAGTEKGVVEPEAT  
FSTCFGAPFMRHPAEYGNLLKELIGRHGVQCWL  
VNTGWTGGAYGTGKRMPKATRAL  
LAAALSGELGQVEFRADTNFGFAVPVSVHGVDS  
ILDPRSTWADKAAYDAQAEKLVSM  
FIANFAKFENHVDGGVRDAAPGVKVAEE"  
/gene="pckA"  
/locus-tag="RL0037"  
/inference="protein  
motif:Pfam:PF01293.8"  
/note="Pfam match to entry  
PF01293.8 PEPCK-ATP"  
/locus-tag="RL0038"  
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/inference="similar to  
sequence:INSDC:C97363"  
/note="similarity:fasta;  
with=UniProt:Q8UJ93 (EMBL:C97363);  
Agrobacterium tumefaciens (strain  
C58/ATCC 33970).; Hypothetical  
protein Atu0036.; length=156; id  
84.615; 143 aa overlap; query  
1-143; subject 13-155"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAK05526.1"  
/db-xref="GI:115254452"  
/db-xref="GOA:Q1MNF8"  
/db-xref="UniProtKB/TrEMBL:Q1MNF8"  
/translation="MASDALYIDDRITTAGWELT  
EQFVLAGGPGGQNVNKVSTAVQLF  
FNIANSPSLNDRVKTNAIKLAGRRLSKDGVLMI  
ASRFRSQDRNREDARDRLKELILE  
AAKPPPPPRKKTRPTKGSVERRLKEKSGRSEVKK  
MRGRPGGSGE"  
/locus-tag="RL0038"  
/inference="protein  
motif:Pfam:PF00472.8"  
/note="Pfam match to entry  
PF00472.8 RF-1"  
/locus-tag="RL0039"  
/locus-tag="RL0039"  
/inference="similar to  
sequence:INSDC:A87250"  
/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:ALKB-CAUCR  
(EMBL:A87250); Caulobacter  
crescentus.; alkB; Alkylated DNA  
repair protein alkB homolog.;  
length=220; id 54.315; 197 aa  
overlap; query 4-200; subject  
22-216 similarity:fasta;  
with=UniProt:Q92TB6  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PROBABLE DNA REPAIR



		<p> SYSTEMATIC NAME: PUTATIVE ALKYLATED DNA  PROTEIN.; length=206; id 73.786;  206 aa overlap; query 1-203;  subject 1-206"  /codon-start=1  /transl-table=11  /product="putative alkylated DNA  repair protein"  /protein-id="CAK05527.1"  /db-xref="GI:115254453"  /db-xref="UniProtKB/TrEMBL:Q1MNGI1"  /translation="MPELLSGIRHLPGYLDRAQ  EALVEVIRTVVAEAPLYVFAMPGT  GKPM5VRMTNCGPLGWVTDKERGYRQPTHPATG  RPWPDMPQQLLDIWNVDVSGYDKPP  EACLVNFYSDEARMGLHQDKDEQLKAPVVISL  GNSCLFRVGGLSRNDRTL5FKLSS  GDLVVLGGEGRLCFHGVDRIHPATSTLLKNGGRI  NLTLRRVNP" </p>
misc-feature	42738..43043	<p> /locus-tag="RL0039"  /inference="protein  motif:Pfam:PF03171.7"  /notes="Pfam match to entry  PF03171.7 2OG-FeII-Oxy" </p>
gene	complement(43056..44051)	<p> /genes="coaA" </p>
CDS	complement(43056..44051)	<p> /locus-tag="RL0040"  /genes="coaA" </p>
		<p> /locus-tag="RL0040"  /inference="similar to  sequence:INSDC:A45727"  /inference="similar to  sequence:INSDC:AE007946"  /notes="similarity:fasta;  with=UniProt:COAA-ECOLI  (EMBL:A45727); Escherichia coli  O157:H7.; coaA; Pantothenate  kinase (EC 2.7.1.33) (Pantothenic  acid kinase) (Rts protein).;  length=EC 2.7.1.3 ( 316; id  53.526; 312 aa overlap; query  23-330; subject 10-316  similarity:fasta;  with=UniProt:COAA-AGRT5  (EMBL:AE007946); Agrobacterium  tumefaciens (strain C58/ATCC  33970).; coaA; Pantothenate kinase  (EC 2.7.1.33) (Pantothenic acid  kinase).; length=EC 2.7.1.3 ( 322;  id 81.988; 322 aa overlap; query  10-331; subject 1-322; putative  pantothenate kinase"  /codon-start=1  /transl-table=11  /product="Pantothenate kinase  (Pantothenic acid kinase) (Rts  protein)."  /protein-id="CAK05528.1"  /db-xref="GI:115254454"  /db-xref="GOA:Q1MNGO"  /db-xref="UniProtKB/TrEMBL:Q1MNGO" </p>

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/translation="MSIATEIIGVPETLDHFQSE
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TSDEVKRLRSMGDPIDLDEVRRILYLSLRLLSAH
VESSQMLFEQRNRFSLSDVTKTP
FVIGIAGSVAVGKSTTARILKELLGRWPSSPKVD
LVTTDGFLHPNAVLQREKLMQRKG
FPESYDTGAILRFLSAIKAGRPDVKAPSYSHLVY
DVLPDEYKIVDRPDILIFEGINVL
QSRDLFAGGKIVPMVSDFDFSGIYIDAAEIEHN
WYVTRFMRLRETAFRDPNSYFHRV
ASISDAEALIEADLWANINLKNLRQNLTPRPR
ADLLKKGKDHILIEQVALRKL"
misc-feature complement(43080..43742 /gene="coaA"
)
/locus-tag="RL0040"
/inference="protein
motif:Pfam:PF00485.7"
/note="Pfam match to entry
PF00485.7 PRK"
gene complement(44048..44371 /locus-tag="RL0041"
)
CDS complement(44048..44371 /locus-tag="RL0041"
)
/inference="similar to
sequence:INSDC:AE007946"
/inference="similar to
sequence:INSDC:ECRFBM"
/note="similarity:fasta;
with=UniProt:HIS2-ECOLI
(EMBL:ECRFBM); Escherichia coli.;
hisI; Histidine biosynthesis
bifunctional protein hisIE
[Includes: Phosphoribosyl-AMP
cyclohydrolase (EC 3.5.4.19)
(PRA-CH); Phosphoribosyl-ATP
pyrophosphatase (EC 3.6.1.31)
(PRA-PH)].; length=203; id 47.126;
87 aa overlap; query 6-92; subject
115-201 similarity:fasta;
with=UniProt:HIS2-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisE; Phosphoribosyl-ATP
pyrophosphatase (EC 3.6.1.31)
(PRA-PH).; length=107; id 71.698;
106 aa overlap; query 1-106;
subject 1-106"
/codon-start=1
/transl-table=11
/product="putative histidine
biosynthesis bifunctional protein"
/protein-id="CAK05529.1"
/db-xref="GI:115254455"
/db-xref="GOA:Q1MNF9"
/db-xref="UniProtKB/TrEMBL:Q1MNF9"
/translation="MSGFSLSDLESIVAERSKAP
PEQSWTAKLVAGGQPKAAKGLGEE
AIEAVMAAVTGDRDNLTYEADVLYHLLVVLKIA
EIPLENVMAELERRTAQSGLKEKA SRQSS"
misc-feature complement(44090..44356 /locus-tag="RL0041"
)
/inference="protein

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motif: Pfam:PF01503.6"
/note="Pfam match to entry
PF01503.6 PRA-PH"
gene      complement(44389..45177 /gene="hisF"
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/locus-tag="RL0042"
CDS       complement(44389..45177 /gene="hisF"
)
/locus-tag="RL0042"
/inference="similar to
sequence:INSDC:ABHISHAFE"
/inference="similar to
sequence:INSDC:AE007946"
/note="similarity:fasta;
with=UniProt:HIS6-AZOBR
(EMBL:ABHISHAFE); Azospirillum
brasiliense.; hisF; Imidazole
glycerol phosphate synthase
subunit hisF (EC 4.1.3.-) (IGP
synthase cyclase subunit) (IGP
synthase subunit hisF) (ImGP
synthase subunit hisF) (IGPS
subunit hisF).; length=261; id
69.767; 258 aa overlap; query
3-260; subject 2-251
similarity:fasta;
with=UniProt:HIS6-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisF; Imidazole glycerol
phosphate synthase subunit hisF
(EC 4.1.3.-) (IGP synthase cyclase
subunit) (IGP synthase subunit
hisF) (ImGP synthase subunit hisF)
(IGPS subunit hisF).; length=258;
id 82.129; 263 aa overlap; query
1-262; subject 1-258"
/codon-start=1
/transl-table=11
/product="putative imadazole
glycerol phosphate synthase
sununit"
/protein-id="CAK05530.1"
/db-xref="GI:115254456"
/db-xref="GOA:Q1MNF7"
/db-xref="UniProtKB/TrEMBL:Q1MNF7"
/translation="MTLKARVIPCLDVKDGRVVK
GVNFLNLVDAGDPVEAAKAYDAAG
ADELCFLDITASDNRETIFDVVSRTADQC FMLP
TVGGGVRTIADIRKLLLCGADKVS
INSAAVSNPDFVTEADKFGDQCIVVSDAKRRR
TQAVGGDNLSAWEIYTHGGRNATG
IDAVEFAQKMWARGAGELLVISM DRDGTGKVGYDL
ELTRAIDAVRPVPIASGGVGDLD
DLVAGVKEGHANAVLAASIFHFGTYSVSEAKHYM
SKCGIDMRLD"
misc-feature complement(44446..45162 /gene="hisF"
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/locus-tag="RL0042"
/inference="protein
motif: Pfam:PF00977.8"
/note="Pfam match to entry

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gene      complement(45178..45924) PF00977.8 His-biosynth
)      /gene="hisA"

CDS      complement(45178..45924) /locus-tag="RL0043"
)      /gene="hisA"
      /locus-tag="RL0043"
      /inference="similar to
sequence:INSDC:ECD840"
      /inference="similar to
sequence:INSDC:SME591782"
      /note="similarity:fasta;
with=UniProt:HIS4-ECOLI
(EMBL:ECD840); Escherichia coli.;
hisA;
1-(5-phosphoribosyl)-5-[(5-phospho
ribosylamino)methylidene amino]
imidazole-4-carboxamide isomerase
(EC 5.3.1.16)
(Phosphoribosylformimino-5-aminoim
idazole carboxamide ribotide
isomerase).;
length=5-phosphoribosyl; id
35.081; 248 aa overlap; query
2-242; subject 1-245
similarity:fasta;
with=UniProt:HIS4-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; hisA;
1-(5-phosphoribosyl)-5-[(5-phospho
ribosylamino)methylidene amino]
imidazole-4-carboxamide isomerase
(EC 5.3.1.16)
(Phosphoribosylformimino-5-aminoim
idazole carboxamide ribotide
isomerase).;
length=5-phosphoribosyl; id
88.066; 243 aa overlap; query
1-243; subject 1-243"
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/transl-table=11
/product="putative
imidazole-4-carboxamide isomerase"
/protein-id="CAK05531.1"
/db-xref="GI:115254457"
/db-xref="GOA:Q1MNC1"
/db-xref="UniProtKB/TrEMBL:Q1MNC1"
/translation="MILFPAIDLKGGQCVRLLKG
DMQQATVYNTDPAAQARSFEDQGF
EWLHVVDLDGAFAGHSANGDAVEAILKATDNPVQ
LGGGIRTLDHIEAWLSRGLRRVIL
GTVAVRNPDLVIEACRKFPPDHVAVGIDAKGGKVA
VEGWAEASELGIIEELARKFEGAGV
AAIIYTDIDRDGILAGINWSTLELADAVSIPVI
ASGGLASLDDIRRMLEPDARKLEG
AISGRALYDGRIDPKEALALIKARAKETA"

misc-feature complement(45232..45921) /gene="hisA"
)      /locus-tag="RL0043"
      /inference="protein
motif:Pfam:PF00977.8"

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		/note="Pfam match to entry PF00977.8 His-biosynth" /locus-tag="RL0044"
gene	complement (45931..46488)	
CDS	complement (45931..46488)	/locus-tag="RL0044"  /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAK05532.1" /db-xref="GI:115254458" /db-xref="UniProtKB/TREMBL:Q1MNC0" /translation="MIHDSFPDANLGGSSRRQNGVSG AGDIAEAVLEFFYIEGEDDLIGLLA YALYERQKRDFVLSHRKRNAGRSPDEAELAAVNS NYLSTDLNRTLDRASQILSSYAE TYVEAMEPQIRLTAVNSDALRQVRVSIKSIKRL GFWRQVRAGFAVTL L L L L L L F G A A A IAAVFFQSDIVDANALMVPTTLRM"
misc-feature	complement (45991..46059)	/locus-tag="RL0044"  /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 144-166"
gene	complement (46485..46676)	/locus-tag="RL0045"
CDS	complement (46485..46676)	/locus-tag="RL0045"  /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAK05533.1" /db-xref="GI:115254459" /db-xref="UniProtKB/TREMBL:Q1MNB9" /translation="MRSMPASRKSQGVFYTLRPS REGLPFFSDIKLPGGTIVIRRVDEA IHRKALSNAAKALKERLDR"
gene	complement (46921..47571)	/gene="hisH" /locus-tag="RL0046"
CDS	complement (46921..47571)	/gene="hisH"  /locus-tag="RL0046" /inference="similar to sequence:INSDC:ECD840" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:HIIS5-ECOLI (EMBL:ECD840); Escherichia coli.; hisH; Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH).; length=196; id

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36.792; 212 aa overlap; query
1-212; subject 1-194
similarity:fasta;
with=UniProt:HIS5-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; hisH; Imidazole
glycerol phosphate synthase
subunit hisH (EC 2.4.2.-) (IGP
synthase glutamine
amidotransferase subunit) (IGP
synthase subunit hisH) (ImGP
synthase subunit hisH) (IGPS
subunit hisH).; length=216; id
81.944; 216 aa overlap; query
1-216; subject 1-216"
/codon-start=1
/transl-table=11
/product="putative imadazole
glycerol phosphate synthase
subunit"
/protein-id="CAK05534.1"
/db-xref="GI:115254460"
/db-xref="GOA:Q1MNB8"
/db-xref="UniProtKB/TrEMBL:Q1MNB8"
/translation="MRVAIIDYSGNLRSAKAF
ERAHEAGIDAHDLTDRÆDVAA
ADRIVLPGVGAYADCRRLDVAVDMAEVLIEAVE
KKARPFLGICVGMQLMSSRGLEKT
VTHGFGWIPGNVVENTPDDPALKIPQIGWNTLDL
KRQHPLFEGIPTGSQGLHAYFVHS
YHLAÆNTEDVIATADYGGPMTAFVGRDNMVGAQ
FHPEKSQKLGGLALIANFLRNP"
/misc-feature complement(46927..47562
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/locus-tag="RL0046"
/inference="protein
motif:Pfam:PF00117.10"
/notes="Pfam match to entry
PF00117.10 GATase"
/gene complement(47574..48059
)
/locus-tag="RL0047"
/CDS complement(47574..48059
)
/inference="similar to
sequence:INSDC:A97364"
/notes="similarity:fasta;
with=UniProt:Q8U5P8 (EMBL:A97364);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; AGR-C-67p.;
length=164; id 32.099; 162 aa
overlap; query 3-161; subject
2-163"
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/transl-table=11
/product="putative transmembrane
protein"
/protein-id="CAK05535.1"
/db-xref="GI:115254461"
/db-xref="GOA:Q1MNB7"
/db-xref="UniProtKB/TrEMBL:Q1MNB7"
/translation="MTSSYIFLTPPGGTSATDE

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TRITRDGFTLLGFLFPWIWLLAHR
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VNMLVGLGQNFVRVRLAAGWNE
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QNKARPNGQHGNAATSLGLFDFDGG R"
misc-feature      complement(join(47805.. /locus-tag="RL0047"
47864,47922..47981))
                    /inference="protein
                    motif:TMHMM:2.0"
                    /note="2 probable transmembrane
                    helices predicted at aa 27-46 and
                    66-85"
sig-peptide       complement(48002..48059 /locus-tag="RL0047"
)
                    /inference="protein
                    motif:SignalP-HMM:2.0"
                    /note="Signal peptide predicted
                    for RL0047 by SignalP 2.0 HMM
                    (Signal peptide probability 0.696)
                    with cleavage site probability
                    0.687 between residues 18 and 19"
gene              complement(48082..48690 /gene="hisB"
)
                    /locus-tag="RL0048"
CDS               complement(48082..48690 /gene="hisB"
)
                    /locus-tag="RL0048"
                    /EC-number="4.2.1.19"
                    /inference="similar to
                    sequence:INSDC:AB091436"
                    /inference="similar to
                    sequence:INSDC:AE007946"
                    /inference="similar to
                    sequence:INSDC:E64967"
                    /note="Similar to C-terminus from
                    codon 160 of Escherichia coli.
                    hisB HIS7-ECOLI (EMBL:E64967) (
                    Histidine biosynthesis
                    bifunctional protein hisB
                    [Includes: Histidinol-phosphatase
                    (EC 3.1.3.15)) ehydratase (EC
                    4.2.1.19) (IGPD)]., and to entire
                    protein of Agrobacterium
                    tumefaciens (strain C58/ATCC
                    33970). hisB HIS7-AGRT5
                    (EMBL:AE007946) (
                    Imidazoleglycerol-phosphate
                    dehydratase (EC 4.2.1.19)
                    (IGPD).), and to entire protein of
                    Burkholderia multivorans. hisB
                    HIS7-BURML (EMBL:AB091436) (
                    Imidazoleglycerol-phosphate
                    dehydratase (EC 4.2.1.19) (IGPD).)
                    similarity:fasta;
                    with=UniProt:HIS7-ECOLI
                    (EMBL:E64967); Escherichia coli.;
                    hisB; Histidine biosynthesis
                    bifunctional protein hisB
                    [Includes: Histidinol-phosphatase
                    (EC 3.1.3.15);
                    Imidazoleglycerol-phosphate
                    dehydratase (EC 4.2.1.19)

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(IGPD)].; length=355; id 48.990;
198 aa overlap; query 4-201;
subject 163-355 similarity:fasta;
with=UniProt:HIS7-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisB;
Imidazoleglycerol-phosphate
dehydratase (EC 4.2.1.19) (IGPD).;
length=198; id 89.286; 196 aa
overlap; query 6-201; subject
2-197 similarity:fasta;
with=UniProt:HIS7-BURML
(EMBL:AB091436); Burkholderia
multivorans.; hisB;
Imidazoleglycerol-phosphate
dehydratase (EC 4.2.1.19) (IGPD).;
length=195; id 54.124; 194 aa
overlap; query 8-201; subject
2-195"
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/transl-table=11
/product="putative histidine
biosynthesis bifunctional protein
hisB"
/protein-id="CAK05536.1"
/db-xref="GI:115254462"
/db-xref="GOA:Q1MNB6"
/db-xref="UniProtKB/TrEMBL:Q1MNB6"
/translation="MAETAASRTGVSRSKTNETS
ISVSVNLDTGKSTISTGVGFDDH
MLDQLSRHSLIDMEIDAKGLDHDHHTVDTGI
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AMDETMTKAAVDLSGRPFVLVNVAFSAPKIGTFD
TELVREFFHALAQNAGITLHILNH
YGANNHHIAETCFKAVARALRTATEIDPRQAGRV
PSTKGTLV"
misc-feature complement(48148..48582
) /gene="hisB"
/locus-tag="RL0048"
/inference="protein
motif:Pfam:PF00475.7"
/note="Pfam match to entry
PF00475.7 IGPD"
gene 48847..49374 /gene="hslV"
/locus-tag="RL0049"
CDS 48847..49374 /gene="hslV"
/locus-tag="RL0049"
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sequence:INSDC:AE007946"
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sequence:INSDC:C91236"
/note="similarity:fasta;
with=UniProt:HSLV-ECOLI
(EMBL:C91236); Shigella flexneri.;
hslV; ATP-dependent protease hslV
(EC 3.4.25.-) (Heat shock protein
hslV).; length=175; id 62.573; 171
aa overlap; query 2-171; subject
1-171 similarity:fasta;
with=UniProt:HSLV-AGRT5
(EMBL:AE007946); Agrobacterium

```



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tumefaciens (strain C58/ATCC
33970).; hslV; ATP-dependent
protease hslV (EC 3.4.25.-).;
length=173; id 91.908; 173 aa
overlap; query 2-174; subject
1-173; putative heat-shock
ATP-dependent protease"
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/transl-table=11
/product="ATP-dependent protease
hslV (Heat shock protein hslV)."
/protein-id="CAK05537.1"
/db-xref="GI:115254463"
/db-xref="GOA:Q1MNB5"
/db-xref="UniProtKB/TrEMBL:Q1MNB5"
/translation="MTTIIIVRKGKGVVMAGDGQ
VSLGQIVMKGNARKVRRIGKGEVV
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LAKDWRTDKYLRNLEAMMLVADKS
ITLAIITNGDVLPEPHGTTAIGSGGNFALAAALA
LMDTDKSAEEIARRALDIAADICV
YTNHNVVVELLDAG"
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/locus-tag="RL0049"
/inference="protein
motif:Pfam:PF00227.11"
/note="Pfam match to entry
PF00227.11 Proteasome"
/gene 49361..49873
CDS 49361..49873
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/inference="similar to
sequence:INSDC:AF360385"
/inference="similar to
sequence:INSDC:AP003005"
/note="similarity:fasta;
with=UniProt:Q93TB3
(EMBL:AF360385); Klebsiella
pneumoniae.; Mutant AAC6'-IbY166A
6'-N-acetyltransferase.;
length=201; id 31.325; 166 aa
overlap; query 9-165; subject
27-192 similarity:fasta;
with=UniProt:Q98CT9
(EMBL:AP003005); Rhizobium loti
(Mesorhizobium loti).;
Aminoglycoside
6'-N-acetyltransferase.;
length=173; id 44.186; 172 aa
overlap; query 1-170; subject
1-170; putative acetyltransferase"
/codon-start=1
/transl-table=11
/product="putative Mutant
AAC6'-IbY166A
6'-N-acetyltransferase."
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/db-xref="GOA:Q1MNB4"
/db-xref="UniProtKB/TrEMBL:Q1MNB4"
/translation="MPKAEPYAFRPLAVADLPLL
AEWLESRRHVRNWSDDPAKALASME
KHIDAASVSCFMVTLSPGKDFAFIQAADLDEVDD"

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misc-feature 49523..49795

gene 49870..51177

CDS 49870..51177

misc-feature 50023..51003

ALAGQPKGTGIDQFIGIEELAGK  
GHGPAFMIGFCNMLFAKGAQRILVDPHPDNAFAI  
RAYTKAGFQGLGETTTNYGRALLM  
ALDRQENDTQ"  
/locus-tag="RL0050"  
/inference="protein  
motif:Pfam:PF00583.9"  
/note="Pfam match to entry  
PF00583.9 Acetyltransf-1"  
/gene="hslU"  
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/locus-tag="RL0051"  
/inference="similar to  
sequence:INSDC:AE007947"  
/inference="similar to  
sequence:INSDC:B86083"  
/note="similarity:fasta;  
with=UniProt:HSLU-ECOLI  
(EMBL:B86083); Shigella flexneri.;  
hslU; ATP-dependent hsl protease  
ATP-binding subunit hslU (Heat  
shock protein hslU).; length=443;  
id 57.942; 447 aa overlap; query  
1-435; subject 1-443  
similarity:fasta;  
with=UniProt:HSLU-AGRT5  
(EMBL:AE007947); Agrobacterium  
tumefaciens (strain C58/ATCC  
33970).; hslU; ATP-dependent hsl  
protease ATP-binding subunit  
hslU.; length=435; id 91.264; 435  
aa overlap; query 1-435; subject  
1-435"  
/codon-start=1  
/transl-table=11  
/product="putative ATP-dependent  
heat shock protease component"  
/protein-id="CAK05539.1"  
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/db-xref="UniProtKB/TrEMBL:Q1MNB3"  
/translation="MTTFSPREIVSELDRIYIGQ  
HDAKRAVAIALRNRWRRQQLDPSL  
RDEVMPKNILMIGTIGVGKTEISRRLAKLAGAPF  
IKVEATKFTVEVGYVGRDVEQIIRD  
LVEVGIGLVREKKRAEVQAKAHVSAEERVLDALV  
GTTASPATRENFRKKLRDGLDDK  
EIDIEVADAGSGMGGFIEIPGMPGANIGVLNLSM  
FGKAMGGRTKKVRTTVKASYSDLI  
RDESDKLIDNEVIQREAVRSTNDGIVFLDEIDK  
IAARDGGMGAGVSEGVQORDLPL  
VEGTTVSTKYGPVKTDHILFIASGAFHVSKPSDL  
LPQLQGRLPVIRVELRPLNKDDFR  
ILTETEASLIRQYRALMETESLSLEFTDDAIDAL  
ADVAVHLNSSVENIGARRLQTVME  
RVLLDISYNAPDRGGTAVTIDAAYVREHVGDLAQ  
NTDLSRFIL"  
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/locus-tag="RL0051"  
/inference="protein  
motif:Pfam:PF00004.12"

gene	51470..52417	/note="Pfam match to entry PF00004.12 AAA" /locus-tag="RL0052" /locus-tag="RL0052" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92TA6 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; CONSERVED HYPOTHETICAL TRANSMEMBRANE PROTEIN.; length=316; id 70.032; 317 aa overlap; query 1-315; subject 1-316" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05540.1" /db-xref="GI:115254466" /db-xref="UniProtKB/TrEMBL:Q1MNB2" /translation="MRRLLTSLMIAVALVNSAPA FAMQTVAGNRHAEQPDIPGASIR RTKGTKSSFDLKYEKVHELLATDRELMKIRKVS SAYGINPIHVVGGAIVGEHTYINVDA YDRLQAIYYKAASYAGESFRFAIDGESVDEFVAR PQFAECKSKSDSYTLWSCREDVWE TDFRGKTVGGTSFPNNRFSVFFQFPFYAGQTFGL GQVNP L TALMLSDLVTRVSGYPKL NEKNAGAVYRAIMDPDISLAFVAASIRRSIDYK EIAGMDSIGNPGLTATLYNVGNR QRAAALAAKNRGAGATVWPEENIYGWLINDKLDE LKGLL"
sig-peptide	51470..51533	/locus-tag="RL0052" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0052 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.991 between residues 22 and 23"
misc-feature	51503..52414	/locus-tag="RL0052" /inference="protein motif:Pfam:PF07182.1" /note="Pfam match to entry PF07182.1 DUF1402"
gene	52466..53878	/locus-tag="RL0053" /locus-tag="RL0053" /inference="similar to sequence:INSDC:A32966" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:CP43-RAT (EMBL:A32966); Rattus norvegicus (Rat).; Cyp4a3; Cytochrome P450 4A3 precursor (EC 1.14.15.3) (CYP4A3) (Lauric acid omega-hydroxylase) (P450-LA-omega 3).; length=EC ( 507; id 27.902; 448 aa overlap; query 37-461;
CDS	52466..53878	

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subject 75-503 similarity:fasta;
with=UniProt:Q92TA5
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE CYTOCHROME
P450 MONOOXYGENASE PROTEIN (EC
1.14.-.-); length=466; id 71.828;
465 aa overlap; query 1-465;
subject 1-465; putative cytochrome
P450 protein"
/codon-start=1
/transl-table=11
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precursor (CYPIVA3) (Lauric acid
omega-hydroxylase) (P450-LA-omega
3)."
/protein-id="CAK05541.1"
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/db-xref="UniProtKB/TrEMBL:Q1MNB1"
/translation="MDMRPDPFVPPAPLPRTVPP
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SDVRQLVLRPILRDGLLTAEGPVW
KRSRKAVAPIFTPRHAQGFAGQMLRQSEDYARKY
EGAGEAGAIFDISTDMTELTFAIL
ADTLFSGEIVTSSGHFADDVNELLRMRGRVDPMD
LMRAPSWVPRVTRIGGQKVLKFR
AIVRNTMDMRLAKMKADRSPADEFLTLLEQAG
PDGLTKEEIEDNLTFTIGAGHETT
ARALAWTLVCVNSPHIREGEMEEIDAVALTGAK
PVEWLDMPQTRAFAFEALRLYPP
APSINRAAISDDFTWSPKGERVELEAGVTVLVMP
WTLHRHELHWDPRAYMPERFLPE
NRASIGRFQFLPFGAGPRVCIGATFALQEAVIAL
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/locus-tag="RL0053"
/inference="protein
motif:Pfam:PF00067.9"
/notes="Pfam match to entry
PF00067.9 p450"
gene 53965..56136
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/locus-tag="RL0054"
/genes="glcB"
CDS 53965..56136
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sequence:INSDC:AY059637"
/inference="similar to
sequence:INSDC:U00096"
/notes="similarity:fasta;
with=UniProt:MASZ-ECOLI
(EMBL:U00096); Escherichia coli.;
glcB; Malate synthase G (EC
2.3.3.9) (MSG).; length=EC
2.3.3.9; id 60.083; 724 aa
overlap; query 4-721; subject
4-722 similarity:fasta;
with=UniProt:MASZ-RHILV
(EMBL:AY059637); Rhizobium
leguminosarum (biovar viciae).;
glcB; Malate synthase G (EC

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/db-xref="GI:115254469"
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/translation="MRIRNAFPVFGLLATLALAG
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FNDAYGLTKDAGYSLPAIPIDRVKQFRRQVVS
YQTTTPTGTTIIVNTRERFLYYILAN
GKAMRYGIGVGKQGFANAGTAYVANKQEWPNWHP
PKEMAVRRPDLAKYVEDGCMGPGLS
NPLGARAMYLFNEDGKDTLFRHLHGTPWASIGTA
ASSGCIRLMNQDVIDLYSRVRPGK
GTSKVVIQ"
misc-feature    complement(56216..56647
)
                /locus-tag="RL0055"
                /inference="protein
motif:Pfam:PF03734.4"
                /note="Pfam match to entry
PF03734.4 ErfK-YbiS-YhnG"
sig-peptide    complement(56803..56890
)
                /locus-tag="RL0055"
                /inference="protein
motif:SignalP-HMM:2.0"
                /note="Signal peptide predicted
for RL0055 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability
0.438 between residues 28 and 29"
gene           57070..57564
CDS            57070..57564
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sequence:INSDC:AF228577"
                /note="similarity:fasta;
with=UniProt:Q9KIP1
(EMBL:AF228577); Rhizobium
leguminosarum (biovar viciae).;
Hypothetical protein.; length=164;
id 98.780; 164 aa overlap; query
1-164; subject 1-164"
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protein"
                /protein-id="CAK05544.1"
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                /db-xref="UniProtKB/TrEMBL:Q1MNA8"
                /translation="MTILSVYNNPLIDGRQSDR
AMMVRRTGTQILLHEMRHVAFLPELP
LASGRRADLITLSEKGEIWIIEIKTSIEDFRVDR
KWPEYRLHCDRLFFATHQDVPLEI
FPEECGLFLSDGYGAHMIREAPEHRMAPATRKSV
TLNFSRAAQRILMAEWANGKPFV VDDV"
misc-feature    57070..57543
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motif:Pfam:PF06319.1"
                /note="Pfam match to entry
PF06319.1 DUF1052"
gene           complement(57585..58163
)
                /locus-tag="RL0057"
CDS            complement(57585..58163
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                /inference="similar to
sequence:INSDC:AF228577"
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with=UniProt:Q9KIP2
(EMBL:AF228577); Rhizobium
leguminosarum (biovar viciae).;
actR; ActR.; length=192; id
99.479; 192 aa overlap; query
1-192; subject 1-192"
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response regulator transcriptional
regulatory protein"
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/db-xref="UniProtKB/TrEMBL:Q1MNA7"
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GLDVIEAIRQRDDTRIIVLTGYG
NIATAVTAVKLGAVDYLAKPADADDVFSALTQRP
GEKAELPENPMSADRVVRWEHIQRV
YEMCERNVSETARRLNMMHRTIQRILAKRAPK"
misc-feature      complement(57744..58103
)
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                  /inference="protein
motif:Pfam:PF00072.9"
                  /note="Pfam match to entry
PF00072.9 Response-reg"
gene              complement(58232..59560
)
CDS               complement(58232..59560 /locus-tag="RL0058"
)
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sequence:INSDC:AF228577"
                  /note="similarity:fasta;
with=UniProt:Q9KIP3
(EMBL:AF228577); Rhizobium
leguminosarum (biovar viciae).;
actS; Sensor histidine protein
kinase.; length=436; id 98.624;
436 aa overlap; query 7-442;
subject 1-436"
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regulator sensor histidine kinase
transcriptional regulator"
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ALIGVAMVCITVLAFSFPFLPWFD
GVEINVHNVQFGVWCISIATMAFAAFYAYRVSM
EASQLADALAATELVLOREKHLsq
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RFREDVMLLRSSQSERCRDILRLT
TLSSGEAHMRRLLPLSSMIEIIVAPHREFGIRLE

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NLINAVDYAREKVIIVTVEHDDKVLIVIEDDGN
GYAPDILTRIGEPYVTKRQKEDTA
GGLGLGLFIKTLERSGASLIFENRDPESAGAR
IRIEWPRMLIDANSTK"
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)
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                /note="Pfam match to entry
                PF02518.9 HATPase-c"
misc-feature    complement(58709..58909 /locus-tag="RL0058"
)
                /inference="protein
                motif:Pfam:PF00512.10"
                /note="Pfam match to entry
                PF00512.10 HisKA"
misc-feature    complement(join(58988.. /locus-tag="RL0058"
59056,59084..59152,
59186..59254,
59405..59473))
                /inference="protein
                motif:TMHMM:2.0"
                /note="4 probable transmembrane
                helices predicted at aa 51-73,
                124-146, 158-180 and 190-212"
gene            complement(59583..62048 /locus-tag="RL0059"
)
CDS             complement(59583..62048 /locus-tag="RL0059"
)
                /inference="similar to
                sequence:INSDC:RM49051"
                /inference="similar to
                sequence:INSDC:SME591782"
                /note="similarity:fasta;
                with=UniProt:Q52902
                (EMBL:RM49051); Rhizobium meliloti
                (Sinorhizobium meliloti).; HelO.;
                length=821; id 74.908; 817 aa
                overlap; query 6-820; subject
                4-820 similarity:fasta;
                with=UniProt:Q92TA0
                (EMBL:SME591782); Rhizobium
                meliloti (Sinorhizobium
                meliloti).; ATP-DEPENDENT HELICASE
                PROTEIN.; length=820; id 74.939;
                818 aa overlap; query 6-821;
                subject 3-820"
                /codon-start=1
                /transl-table=11
                /product="putative ATP-dependent
                helicase protein"
                /protein-id="CAK05547.1"
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                /db-xref="GOA:Q1MNA5"
                /db-xref="UniProtKB/TrEMBL:Q1MNA5"
                /translation="MTISASLPVSHVLPVVA
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                IEVVTGCVFARMILDDPELTGVSVVFDEFHERS
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VMSATLDVERVAALLDHPPVIESLGRSFPIDIRY  
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 YGNLSQKEQDAAIRPASQGMRKIV  
 LATSIAETSITIDGVRVIDSGLQRLPVFEASTG  
 ITRLETVVRVSASADQRAGRAGRT  
 EPGTAVRLWHQGTAAALPAFTPPQILSSDLSGLV  
 LDLAHWGVQDPASLAFVDQPPETT  
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 LTEQGLGGTSVDIEERLRRFKVERGERAEASRRL  
 AGRLASGLDRGAATAPALAGQLL  
 HAFPDRIALQRRGRFRVMANGRAELPETERLA  
 GSQMLVIADLTGRAAQARVLAAAE  
 VTRGDIEAELPGEIKTGDQIFFDRQSRQIRARRA  
 TRLGAIVFEETPLPRPSGAAVTQA  
 LVEGVRELGLDQLSFSKEAVQLRERIGFLHRTIG  
 EPWFVDVSDALLSRLDDEWFAPFQT  
 EARGLSEISAAGLSNGLMSLVPHELQRLDLSRLAP  
 THFEAPTGRHPHPIQYEGEPEVLTII  
 RVQELFGLKQHPAIAAGRLPLLELTSPAHRPPIQ  
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gene	complement(62045..62992 )	/locus-tag="RL0060"
CDS	complement(62045..62992 )	/locus-tag="RL0060"  /inference="similar to sequence:INSDC:AE007928" /inference="similar to sequence:INSDC:AP003001" /note="similarity:fasta; with=UniProt:OCD-AGRT5 (EMBL:AE007928); Agrobacterium tumefaciens (strain C58/ATCC 33970).; arcB; Ornithine cyclodeaminase (EC 4.3.1.12) (OCD).; length=354; id 30.882; 272 aa overlap; query 44-313; subject 57-320 similarity:fasta; with=UniProt:Q98GR8 (EMBL:AP003001); Rhizobium loti (Mesorhizobium loti).; Ornithine cyclodeaminase; Ocd2.; length=321;

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ornithine cyclodeaminase"
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(OCD)."
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QAAEKIAAEARALGLNAEAVADAEEAARTADIIS
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GAFKPSMRESDDAAIRRASVYVDTRAGAI AEAGD
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GAHGGRSMDAEITLFKSVGALEDLAGAILAYKT
VTGQK"
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/note="Pfam match to entry
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gene              65462..65538
tRNA              65462..65538
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gene              69432..69551
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gene              69764..69840
tRNA              69764..69840
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gene              complement(70180..71670
)
CDS               complement(70180..71670
)
/inference="similar to
sequence:INSDC:AP006577"
/note="similarity:fasta;
with=UniProt:Q7NGT7
(EMBL:AP006577); Gloeobacter
violaceus.; Glr2801 protein.;
length=453; id 44.892; 372 aa
overlap; query 5-374; subject
1-355"

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family protein"
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YVVDHLLGGPQGLAVARSMHLERGLRLILDFVPN
HVAPDHLWVRDQPGYFVQGSDDDA
RNDPASFATVGSKVFARGRDPEFFPAWPDVLQLNT
FSPALRETIVETIAEIIAGQCEGVR
CDMAMLVLNTIFERTWGDHAGAKPDDDYWTIIP
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QQGFDYCYDKKLYDRMEHGDAESVRQHLLADSTY
QEKMVRFIEINHDEPRAAAAFPLEK
ARAAAVAMLTTLTGAKLLHEGQFEGATTRLPIFLG
RRPVASVDCDLSAFYARLLTAIHG
DVFKNGEWRLCETSGWSDNQSCRNLISWCWAKGE
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/note="Pfam match to entry
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CDS             complement(71667..74426
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id 59.935; 926 aa overlap; query
5-916; subject 1-908"
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SWIAETSRAARKPNLRQIEAAAGQSTVAATDSVG
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TKVAHYRMTIAPGQSATVRLRLS
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RSLSKVHERDPYVFQVQGGQYRVDYLPSESNTGM
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gene      complement(74746..76002 /locus-tag="RL0063"
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CDS       complement(74746..76002 /locus-tag="RL0063"
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          /note="similarity:fasta;
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          meliloti).; Putative membrane
          protein.; length=420; id 76.667;
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          subject 1-420"
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          LKNFPDWSLRIVGHTDASGNAETNERLSLERANA
          IKAALVERGVNTRDLLAAGAGQTR
          PIASNETAEGKALNRRVELVRLTDSAEAKLLKG
          MSDYLAAQKTIISFAYDANLQVVTN
          SEQKGLTSSGTVVLSPDKVHTTRSGGFVEIEA
          LFDGKTLTLLGKNLNKYTQVDIPG
          TVDHLIDELKDRYGLPLPAADLLMTNSYDELMQ
          G
          VYDSKDLGSGVINGAECDSLAFRK
          DEVDFQIIVAQGAQPYPCRLVITSRMVKGGPEYS
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          motif:Pfam:PF00691.7"
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gene      complement(76906..78225 /locus-tag="RL0064"
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CDS      complement(76906..78225 /locus-tag="RL0064"
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        (EMBL:AP003006); Rhizobium loti
        (Mesorhizobium loti).; M115242
        protein.; length=468; id 49.423;
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        YKGFFYHFLDIETGRRVWQCELSIDSAFLFAGA
        LTVATYFDRDTADEAEIRGLATAL
        YERADWNWARDGGATLTHGNRPESGFIPYRWRY
        DEGLLLYIIGLGSPTHELPPESYA
        AYTESYEWARNIYGRELLYSGLFTHQLSHMWIDF
        RGIRDAFMREHDTDYFENTRHATY
        VQQEYAIRNPMNMFAGYGEHCWGFTACDGPWGKR
        TTEGVDREYFDYIARGAPFGDDG
        TIAPWVAVASLFFAPEIVVPTVRNFARMNLGMTR
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gene      complement(78231..82121 /locus-tag="RL0065"
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CDS      complement(78231..82121 /locus-tag="RL0065"
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        meliloti).; ndvB; Protein ndvB.;
        length=2832; id 40.078; 1290 aa
        overlap; query 17-1282; subject
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        with=UniProt:Q7X325
        (EMBL:AY281354); uncultured
        Acidobacteria bacterium.; Putative
        cyclic beta 1'-2' glucan
        synthetase.; length=2714; id
        44.648; 1308 aa overlap; query
        2-1296; subject 1418-2711 Similar
        to codons 1550 to the C-terminus
        of Rhizobium meliloti
        (Sinorhizobium meliloti) Protein
        ndvB (2832 aa), and similar to
        codons 1420 to the C-terminus of

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uncultured Acidobacteria bacterium  
 Putative cyclic beta 1'-2' glucan  
 synthetase (1308 aa)"  
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 ERTLELTSYAEVCLYNRSADMAHP  
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 VHVSSNLQPAQAAQYETDRLRFL  
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 TVRLAPGADARIAFVTGAADDQSA  
 VQLIAKRYAEIDAVEQAFSDASRRYSESELQTLGL  
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 TSNYQSGGAYGFRDQLQDVMAVY  
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 IDAIPQAWAVISGEADAERASQAM  
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 SASWLRYVALEAILGRQEGRLRFEPVCVPAGWP  
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gene              complement(82152..84617 /locus-tag="RL0066"
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CDS               complement(82152..84617 /locus-tag="RL0066"
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                  length=787; id 51.216; 781 aa
                  overlap; query 25-802; subject
                  6-783 similarity:fasta;
                  with=UniProt:PHK1-RHIME
                  (EMBL:SME591782); Rhizobium
                  meliloti (Sinorhizobium
                  meliloti).; Probable
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FKQFSFPGGIPSHVAPETPGSIHE
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FVEGSDPENVHQQLAGVLDTAVID
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TYRRTNHGNLHVRYGKEEGTTTP
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PF03894.3 XFP"
gene complement(84994..85662 /locus-tag="RL0067"
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CDS complement(84994..85662 /locus-tag="RL0067"
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with=UniProt:Q92ZW4
(EMBL:AE007225); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein.;
length=217; id 57.746; 213 aa
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1-213"
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DLLKAIVTADQDETASGDEAIRRS
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ECKKAARVAEESVRGVRVVEHFS  EDRR"
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PF04972.3  BON"
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/inference="protein
motif: Pfam:PF00571.13"
/note="Pfam match to entry
PF00571.13  CBS"
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/inference="protein
motif: Pfam:PF00571.13"
/note="Pfam match to entry
PF00571.13  CBS"
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CDS             complement(85775..87463 /locus-tag="RL0068"
)
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with=UniProt:Q8DM98
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elongatus (Thermosynechococcus
elongatus).; ATP-binding protein
of ABC transporter.; length=616;
id 38.973; 526 aa overlap; query
30-555; subject 84-608"
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86882..86950,
86969..87037,
87179..87238,
87299..87367))
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motif:TMHMM:2.0"
/note="6 probable transmembrane
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76-95, 143-165, 172-194,261-283
and 290-312"
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/inference="protein
motif:Pfam:PF00664.9"
/note="Pfam match to entry
PF00664.9 ABC-membrane"
gene              complement(87586..89265 /locus-tag="RL0069"
)
CDS               complement(87586..89265 /locus-tag="RL0069"
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with=UniProt:Q59152 (EMBL:I39710);
Agrobacterium tumefaciens.; celd;
Celd protein.; length=584; id
64.159; 452 aa overlap; query
10-460; subject 1-452
similarity:fasta;
with=UniProt:Q8UAR8
(EMBL:AE009260); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; celd; Cellulose
biosynthesis protein.; length=553;
id 62.202; 545 aa overlap; query
7-545; subject 3-547"
/codon-start=1
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biosynthesis protein"
/protein-id="CAK05557.1"
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/db-xref="UniProtKB/TrEMBL:Q1MN95"
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FEAVRENWDQVFMEDPDAQHFLSW
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LITHLNEKTGLFYDEIIMAGNFPA
DYTGFIVRPDYEHHAIAGFASFLKHQNWTDLKL
EYFSGPAGRREKMI EALQGPEVMFR
DSSPKNSENIDNTICPIVPLPASFDYLEQRMSS
QTRQKLRRFLRKVEGDDVYRITMA
TAETIDRDLIDILNLRKWSARKGTERTERLII
TTREMLMDSFNCNLEVPVFVWHGD

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QPLGALANIIDRQKKAILFYITGRDENWKTPSPG
LILHGYCIRRAIEHGFKTYDFLRG
NEPYKYMFGVEERRISCTLFRTNRGQNLHGVLNP
RSIRFVYEQALDMYRNGARSKAEI
AFNQVLQSQAPGHTGAEFGLANLLFDRGKLTEAQA
AYKVLVEQAPDPTPIQMRLGDTQL
ALHQYDQAAETFRQIGIOPHLIQAHYKRGIALA
ASKRLAEAEAVFAAIQEVHSDPT
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misc-feature complement(87748..87849 /locus-tag="RL0069"
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/note="Pfam match to entry
PF00515.11 TPR"
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motif: Pfam:PF00515.11"
/note="Pfam match to entry
PF00515.11 TPR8"
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motif: Pfam:PF00515.11"
/note="Pfam match to entry
PF00515.11 TPR8"
gene complement(89508..89999 /locus-tag="RL0070"
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CDS complement(89508..89999 /locus-tag="RL0070"
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sequence: INSDC:B98318"
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with=UniProt:Q8UAP9 (EMBL:B98318);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Hypothetical
protein Atu3324.; length=170; id
77.160; 162 aa overlap; query
1-162; subject 7-168"
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/transl-table=11
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/protein-id="CAK05558.1"
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TESLLIYIIAHLRV EKDAIVVF
LT LNTTRARID LIERLSKLASTSP SDRKAILSAM
SRLKESKTRNKYNHC IYSFDEKG
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KSIAEIVAI SRTLWAFIHAS PQIS GEL"
/locus-tag="RL0071"
gene complement(90117..91466
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CDS complement(90117..91466 /locus-tag="RL0071"
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/inference="similar to
sequence: INSDC:C95953"
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sequence: INSDC:C98318"

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Rhizobium meliloti (Sinorhizobium
meliloti).; Hypothetical protein
expD2.; length=Hypothetical
protein; id 32.710; 428 aa
overlap; query 24-448; subject
52-472 similarity:fasta;
with=UniProt:Q8UAQ0 (EMBL:C98318);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Secretion
protein, HlyD family.; length=497;
id 80.778; 437 aa overlap; query
13-449; subject 61-497; putative
HlyD family secretion protein"
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/transl-table=11
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expD2."
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/db-xref="GI:115254485"
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/db-xref="UniProtKB/TrEMBL:Q1MN93"
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SRSNRMLQLRRLRLAEVVARLRAEAQGLRQFQL
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FERQLSLLTEERDSKARLVKVGVM
RKTDLLAIERAIADAMGDIARLNGELNESEAEIA
KFRQEAIVAVNSNKAALDALETA
ETDLDVSVREQMREAAGVLERTTIRSPVSGTVVRS
YFHTAGGVITTKPIMEILPSHVP
LILEAKVLRISIDQLHEGETASIRLTALNRRTTP
VLQGVFYVSADSIENAGASVKD
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misc-feature complement(90336..91271 /locus-tag="RL0071"
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/inference="protein
motif:Pfam:PF00529.8"
/note="Pfam match to entry
PF00529.8 HlyD"
misc-feature complement(91323..91391 /locus-tag="RL0071"
)
/inference="protein
motif:TMHMM:2.0"
/note="1 probable transmembrane
helix predicted at aa 26-48"
gene complement(91472..93769 /locus-tag="RL0072"
)
CDS complement(91472..93769 /locus-tag="RL0072"
)
/inference="similar to
sequence:INSDC:AE009262"
/note="similarity:fasta;
with=UniProt:Q8UAQ1
(EMBL:AE009262); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; ABC transporter,

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nucleotide binding/ATPase  
protein.; length=690; id 82.138;  
683 aa overlap; query 88-765;  
subject 9-690 Similar, but  
truncated at the N-terminus to  
Agrobacterium tumefaciens (strain  
C58/ATCC 33970) ABC transporter,  
nucleotide binding/ATPase protein  
(690 aa)"

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component of ABC transporter"  
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/db-xref="UniProtKB/TrEMBL:Q1MN92"  
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AVAQGLATAKTPEAPARFPQIEARVSPQPKKIE  
LKSSPTMPFAKTIEGSGPISENN  
RRMRAGGGGNGKSDPGGGGGGGGGGGFHKRS  
EPVNFASLSRGMMAVRHNMVVVM  
MFTIAINVLLAIPLYLFQISDRVLTSSVDTLV  
MLSIAVIGAVLLQAFMDSVRRFIL  
MRTAVELEVQLGAPILSAAARASLHGSGKDYQTL  
QDLQLLRGFLTSGTLIAFLDAPLM  
PPFVVVVYFVHPHGLGIIIMVCCAVLFVIAYNQK  
FTARQFAESNGYLSRANFHLDSMS  
RNSQIINAMAPIEAVKMWGRETAGSLKSQVEAQ  
DRNIIFSGISKACRMITQVTLGLW  
GAHLSLSGELTGMVIAASTISGRALPIEGAIIE  
GWNQFNRSAAAYSRIKGLLLNSPL  
NFFRLRLPNPEGRDLVERILFVPPQKKVILNGI  
SFSLRKGESLAIIGNSGSGKTLTG  
KMLVGSIVPTSGNVRLDLMDLRNWDQRQFGESIG  
YLPQDVQLFPGTIKANICMRDDV  
DDHQIYDAVLAADVHELIAGFPQGYETIVAADGA  
PLSGGQKQRIALARAFFGNPKFVV  
LDEPNSNLDTQGEAALAKALIHAKKQGITVTIT  
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misc-feature complement(91568..92125  
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/inference="protein  
motif:Pfam:PF00005.11"  
/note="Pfam match to entry  
PF00005.11 ABC-tran"  
/locus-tag="RL0072"

misc-feature complement(92333..93130  
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motif:Pfam:PF00664.9"  
/note="Pfam match to entry  
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/locus-tag="RL0072"

misc-feature complement(join(92363..  
92431,92675..92743,  
92756..92824,  
92966..93019,  
93062..93130))

/inference="protein"

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motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted at aa 214-236,
251-268, 316-338,343-365 and
447-469"
gene      complement(93795..95831 /locus-tag="RL0073"
)
CDS       complement(93795..95831 /locus-tag="RL0073"
)

/inference="similar to
sequence:INSDC:AE009262"
/note="similarity:fasta;
SWALL:Q8UAQ2 (EMBL:AE009262);
Agrobacterium tumefaciens;
hypothetical protein atu3321;
length 680 aa; 687 aa overlap;
query 1-678 aa; subject 8-680 aa"
/codon-start=1
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protein"
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VNALYDDDYLDMDTGVHAPRDTSF
VIERLADFSTKAEIFTFFASLHRTDTYDGALKVA
EDLEVYIQNAQNTEDSGTTSLGTD
ATHEFVRLDPGVNDITVYINGKAETDIPVLDLFLP
DRGLAKLPEEPDDSNITSVEQDDPS
GTSLEVTAGANLVNVASVINTGVITSVTAVMGN
YHQVDAISQAFVYSDNDEIASTLH
SSDRSGEAAETIAKNIALFEHSTFEASSHADTDA
TEPTFPNSWRVSVIDGDVSVFQWI
EQYQFVIDNDTMTVITSGETTVLTGNTSINFS
SFFGMGMQYDLVIIGGNVLDINSI
TQISLLYDNDWVRAEDGVDPGADIQTGDNLIWNF
ASIHNVGTDSFPAAMPDYMAATQK
AIEDRDPNMEPLSFDVNFQGYAGLNVLYITGNL
YDMTIIKQVSILGSDDDVTLAAS
ILENNPDAITVTIDTGSNAVVNIAEIVDYDSFGQT
TYLAGQLYSDAILIQGGLVEHDTT
QPQPADDRLANEVIAFFDNDPAGGDCADGVINA
GNDFSWSSTHPADVMQAMVA"
gene      complement(95973..96929 /locus-tag="RL0074"
)
CDS       complement(95973..96929 /locus-tag="RL0074"
)

/inference="similar to
sequence:INSDC:AE008350"
/note="similarity:fasta;
with=UniProt:Q8UAQ3
(EMBL:AE008350); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Fibrinogen binding
protein (AGR-L-3004p).;
length=321; id 65.109; 321 aa
overlap; query 6-317; subject

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		/transl-table=11
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		/protein-id="CAK05562.1"
		/db-xref="GI:115254488"
		/db-xref="UniProtKB/TreMBL:Q1MN90"
		/translation="MSDDTEITKVGALADGFANS AINSTEIDDDSTGYVGGVANGDNR DNTDNSVDVDVKAIEDVATNNGDNRDNEYDWSYK SDDDTSTKTTTITDIDTKTDYDWS YDSKTYSDNDITDKTITDIDTKTVITDIDIKTVIE TETDITKTVTDSNNTSDSFNKTDTD FAVIEDVKDSNLGVAGHDLTFNLGDDFSFTLDVD SILNNSLTGAGNDSGFSVAQANH ADQDSAWNTKMENEGAQNHLNANGGTANSAGME MDGKSWDLKAGDDANGASTADASA ILANSGFHLELVQGANLLSNTVSSVIGGNSHTS DVGEDTST"
repeat-unit	complement (96580..96593)	/locus-tag="RL0074"
repeat-unit	96622..96632	/note="accgacaccaagac"
repeat-unit	complement (96640..96653)	/rpt-unit-seq="tagctccagtc"
		/locus-tag="RL0074"
repeat-unit	96700..96710	/note="accgacaccaagac"
repeat-unit	96767..96780	/rpt-unit-seq="tagctccagtc"
repeat-unit	complement (96767..96780)	/note="cgctcgagctcgagc"
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gene	97773..98555	/note="cgctcgagctcgagc"
CDS	97773..98555	/locus-tag="RL0075"
		/locus-tag="RL0075"
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		/inference="similar to sequence:INSDC:I39835"
		/note="similarity:fasta; with=UniProt:DEGU-BACBR (EMBL:I39835); Bacillus brevis (Brevibacillus brevis).; degU; Transcriptional regulatory protein degU.; length=236; id 28.821; 229 aa overlap; query 24-239; subject 12-223 similarity:fasta; with=UniProt:Q8UAQ5 (EMBL:BM3181); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Transcriptional regulator, LuxR family (AGR-L-3006p).; length=265; id 59.231; 260 aa overlap; query 1-260; subject 10-265"
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		/transl-table=11
		/product="putative GerE family transcriptional regulator"
		/protein-id="CAK05563.1"
		/db-xref="GI:115254489"
		/db-xref="GOA:Q1MN89"
		/db-xref="UniProtKB/TreMBL:Q1MN89"
		/translation="MFMTGSGMENADGRKLGSG"

		<p> GDTILVVAADLFSECEMVEALAKK  FPNCEVASITSTKPILDKSDMKLVLFYHIPGP  ELHEALQAARENHPETSIGLVVEA  IDMLPEFYVSRLEARIIDGVLPLNLRDVFMAAV  DLLMKGGEHFPSSALLNRLTNKNAQ  LEPSLYQTKSVDAARSNALKLRDSISALTREV  QILDICKGTQNKIIADKLHLSN  TVKVHVRNIYKKMNVNRNTEAASRFFNEHPAGEE  DMSGRWRRN" </p>
misc-feature	98328..98501	<p> /locus-tag="RL0075"  /inference="protein  motif:Pfam:PF00196.8"  /note="Pfam match to entry  PF00196.8 GerE" </p>
gene	complement(98571..98891)	/locus-tag="RL0076"
CDS	complement(98571..98891)	<p> /locus-tag="RL0076"    /inference="similar to  sequence:INSDC:A98319"  /note="similarity:fasta;  with=UniProt:Q8UAQ6 (EMBL:A98319);  Agrobacterium tumefaciens (strain  C58/ATCC 33970).; Hypothetical  protein Atu3317 (AGR-L-3007p).;  length=116; id 37.864; 103 aa  overlap; query 13-104; subject  15-116"  /codon-start=1  /transl-table=11  /product="conserved hypothetical  protein"  /protein-id="CAK05564.1"  /db-xref="GI:115254490"  /db-xref="UniProtKB/TrEMBL:Q1MN88"  /translation="MVKKQDAQAQLKGRIRSAMF  AWGTALLAIGFTACTVDDHIAV  AKKNIPVVEAPRVSKAYAYPANRVGRPAAATVRT  VAYHGSAFYICSPSGFGQKSRCA RPPI" </p>
misc-feature	complement(98781..98849)	/locus-tag="RL0076"
gene	99276..100301	<p> /inference="protein  motif:TMHMM:2.0"  /note="1 probable transmembrane  helix predicted at aa 15-37"  /locus-tag="RL0077"  /locus-tag="RL0077" </p>
CDS	99276..100301	<p> /inference="similar to  sequence:INSDC:AT8927"  /inference="similar to  sequence:INSDC:B98319"  /note="similarity:fasta;  with=UniProt:Q9LFG7 (EMBL:AT8927);  Arabidopsis thaliana (Mouse-ear  cress).; F4P12-220; DTD-  glucose 4-6-dehydratase-like protein  (UDP-glucuronic acid  decarboxylase).; length=433; id  50.303; 330 aa overlap; query  2-328; subject 96-420  similarity:fasta;  with=UniProt:Q8UAQ7 (EMBL:B98319); </p>



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Agrobacterium tumefaciens (strain
C58/ATCC 33970).; DTD-glucose
4-6-dehydratase (AGR-L-3008p).;
length=340; id 72.093; 344 aa
overlap; query 1-341; subject
1-340"
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4-6-dehydratase-like protein
(UDP-glucuronic acid
decarboxylase)"
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YQRDPVGTLLTNVLGAVNTLDCARKTGAIVVQSS
TSEVYGDPIHSPQHECYCGNVNQI
GPRGCYDEGKRSSETLFFDYHRTYGVDVKVGRIF
NTYGPRLDDGRVVSNFIVQALR
NADLTIYGDGQQTSTFCYVDLLIEGFLRFSTAGS
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/inference="protein
motif:Pfam:PF01370.8"
/note="Pfam match to entry
PF01370.8 Epimerase"

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gene 100303..101286
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/inference="similar to
sequence:INSDC:RLEXOBGEN"
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(EMBL:RLEXOBGEN); Rhizobium
leguminosarum (biovar trifolii).;
exoB; UDP-glucose 4-epimerase (EC
5.1.3.2) (UDP-galactose
4-epimerase) (Galactowaldenase).;
length=EC 5.1 ( 327; id 51.757;
313 aa overlap; query 5-317;
subject 6-317 similarity:fasta;
with=UniProt:Q8UAQ8 (EMBL:C98319);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; galE;
UDP-glucose 4-epimerase.;
length=356; id 74.695; 328 aa
overlap; query 1-327; subject
30-356"
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/transl-table=11
/product="putative UDP-glucose
4-epimerase (UDP-galactose

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misc-feature 100315..101280

gene 101283..103151

CDS 101283..103151

4-epimerase)"

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EACLDQDIDRIVFSSSCATYGVFASLPPIREESQ  
HPVNPYGRTKLIFEMAELEDFAAAY  
GIRFAALRYFNAAAGADPDGELAERHQPEETHLIPR  
ALLAAAGRLERLIDFGTDYATEDG  
TCVRDYIHVSDLAQAHLAAVNHLADGGSLSVNL  
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/gene="exoB"

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/inference="protein  
motif:Pfam:PF01370.8"

/note="Pfam match to entry  
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/gene="acsAB"

/locus-tag="RL0079"

/gene="acsAB"

/locus-tag="RL0079"

/EC-number="2.4.1.12"

/inference="similar to  
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/inference="similar to  
sequence:INSDC:AXCCPENG"

/note="similarity:fasta;  
with=UniProt:ACSL-ACEXY  
(EMBL:AXCCPENG); Acetobacter  
xylinus.; acsAB; Cellulose  
synthase 1 [Includes: Cellulose  
synthase catalytic domain  
[UDP-forming] (EC 2.4.1.12);  
Cyclic di-GMP binding domain  
(Cellulose synthase 1 regulatory  
domain)].; length=1550; id 24.421;  
561 aa overlap; query 38-567;  
subject 80-606 similarity:fasta;  
with=UniProt:Q8UAQ9  
(EMBL:AE008351); Agrobacterium  
tumefaciens (strain C58/ATCC  
33970).; Cellulose synthase  
(AGR-L-3012p).; length=AGR-L-3012p; id 65.772; 596  
aa overlap; query 14-608; subject  
14-607"

/codon-start=1

/transl-table=11

/product="putative transmembrane  
cellulose synthase"

/protein-id="CAK05567.1"

/db-xref="GI:115254493"

/db-xref="GOA:Q1MN85"

/db-xref="UniProtKB/TrEMBL:Q1MN85"

/translation="MSSVSQIGHGVRTAKAATVE  
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 AYFILIFLDARTVSPRAGLPEGRV  
 AMVVTKAPSEPAVVRTTLQAMLDQIGVDFDVWL  
 ADEDPSEETRRWCEEHGVLISTRK  
 GVAEYHRTTWPRTRCKEKNLAYFYDHFYARYD  
 FVAQFDADHVPTPTYLREILRPFA  
 DPEIGYVSAPSIDANAGTSWAARGRLYAEASLH  
 GSLQGTGYNNGWAPLCIGSHYAVRT  
 SALRQIGGLGPELAEDHSTLTMNNSGGWRGVHAV  
 DAIAHGDPANFTDLVVQEFQWSR  
 SLVTILLQHSRRHIMHLPWRLRFQFVFSQLWYPL  
 FSVFAMMMFLLPVAALLTGRVFN  
 VTYPDFLLHFVPMMSVLTLFAFFWRTTATFRPHD  
 AKLLGWEGLAIFLRWPWSLAGSL  
 AAVRDYICGSFVDFRITPKGRQQQORSLPLRVIAF  
 YIGLAGLSAAAMMFATDAAAQGF  
 YVFAMMNLVYVYALITVLIVVRHAVENDLPLLPQS  
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 /gene="acsAB"

misc-feature      order(101376..101435,  
                     101472..101540,  
                     102369..102437,  
                     102474..102542,  
                     102585..102653,  
                     102711..102779,  
                     102807..102875,  
                     102912..102980)

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 64-86, 363-385, 398-420,435-457,  
 477-499, 509-531 and 544-566"

misc-feature      101586..102131

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 /inference="protein  
 motif:Pfam:PF00535.10"  
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 PF00535.10 Glycos-transf-2"  
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gene                103148..103711  
 CDS                103148..103711

/inference="similar to  
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 with=UniProt:Q8UAR0  
 (EMBL:AE009261); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; Hypothetical protein  
 Atu3313.; length=173; id 50.000;  
 152 aa overlap; query 26-177;  
 subject 21-169"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 exported protein"  
 /protein-id="CAK05568.1"  
 /db-xref="GI:115254494"  
 /db-xref="UniProtKB/TrEMBL:Q1MN84"  
 /translation="MSRRNRQVSSMEDVMSIGSR  
 LWGAALALSCLLPVATHGAIEAVKT

		KAPTPLSAYELYRIYGDKTWTWNTGGGRRFFYDGR RFVAVSNDKKGKPSFAEGRWVVDDL GQLCMRATWTNAEGAARASTCFGHRKIGNTIYQR RQPNGEWYVFRHASVRQGDEFQKL VPTDTSYSAKASEVKQILLSQEVARKGG" /locus-tag="RL0080" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0080 by SignalP 2.0 HMM (Signal peptide probability 0.995) with cleavage site probability 0.977 between residues 38 and 39"
sig-peptide	103148..103259	
misc-feature	103202..103648	/locus-tag="RL0080" /inference="protein motif:Pfam:PF06191.1" /note="Pfam match to entry PF06191.1 DUF995" /locus-tag="RL0081" /locus-tag="RL0081" /inference="similar to sequence:INSDC:AB039953" /inference="similar to sequence:INSDC:AE008351" /note="similarity:fasta; with=UniProt:Q8RS40 (EMBL:AB039953); Alcaligenes sp. XY-234.; 3xynAlc; Beta-1,3-xylanase.; length=469; id 28.105; 153 aa overlap; query 87-229; subject 65-209 similarity:fasta; with=UniProt:Q7CS49 (EMBL:AE008351); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-L-3016p.; length=320; id 66.901; 284 aa overlap; query 34-317; subject 32-315 Codons 85 to 235 are similar to codons 65 to 215 of Alcaligenes sp. XY-234 Beta-1,3-xylanase (469 aa), and entire protein is similar to Agrobacterium tumefaciens (strain C58/ATCC 33970) AGR-L-3016p (320 aa)" /codon-start=1 /transl-table=11 /product="putative polysaccharide degradation protein" /protein-id="CAK05569.1" /db-xref="GI:115254495" /db-xref="UniProtKB/TrEMBL:Q1MN83" /translation="MKKLMKKNLSTAAIALLLC VADLPGRSEVQYAGIAPNPAAAVR TIIDKRPVLHADGKFGAYDPHGDFGAQASVATE ALFLPWEDVDLETLRVADAYAQAAR GRNLLITVEPWSWDVDWRLTSAELRAKVLRGDYD VNMRAIAQMISELKSPVIVRWGQE MEDKSGRFSWSGWSPODYITAYKRMMDIVRQEAP GTELMWSPKGPGLQAYYPGDDYV DLVGLSVFGLQRYDELAYNGHRTFSEALKQGYDL VAGYGPKIWVAELGYGGDAYMKP
gene	103715..104686	
CDS	103715..104686	

		WIETVALKQSAFPNLQEVVYFNDRDVHAWPFDLG RPDWRVVESLANR" /locus-tag="RL0081" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0081 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.849 between residues 22 and 23"
sig-peptide	103715..103778	
gene	complement(104748..106034)	/locus-tag="RL0082"
CDS	complement(104748..106034)	/inference="similar to sequence;INSDC:RME591985" /note="similarity:fasta; with=UniProt:Q92W28 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative solute-binding protein.; length=428; id 72.326; 430 aa overlap; query 1-427; subject 1-426" /codon-start=1 /transl-table=11 /product="putative solute-binding component of ABC transporter" /protein-id="CAK05570.1" /db-xref="GI:115254496" /db-xref="GOA:Q1MN82" /db-xref="UniProtKB/TrEMBL:Q1MN82" /translation="MQVNRRSFLMGSAGAAAGLA FGAGSAIPAFEDAQLRAMW*GSN DRAKRTLDVAKLYQSKTPGVITIVGESLSGDGYWT KLATQMAGRSIADIFQLEPGTISD YSKRGACMPLDEFVPSLQVDSFGADMCLKTTID GKLYGVGLGLNSFSMFFDTVEFEK AGIPVPTPDLTWDEYAKLAVELAKSSGKSGGPYA ARYAYVFDAWLRQRGKSLFARFV GLGFTADDAREWFDYWEKLRKAGGIVAADVQTLD QNTIDTNALGLGKSVIGMAYSNQM IGYQLIIKNKLGITMLPREKKGSPSGHYRPAFI WSVGATTKNGEAAAFIDFFVNDI EAGKILGVERGVPMSPTVREAILPQLNPTEQETV KYVNLKDKQVGEYPPVPVPMGATQF DQRVLRPICDELAFERVSADAAATRLIEEGKATI KG"
misc-feature	complement(105024..106010)	/locus-tag="RL0082"
		/inference="protein motif:Pfam:PF01547.11" /note="Pfam match to entry PF01547.11 SBP-bac-1"
sig-peptide	complement(105938..106034)	/locus-tag="RL0082"
		/inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0082 by SignalP 2.0 HMM (Signal peptide probability 1.000)

		with cleavage site probability 0.981 between residues 31 and 32"
misc-feature	complement(105948..106016)	/locus-tag="RL0082"
		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 7-29"
gene	106182..107201	/locus-tag="RL0083"
CDS	106182..107201	/locus-tag="RL0083" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:Q92W29 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative transcriptional regulator protein.; length=342; id 66.964; 336 aa overlap; query 1-336; subject 1-336" /codon-start=1 /transl-table=11 /product="putative LacI family transcriptional regulator" /protein-id="CAK05571.1" /db-xref="GI:115254497" /db-xref="GOA:Q1MN81" /db-xref="UniProtKB/TrEMBL:Q1MN81" /translation="MNDQKIRRPQADIATLAGV SVSTVSRVLNPEFGISESVRLQIL KVAENGYPVKPASEAVAGGLALIASDGVGTGLS VFYEAIVDGLRAGAAEAGMPFEVR LVREDRTTPDAVRDYMQTAGAEGFLVGIDPNES LRDWLQASMTPTVLVNGTIDPRMQF DGVSPANFFGAYEATSRLLTKAGHRRILHLSGSHR HTIRERVVRGFEEAIAAVSGAEGRL VSLALQGSASREAHERTTEALAENAGFTAFCMN DFIAVGVLAVTEAGLRVPEDFAI VGFDLLPCAQMTNPQLSTMRVDRAALGREAVSLM LSRFRNRTASARHICQAVRIPGG TVPNA" /locus-tag="RL0083" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0083 by SignalP 2.0 HMM (Signal peptide probability 0.906) with cleavage site probability 0.895 between residues 30 and 31"
sig-peptide	106182..106269	
misc-feature	106206..106283	/locus-tag="RL0083" /inference="protein motif:Pfam:PF00356.8" /note="Pfam match to entry PF00356.8 LacI"
misc-feature	106365..107198	/locus-tag="RL0083" /inference="protein motif:Pfam:PF00532.8" /note="Pfam match to entry PF00532.8 Peripla-BP-1"
gene	107329..109185	/locus-tag="RL0084"
CDS	107329..109185	/locus-tag="RL0084" /inference="similar to

gene 109182..110192  
CDS 109182..110192

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sequence:INSDC:C95906"
/note="similarity:fasta;
with=UniProt:Q92W30 (EMBL:C95906);
Rhizobium meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMB20536.; length=617; id 75.121;
619 aa overlap; query 1-618;
subject 1-617"
/codon-start=1
/translation=11
/product="conserved hypothetical
protein"
/protein-id="CAK05572.1"
/db-xref="GI:115254498"
/db-xref="UniProtKB/TrEMBL:Q1MN80"
/translation="MTYDPASANPLAGNPLETRA
DMSRALLALFDPELLACFSKGNARV
TLNGGGAHFDRAAADLEGFARPLWGLAPLGAGNG
DFAHWHRFAGEGLANGTDPAHPEYW
GTVNGRDQRMVELAALGFALALVPEKIWEPLDAR
ARGNVVAYLKHARQFDYADNNWKF
FRIFVDIALDRLGADFRSLTRQYLEELEGFYIG
DGWYRDGNVRRIDHYIPFAMHFG
LIYSKLVDDDYAKRYRERAVLFARDFRHWFAADG
ATIPFGRSILTYRFACAGFWALAF
ADVEALPWGEVKHLCLOHLRWWKDKPIADR DGV
SIGFGYPNLLMSESYNSAGSPYWA
FKAFPLAIAEDHPFWTAKEKVEQAPDIIPQRH
PGMVMIRAGGDVVALLSSGQENLQM
RCGTEKYAKFAYSARYGFSVEADERAFALAAFD
ALAFSDDDLHYRVRETNEEAKIAG
EVLFAKWSPFADVDTWLVPAAPWHIRLHRI
SRPLRIAEGGFAIGRRDFELDTLS
ASGGVAYAVGEADFTGILDGSSVKRSLVQKAM
PNTNVIVAKTLVPQLRGQIPTGET
ILVTAVLALDDPAALSSAWARFPKAPDIAALEAL
VREKGVTVSAIEAPGQMP"
/locus-tag="RL0085"
/locus-tag="RL0085"
/inference="similar to
sequence:INSDC:B95906"
/inference="similar to
sequence:INSDC:MESERCYC"
/note="Codon 70 to the C-terminus
are similar to codons 60 to the
C-terminus of Methylobacterium
extorquens. HprA DHGY-METEX
(EMBL:MESERCYC) ( Glycerate
dehydrogenase (EC 1.1.1.29)
(NADH-dependent hydroxypyruvate
reductase) (HPR) (GDH)
(Hydroxypyruvate dehydrogenase)
(Glyoxylate reductase) (HPR-A).),
and to entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
Putative dehydrogenase protein.
Q92W31 (EMBL:B95906) (336)
similarity:fasta;
with=UniProt:DHGY-METEX
(EMBL:MESERCYC); Methylobacterium
extorquens.; hprA; Glycerate
dehydrogenase (EC 1.1.1.29)

```

```

(NADH-dependent hydroxypyruvate
reductase) (HPR) (GDH)
(Hydroxypyruvate dehydrogenase)
(Glyoxylate reductase) (HPR-A).;
length=313; id 36.047; 258 aa
overlap; query 75-322; subject
63-307 similarity:fasta;
with=UniProt:Q92W31 (EMBL:B95906);
Rhizobium meliloti (Sinorhizobium
meliloti).; Putative dehydrogenase
protein.; length=336; id 64.881;
336 aa overlap; query 1-336;
subject 1-336"
/codon-start=1
/transl-table=11
/product="putative glycerate
dehydrogenase"
/protein-id="CAK05573.1"
/db-xref="GI:115254499"
/db-xref="GOA:Q1MN79"
/db-xref="UniProtKB/TrEMBL:Q1MN79"
/translation="MSQPAIIAMQPSRTQHVLP
DEVLRRLGGIGRLLDSKFLQRFDD
ERARRLLAAEAILITGWGGPYVGPEIPTAAPHLK
FIVHAAGTVKGVIDDAIFEAGIPV
SHSAEANAVPVAEFTLAAIIFAGKRVFRFRDLYV
ADRNRRNRTHLMQREAIIGNRYRTVG
IVGASRIGRRVIELLKPFDFYRLLLSDPFLDAAEA
AGLGTEKIDLDLMRQSDIVSLHA
PSLPSTQHMIDARRLSLMKDGATLINTARGILID
EAALLSVLKTGRIDAVLDVDTPEI
PEAGSAFYDLPNVFLTPHIAGAIGLERARLGEMA
VDEIERFVTGQPLLYQIHQANLAN IA"
misc-feature 109518..110063
/locus-tag="RL0085"
/inference="protein
motif:Pfam:PF02826.5"
/note="Pfam match to entry
PF02826.5 2-Hacid-dh-C"
gene complement(110281..1116
09)
CDS complement(110281..1116 /locus-tag="RL0086"
09)
/inference="similar to
sequence:INSDC:B95991"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:MI2D-RHIME
(EMBL:B95991); Rhizobium meliloti
(Sinorhizobium meliloti).; idhA;
Inositol 2-dehydrogenase (EC
1.1.1.18).; length=330; id 26.471;
204 aa overlap; query 22-225;
subject 4-194 similarity:fasta;
with=UniProt:Q92T57
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
OXIDOREDUCTASE PROTEIN.;
length=433; id 82.892; 415 aa
overlap; query 20-434; subject
5-419 N-terminus to codon 230 is

```



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similar to the N-terminus to codon
200 of Rhizobium meliloti
(Sinorhizobium meliloti) Inositol
2-dehydrogenase (330 aa), and
entire protein is similar to
Rhizobium meliloti (Sinorhizobium
meliloti) PUTATIVE OXIDOREDUCTASE
PROTEIN. (433 aa)"
/codon-start=1
/transl-table=11
/product="putative GFO/IDH/MocA
family oxidoreductase"
/protein-id="CAK05574.1"
/db-xref="GI:115254500"
/db-xref="GOA:Q1MN78"
/db-xref="UniProtKB/TrEMBL:Q1MN78"
/translation="MGLISVFVSSRMQEDHSMEK
RRFALIGTGNRGTTMWGKDLLAGW
REHVDLTAIVEKNSLRGERARNMIGSNAPLYENI
DSMLAEQKPDLVIVCTPDHTHDDI
VVRALESgidvITEKPMTTTSVEKIRRILDAEKRT
GRRVDVTSFNRYAPTAAKIKELLN
AGEIGRVTSVDFFHWYLNTHKGADYFRRWHAYKEN
SGSLFVHKATHHFDLLNWYLDSDP
EAVTSFADLQNYGRKGPFGRGPRCKLCPHTHECDY
YLDLEADPFELDSLYEDPSKIDGYF
RDGCVFREDIDIPDTMVSLRYRNNVHVSYSLNT
FQPIEGHHLAFNGTKGRIELRQYE
AQPWEEPKQDTILLIRNFPDGKEAVERIVVPHFT
GGHYGGDDRRNMIMIFKPDTEDLA
QRAGTRAGAMSVLCGIAALESSRTGKVVDIADLM
PELANDGSPNSLRTSR"
/misc-feature complement(110833..1111 /locus-tag="RL0086"
44)
/inference="protein
motif:Pfam:PF02894.4"
/notes="Pfam match to entry
PF02894.4 GFO-IDH-MocA-C"
/misc-feature complement(111178..1115 /locus-tag="RL0086"
49)
/inference="protein
motif:Pfam:PF01408.8"
/notes="Pfam match to entry
PF01408.8 GFO-IDH-MocA"
/gene complement(111710..1125 /locus-tag="RL0087"
34)
/CDS complement(111710..1125 /locus-tag="RL0087"
34)
/inference="similar to
sequence:INSDC:A69646"
/inference="similar to
sequence:INSDC:AY316746"
/notes="similarity:fasta;
with=UniProt:IOLI-BACSU
(EMBL:A69646); Bacillus subtilis.;
ioli; Ioli protein.; length=278;
id 26.429; 280 aa overlap; query
6-265; subject 3-263
similarity:fasta;
with=UniProt:Q6W2E1
(EMBL:AY316746); Rhizobium sp.
(strain NGR234).;

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3-dehydroshikimate dehydratase (EC
4.2.1.-).; length=EC ( 274; id
85.766; 274 aa overlap; query
1-274; subject 1-274"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05575.1"
/db-xref="GI:115254501"
/db-xref="UniProtKB/TrEMBL:Q1MN77"
/translation="MQVEGLSINLATIREQCGFA
EAVDICKLKHGITAIAPWDQVAKV
GLDEAVRIVKSNIGIKLTGLCRGGFFFAANDADWQ
KNLDDNRRRAIDEEAAAFSADCLVLV
VGGLPGSSKDIVAARRMVFDGIAAVLPHAQAAGV
KLAIEPLHPMYAADRACVNTLQQA
LDLCEQLGEDVGAVDVYHVWDPDLANQIARAG
RMKRIFAHHICDWLVP TKDMLLDR
GMMGDGVIDLKGI RRMVEAAGFFGAQEVEIFS AE
NWWKRPAEEVIATCVERFRSCC"
gene      complement(112672..1138 /locus-tag="RL0088"
35)
CDS        complement(112672..1138 /locus-tag="RL0088"
35)
           /inference="similar to
           sequence:INSDC:SME591782"
           /note="similarity:fasta;
           with=UniProt:Q92T60
           (EMBL:SME591782); Rhizobium
           meliloti (Sinorhizobium
           meliloti).; Hypothetical protein
           SMC04132.; length=387; id 84.197;
           386 aa overlap; query 1-386;
           subject 1-386"
           /codon-start=1
           /transl-table=11
           /product="conserved hypothetical
           protein"
           /protein-id="CAK05576.1"
           /db-xref="GI:115254502"
           /db-xref="UniProtKB/TrEMBL:Q1MN76"
           /translation="MTTINLPLDGKIVPYTLTGT
           FIALAKRDAKAFPRIAFAAAHVVA
           DPLADNDFWLTPAIDWERTLAFRHRLWDLGLGVA
           EAMDTAQRGMGLGWPEARDLIRRA
           LSEAAGRKDALIACGAGTDHLTPGPDVTVDTILS
           AYEEQIETVEAAGGRIILMASRAL
           AAAAKPGDDYIRVYDRILRQVKEPVIIHWLGEMF
           DPALEGYWGNGDHIQAMSTCLEVI
           EAHADKVDGIKISLLSKEKEVAMRRRLPKGV RMY
           TGDDFN YAE LIA GDEEGHS DAL LG
           IFDAIAPAASAALEALGRKSNHEFFDLLEPTVPL
           SRHIFKAPTRFYKTGVVFLAYLNG
           LQDHFVMVGGQQSTRSLTHLAELFRLADKARVLA
           DPELATARMQVLAVHGVN"
           /locus-tag="RL0088"
misc-feature complement(112678..1138
32)
           /inference="protein
           motif:Pfam:PF06187.1"
           /note="Pfam match to entry
           PF06187.1 DUF993"

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gene complement(113839..1149 /locus-tag="RL0089"  
87)

CDS complement(113839..1149 /locus-tag="RL0089"  
87)

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sequence:INSDC:AY316746"  
/note="similarity:fasta;  
with=UniProt:Q6W2E4  
(EMBL:AY316746); Rhizobium sp.  
(strain NGR234).; Oxidoreductase  
(EC 1.1.1.-).; length=382; id  
91.099; 382 aa overlap; query  
1-382; subject 1-382"  
/codon-start=1  
/transl-table=11  
/product="putative oxidoreductase"  
/protein-id="CAK0577.1"  
/db-xref="GI:115254503"  
/db-xref="GOA:Q1MN75"  
/db-xref="UniProtKB/TrEMBL:Q1MN75"  
/translation="MARLGIILHGVIGRMGYNQH  
LVRSLAIFRDQGGITLKSSEKLEI  
DPIIVGRNGAKMEELAKKHNIKRWSTDLDAALAN  
PDDTIFFDAGTTLMRAELLKSKALD  
AGKHVYCEKPISSDDLQVALDLARKARRSGLKHGV  
VQDKLFLPGLRKLALLRDSGFFGK  
ILSVRGEFGYWFEGDWGVPAQRPSWNYRKGDDG  
GIIDMLCHWRVYLDNLFGGEVAV  
SCLGATHIPRRIDEQKGPYDCDDDAAYATFELE  
GGAIAQVNSSWAVRVRDDLVTFQ  
VDGTHGSAGVAGLTKCWSQHRVNTPKPVWNPDPQ  
TIDFYKTWDEVPTQAFDNGFKAQ  
WEMFIRHVVEDAPWYGLEAGAGVQLAELGLKS  
WAERRWLDVPALEF"

misc-feature complement(114166..1145 /locus-tag="RL0089"  
10)

/inference="protein  
motif:Pfam:PF02894.4"  
/note="Pfam match to entry  
PF02894.4 GFO-IDH-MocA-C"

misc-feature complement(114574..1149 /locus-tag="RL0089"  
84)

/inference="protein  
motif:Pfam:PF01408.8"  
/note="Pfam match to entry  
PF01408.8 GFO-IDH-MocA"

gene complement(115119..1157 /locus-tag="RL0090"  
96)

CDS complement(115119..1157 /locus-tag="RL0090"  
96)

/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:Q92T62  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE TRANSCRIPTION  
REGULATOR PROTEIN.; length=225; id  
75.111; 225 aa overlap; query  
1-225; subject 4-225"  
/codon-start=1  
/transl-table=11

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/product="putative TetR family
transcriptional regulator"
/protein-id="CAK05578.1"
/db-xref="GI:115254504"
/db-xref="GOA:Q1MN74"
/db-xref="UniProtKB/TrEMBL:Q1MN74"
/translation="MNSGGNGEKKRSRRPSAER
TAQRDPERTRAAILDAATREFAEN
GMGGARVDAIAERAGTNKRMLYHYFGDKEQLYLR
VLEEAYVGIRTAERALHIGDRSPE
EGISELALFTWRYFLQHPEFLSLGLTENLHRRW
LRQSVRLKELHSHLIGELSDVLEQ
GKKQGVFIETADPLHYLTIASLGIFYLSNQYTL
STIFGRDLMEPTHLNAWERHIVHV TLASIKR"

misc-feature      complement(115560..1157
00)               /locus-tag="RL0090"

                  /inference="protein
motif:Pfam:PF00440.8"
                  /note="Pfam match to entry
PF00440.8 TetR-N"

gene              115995..117281
CDS               115995..117281
                  /locus-tag="RL0091"
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                  /inference="similar to
sequence:INSDC:SME591782"
                  /note="similarity:fasta;
with=UniProt:Q92T63
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE PERIPLASMIC
BINDING ABC TRANSPORTER PROTEIN.;
length=427; id 69.159; 428 aa
overlap; query 1-428; subject
1-427"
                  /codon-start=1
                  /transl-table=11
                  /product="putative ATP-binding
component of ABC transporter"
                  /protein-id="CAK05579.1"
                  /db-xref="GI:115254505"
                  /db-xref="GOA:Q1MN73"
                  /db-xref="UniProtKB/TrEMBL:Q1MN73"
                  /translation="MTRFVSRNFVAGGATLLSL
SALGTSALAQETRLRLLLWGSQPR
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ATQVAGRNAPDVQMDYRIYVQYA
RRGALAPLESYMPAKLNLDDFDKAQIEGGSVDGH
LYGVSGLGANSAAATVLNTTAFKEAG
VDLPTQATTWEEFGRIGAEITKAGKRKGMFGIAD
GSGGEPLFENWLRLQRKALYTDG
KIAFDVDDASEWYDMWAKFREAGACVPADIQALD
KNDIETINTVSLGKSAAGFAHSNQF
VAYQAMNKDKLALNTNMRKIPESKGGHYRKPSMF
FSVSAQSKAVDLAVDYVNFVKNP
EAALLLDVERGIPESAMREVVAAKLDENGKVAL
AYVSGLDLAGKLPPPPFAGAGEG
ELMLRNIAEQVGFGQLSPSDGGKQLVAEITQILAR
G"

sig-peptide      115995..116079
                  /locus-tag="RL0091"
                  /inference="protein
motif:SignalP-HMM:2.0"
                  /note="Signal peptide predicted
for RL0091 by SignalP 2.0 HMM

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		(Signal peptide probability 1.000) with cleavage site probability 0.997 between residues 29 and 30" /locus-tag="RL0091" /inference="protein motif:Pfam:PF01547.11" /note="Pfam match to entry PF01547.11 SBP-bac-1"
misc-feature	116025..117005	
gene	117288..118247	/locus-tag="RL0092"
CDS	117288..118247	/locus-tag="RL0092" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T64 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSPORT SYSTEM PERMEASE ABC TRANSPORTER PROTEIN.; length=315; id 80.952; 315 aa overlap; query 5-319; subject 1-315" /codon-start=1 /transl-table=11 /product="putative transmembrane component of ABC transporter" /protein-id="CAK05580.1" /db-xref="GI:115254506" /db-xref="GOA:Q1MN72" /db-xref="UniProtKB/TrEMBL:Q1MN72" /translation="MSNAMRTPAGAINVERYQGA VADGRFRLLWNANAPGYLFLLPWL IGFFGLTLGPALISLYLSFTDFDMLQSPRWGMA NYVRIATADPKFSAAMYVTLYTVV FSVPFKLTFALLVAMALNRGLRGLSVYRAIFYLP SLLGGSVAIAVLWRQLFASDGLVN AALSIFYGIEGFSWISHPNYSIYTLVALSVWQFGS PMIIFLAGLRQIPQDMYEAASLDG ASKFRQFYKITLPLLTPVIFNAVVTIDAFKAF TPAFIISGGTGGPINSTLFYTYL YQEAFGNFRMGYASALAWILVVIIAIFTAFSFLT SRYVWHYDD" /locus-tag="RL0092"
misc-feature	order(117396..117464, 117573..117641, 117678..117746, 117828..117896, 117957..118025, 118053..118112, 118149..118217)	
		/inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted at aa 37-59, 96-118, 131-153, 181-203,224-246, 256-275 and 288-310" /locus-tag="RL0092" /inference="protein motif:Pfam:PF00528.10" /note="Pfam match to entry PF00528.10 BPD-transp-1"
misc-feature	117555..118235	/locus-tag="RL0093"
gene	118249..119127	/locus-tag="RL0093"
CDS	118249..119127	/locus-tag="RL0093" /inference="similar to

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sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q92T65
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE TRANSPORT
SYSTEM PERMEASE ABC TRANSPORTER
PROTEIN.; length=295; id 85.567;
291 aa overlap; query 2-292;
subject 5-295"
/codon-start=1
/transl-table=11
/product="putative transmembrane
component of ABC transporter"
/protein-id="CAK05581.1"
/db-xref="GI:115254507"
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/db-xref="UniProtKB/TrEMBL:Q1MN71"
/translation="MTASVTAARPPSDITKRSLP
ASLIHALLIAASLLMLYPLLWMV
SASVRPETEIFSSTSLLIPSSIDFSSYARGWVGLD
VSFGRFFWNSLVISLLVVTGNVIA
CSLTAFAFARLRFAGRNFWFAIMLGLTLMIPYHVT
LIPQYVLFLLDLGWVNTILPLVVPK
FLASDAFFIFLMVQFFRGIPRELEDAAMMDGCSA
WRIYWKIMLPPLSLPVLATAAIFSF
IWTWDDFFGFLIYLNDMNTYTIQLGLRTFVDSTS
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FQRLLEIGIATTGMRK"
/locus-tag="RL0093"

misc-feature      order(118309..118377,
118510..118578,
118612..118680,
118708..118776,
118837..118905,
119026..119094)

/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted at aa 21-43,
88-110, 122-144, 154-176,197-219
and 260-282"

misc-feature      118489..119109
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motif:Pfam:PF00528.10"
/note="Pfam match to entry
PF00528.10 BPD-transp-1"

gene              119151..120224
CDS               119151..120224
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sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q92T67
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
OXIDOREDUCTASE PROTEIN.;
length=357; id 82.913; 357 aa
overlap; query 1-357; subject
1-357"
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/transl-table=11
/product="putative GFO/IDH/MocA

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family oxidoreductase"
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/db-xref="UniProtKB/TrEMBL:Q1MN70"
/translation="MSIRTVAIVCGIGRSHIVE
GYLPHSDKFKVVAICDLNEORMAA
VGDEFGIERRRTSFAELLADDTIDIIDICTPPGI
HLEQVVAALAAGKHVVCEKPLTGS
LAAVDTIMAAEKTAGVLMPIFYRYGDGIQKAK
RIIDAGIAGKPYTASVETFWLRKP
EYYAVPWRGKWATELGGVLVTHALHLHDLMLHLM
GPAARVFGRVATRVNDIEVEDCAS
ASLLMESGAFVLSCTLGSEQEISRLRLHFENV
FESSHEPYTPGKDPWKIIAANDDV
REQIDRVVGDWQFVAPRFTTQMCFHAFSLGHAP
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GADVPLPVGPDSPKYADWRARTK"
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/inference="protein
motif:Pfam:PF01408.8"
/notes="Pfam match to entry
PF01408.8 GFO-IDH-MocA"
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/locus-tag="RL0094"
/inference="protein
motif:Pfam:PF02894.4"
/notes="Pfam match to entry
PF02894.4 GFO-IDH-MocA-C"
/gene 120256..121332
CDS 120256..121332
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/inference="similar to
sequence:INSDC:SME591782"
/notes="similarity:fasta;
with=UniProt:Q92T68
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE ATP-BINDING
ABC TRANSPORTER PROTEIN.;
length=360; id 84.680; 359 aa
overlap; query 1-358; subject
1-359"
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/transl-table=11
/product="putative ATP-binding
component of ABC transporter
protein"
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/db-xref="GI:115254509"
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/db-xref="UniProtKB/TrEMBL:Q1MN69"
/translation="MATSVVLQKVEKRYGAMDVI
HGIDLTIIDPGEFVVEVGPSCGKS
TLLRMIAGLEEITGGLLLDNERNMNEVAPAKRGI
AMVFQSYALYPHMSVYKNLAFGLE
TAGYKKAELIEPKVKRAAEILQIEKLLERKPKALS
GGQQRQVAIGRAIVREPRIFLFE
PLSNLDAELRVQMRVEISRLHSLGNTMIYVTHD
QVEAMTMADKIVVLNSGRIEQVGA
PLDLYNNPANRFVAGFIGSPKMNFLKARIEQAGE
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TMLYTTTPDNQLLTVALDGGQKVE

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gene	121601..122494	
CDS	121601..122494	
misc-feature	121724..122464	
gene	122495..124945	
CDS	122495..124945	



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/inference="similar to
sequence:INSDC:AP003006"
/note="similarity:fasta;
with=UniProt:O46504
(EMBL:AF026954); Bos taurus
(Bovine).; Pyruvate dehydrogenase
phosphatase regulatory subunit.;
length=878; id 37.772; 826 aa
overlap; query 5-806; subject
38-857 similarity:fasta;
with=UniProt:Q98BZ1
(EMBL:AP003006); Rhizobium loti
(Mesorhizobium loti).; Sarcosine
dehydrogenase.; length=869; id
63.171; 820 aa overlap; query
2-816; subject 52-869; putative
dehydrogenase"
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/product="Pyruvate dehydrogenase
phosphatase regulatory subunit."
/protein-id="CAK05585.1"
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/db-xref="GOA:Q1MN67"
/db-xref="UniProtKB/TrEMBL:Q1MN67"
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VDDLVGAAFLPTDGGQANPSDITQA
LAKGARMGSGVSIFEDTEVLDLEIDKGRIRAVITA
QGRIECERVVVCAGOWTRAFAARF
GVNVPLVSVVEHQYIITESFGVPSNLPTLRDPDRL
TYEKEVGGIVMGGYEPNIPWAA
NGIPDGFHYTLDSNFDHFEQIMEQALGRVPALE
NVGVKQLLNGPESFTPDGNFILGE
APELKNFFVVGAGFNAFGIASAGGAMALAEWVK
GEPFYDLWPVDIRRFGRPHFDDTW
VVRTLEAYGKHYYTMAWPFEEHSSGRPCRKSPLY
DRLKAQGACFGEKLGWERPNWFA
LFANEKPKDVYSYTRQNWDAVGREHKAVREAAA
IFDQTSFAKFVLKGRDAEALSWI
ASNDVARPVGSLVYITQMLNDKGGIECDVTVARIA
ENEYYIVTGTGFATHDFDWIARNI
PAEMHAEIIVDVTSAYSVLSIMGPNRAVLEKVTG
SDVSNAAFPFGKVRTIGIAGCPVR
ALRITYVVGELGYELHIPVEYATTIVYDVLMAAGGE
LGLVNAGYRAIESCRLEKGYRAWG
SDIGPDHTPVEAGLGWAVKMRKSIPIRGREAIER
QLSGGVKKRLACFVEDADTVLLG
RETIYRDGKRVGWLSSGGFGYTLGKPIGYGYVRN
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PF01266.8 DAO"
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misc-feature 122519..123595

misc-feature 123947..124921

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motif:Pfam:PF01571.8"
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PF01571.8 GCV-T"
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32)
CDS complement(125075..1265 /locus-tag="RL0098"
32)
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sequence:INSDC:AF007800"
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sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:O08355
(EMBL:AF007800); Pseudomonas
fluorescens.; mt1D; Mannitol
dehydrogenase (EC 1.1.1.67).;
length=493; id 40.959; 459 aa
overlap; query 6-459; subject
6-459 similarity:fasta;
with=UniProt:Q92TQ9
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative D-mannionate
oxidoreductase protein (EC
1.1.1.57).; length=487; id 47.468;
474 aa overlap; query 6-478;
subject 6-475"
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/transl-table=11
/product="putative mannitol
dehydrogenase"
/protein-id="CAK05586.1"
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/db-xref="GOA:Q1MN66"
/db-xref="UniProtKB/TrEMBL:Q1MN66"
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VAPRPDAGLLARLEDPAIRIVSMTVTEKAYGDFP
ATGGLDLKHPDIVADLVSRHTPRG
VIGYLVEGLARRRQKGIAPFTPLSCDNLPNSGAV
LKRVLVEFASRIDPLHRWIEASV
FPFSTMVDRITPASTEATYADAERLTGRITDMAAV
ETEFPTQWVIEDHFANGRPWEKV
RGALMVEEVSAYEKKMLRLNGAHSLLAYLGYIG
GYEFIRDVMDDAALAAALAYRHMHA
AARTLDPVPGIDLDYASELIARFANKAIAHRTY
QIAMDGTQKLPORLLEPASEALAH
GDRAETYAIAVAAMWRYAIGEHGNGERYELRDP
AGEIAALAIADIPRTGLAISAALEFT
LPGLFPAALTGHRAWTDQVADKLEILIQDDRLLP
F"
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54)
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motif:Pfam:PF01232.10"
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PF01232.10 Mannitol-dh"
gene complement(126529..1279 /locus-tag="RL0099"
44)
CDS complement(126529..1279 /locus-tag="RL0099"

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sequence:INSDC:A65098"
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sequence:INSDC:B95958"
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(EMBL:A65098); Shigella flexneri.;
uxaC; Uronate isomerase (EC
5.3.1.12) (Glucuronate isomerase)
(Uronic isomerase).; length=EC
5.3.1.12; id 28.670; 436 aa
overlap; query 24-445; subject
16-441 similarity:fasta;
with=UniProt:UXAC-RHIME
(EMBL:B95958); Rhizobium meliloti
(Sinorhizobium meliloti).; uxaC;
Uronate isomerase (EC 5.3.1.12)
(Glucuronate isomerase) (Uronic
isomerase).; length=EC 5.3.1.12;
id 56.103; 467 aa overlap; query
6-471; subject 3-469"
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isomerase (glucuronate isomerase)"
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/db-xref="GOA:Q1MN65"
/db-xref="UniProtKB/TrEMBL:Q1MN65"
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RTVARDLYETVRNLFIVSPHGHT
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TLDLGVPRLDGKPVASGRAIWRTF
AAHYHLFRGTPSSLWVDHMSAVLGCTEPLTPDN
ADALYDHINAQALFEPFRALHQ
RFGIETIATTDGALDPLAHHQKMAADGWIGKVRT
TYRPDSVTDPDVAVGFRDNLVKFGE
ITGTEVTRWDGLIEAHRRRRAYFRQFGATAIDHG
VPTAFTADLPLTEKQALLDKALKG
PLSAEDAELFRGQMMTEAGLSAEDGMVMQIHAG
SRRNTDSGLFATRGPNMGADIPTS
TDMVGGNLALLSKYGHAPGLRVLLFTLDETTYAR
ELAPMVGHWFCLMIGPPWFHDSP
LGIRRYLDQVVETAGFANMAGFNDDTRALLSIPA
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REAEIVAGELSYGNAKKAYKL"
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misc-feature complement(126532..1279
32)

gene 128125..128334
CDS 128125..128334

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/note="Pfam match to entry
PF02614.4 UxaC"
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/inference="similar to
sequence:INSDC:B97373"
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sequence:INSDC:C85999"
/note="similarity:fasta;
with=UniProt:SLYX-ECOLI
(EMBL:C85999); Escherichia coli

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O157:H7.; slyX; Protein slyX.;
length=72; id 33.333; 63 aa
overlap; query 8-69; subject 10-72
similarity:fasta;
with=UniProt:SLYX-AGRT5
(EMBL:B97373); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; slyX; Protein slyX
homolog.; length=70; id 82.857; 70
aa overlap; query 1-69; subject
1-70"
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/protein-id="CAK05588.1"
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/db-xref="UniProtKB/TrEMBL:Q1MN64"
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TIELSDQLAEQWKIVQMRKLD
RLTERFLSLEEQSLDAPAITRPPHY"
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/inference="protein
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/note="Pfam match to entry
PF04102.2 SlyX"
gene      complement(128390..1298
71)      /gene="gabD"
CDS       complement(128390..1298
71)      /locus-tag="RL0101"
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          /locus-tag="RL0101"
          /EC-number="1.2.1.16"
          /inference="similar to
sequence:INSDC:C95948"
          /inference="similar to
sequence:INSDC:ECD890"
          /note="similarity:fasta;
with=UniProt:GABD-ECOLI
(EMBL:ECD890); Escherichia coli.;
gabD; Succinate-semialdehyde
dehydrogenase [NADP+] (EC
1.2.1.16) (SSDH).; length=482; id
65.409; 477 aa overlap; query
15-491; subject 6-481
similarity:fasta;
with=UniProt:Q92V65 (EMBL:C95948);
Rhizobium meliloti (Sinorhizobium
meliloti).; Putative
succinate-semialdehyde
dehydrogenase (NAD(P)+) protein
(EC 1.2.1.16).; length=491; id
67.814; 494 aa overlap; query
1-493; subject 1-491; putative
succinate-semialdehyde
dehydrogenase [NAD(P)+]"
/codon-start=1
/transl-table=11
/product="Succinate-semialdehyde
dehydrogenase [NADP+] (SSDH)."
/protein-id="CAK05589.1"
/db-xref="GI:115254515"
/db-xref="GOA:Q1MN63"

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misc-feature	complement(128396..129790)	/locus-tag="RL0101" /inference="protein motif:Pfam:PF00171.9" /note="Pfam match to entry PF00171.9 Aldedh" /gene="gabT"
gene	complement(130039..131319)	/locus-tag="RL0102" /note="synonym: goaG" /gene="gabT"
CDS	complement(130039..131319)	/locus-tag="RL0102" /inference="similar to sequence:INSDC:A64879" /inference="similar to sequence:INSDC:AF335502" /note="similarity:fasta; with=UniProt:GOAG-ECOLI (EMBL:A64879); Escherichia coli.; goaG; 4-aminobutyrate aminotransferase (EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (Glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-AT).; length=421; id 61.575; 419 aa overlap; query 1-419; subject 1-419 similarity:fasta; with=UniProt:Q9AGD3 (EMBL:AF335502); Rhizobium leguminosarum.; gabT; 4-aminobutyrate aminotransferase (EC 2.6.1.19).; length=E ( 426; id 100.000; 426 aa overlap; query 1-426; subject 1-426" /codon-start=1 /transl-table=11 /product="putative 4-aminobutyrate aminotransferase" /protein-id="CAK05590.1"

		/db-xref="GI:115254516" /db-xref="GOA:Q1MN62" /db-xref="UniProtKB/TrEMBL:Q1MN62" /translation="MNATSLTDRKNAAISRGVGM TTQIYADRAENAEIWDKEGRYYID FAAGIAVLNTGHRHPRVIAAVKDQLDRFTHTCQ VVPYSEYVHLAERLNALLPGDFEK KTIFFVTGAAEAVENAVKIAARAATGRSAVIAFGGG FHGRTFMGMALTKGVVVPYKVGFGA MPGDVFHIFPPVELHGVADQSLAALKKLFADVD DPQRVAAIIIEPVQGGEGFYSAFA AFMKALRELCDQHIGILLIADVEQTGFARTGRMFA MDHHEVAPDLTTMAKSLAGGFPLA AVTGRAAIMDAPGPGGLGGTYGGNPLGIAAAHAV LDVIVDEDLCNRANLLGGRLLKQRL ESMRETVPEIVDIRGPGFMNAVEFNDRTTGLPSA EFANRVRLIALDKGLILLTCGVHG NVIRFLAPITIQDEIFGEALDILEASMLQASAAK "
misc-feature	complement (130051..131283)	/gene="gabT"
gene	131486..132295	/locus-tag="RL0102"
CDS	131486..132295	/inference="protein motif:Pfam:PF00202.8" /note="Pfam match to entry PF00202.8 Aminotran-3" /locus-tag="RL0103" /locus-tag="RL0103" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:Q92V63 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein Smb21187.; length=276; id 75.362; 276 aa overlap; query 1-269; subject 1-276" /codon-start=1 /transl-table=11 /product="putative MerR family transcriptional regulator" /protein-id="CAK05591.1" /db-xref="GI:115254517" /db-xref="GOA:Q1MN61" /db-xref="UniProtKB/TrEMBL:Q1MN61" /translation="MNDNGPVRYKVAEAAARLAGV SASTLRLEWESQGLVVPGRSETGHR QYSADGVARLKRIWYRVERGLNPAAIREALESE EPSADGAESQDTGLGRKLRLRH ANGKTLDDQVAGDIGVTSSTLSTLERTSQGVSFKT LHDLAEEYGTTVSRLSGEESGDPV VLVRAGEWRKWPETTPGVTVQLLAEGRRMMDCHR FVLAPGAASEGAYRHEGEEFMHVL SGRLELVLDGQDFDLGPGDSLYFESRRDHSWRN RHDGETVLLWINTPPTF"
misc-feature	131513..131623	/locus-tag="RL0103" /inference="protein motif:Pfam:PF00376.9" /note="Pfam match to entry PF00376.9 MerR"
misc-feature	131774..131938	/locus-tag="RL0103"

gene	132535..133161	/inference="protein
CDS	132535..133161	motif:Pfam:PF01381.9"
		/note="Pfam match to entry
		PF01381.9 HTH-3"
		/locus-tag="RL0104"
		/locus-tag="RL0104"
		/inference="similar to
		sequence:INSDC:AE008273"
		/inference="similar to
		sequence:INSDC:ECD823"
		/note="similarity:fasta;
		with=UniProt:RND-ECOLI
		(EMBL:ECD823); Escherichia coli.;
		rnd; Ribonuclease D (EC 3.1.26.3)
		(RNase D).; length=375; id 31.847;
		157 aa overlap; query 13-168;
		subject 14-166 similarity:fasta;
		with=UniProt:Q8U8I4
		(EMBL:AE008273); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; rnd; Ribonuclease D
		(AGR-L-1490p).;
		length=AGR-L-1490p; id 88.942; 208
		aa overlap; query 1-208; subject
		1-208 Similar to the N-terminus to
		codon 170 of Escherichia coli
		Ribonuclease D (375 aa), and
		entire protein is similar to
		Agrobacterium tumefaciens (strain
		C58/ATCC 33970) Ribonuclease D
		(208 aa)"
		/codon-start=1
		/transl-table=11
		/product="putative ribonuclease"
		/protein-id="CAK05592.1"
		/db-xref="GI:115254518"
		/db-xref="GOA:Q1MN60"
		/db-xref="UniProtKB/TrEMBL:Q1MN60"
		/translation="MAATIRYHEGDISAADVARY
		TGAIAIDTETLGLVPRRDLRCVVQ
		LSPGDGTADIIRIAGQKEAPNLVALLEDPTHQK
		IFHYGRFDIAVLHFTFSVTTTFVF
		CTKIASRLIRITYTDHGLKDNLEMLDVEDVSKAQ
		QSSDWAARLSPAQLEYAASDVLY
		LHALRDKLTERLIRDGRYDHATACFEFLPRAKL
		DLWGEEADIFAHS"
misc-feature	132547..133053	/locus-tag="RL0104"
		/inference="protein
		motif:Pfam:PF01612.10"
		/note="Pfam match to entry
		PF01612.10 3-5-exonuc"
		/locus-tag="RL0105"
gene	133393..134958	/locus-tag="RL0105"
CDS	133393..134958	/inference="similar to
		sequence:INSDC:AE008273"
		/note="similarity:fasta;
		with=UniProt:Q8U8I7
		(EMBL:AE008273); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; Hypothetical protein
		Atu4105 (AGR-L-1495p).;
		length=513; id 26.449; 552 aa

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overlap; query 1-519; subject
1-511"
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/transl-table=11
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protein"
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/db-xref="UniProtKB/TrEMBL:Q1MN59"
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AIVASGLGQSVIAPAPVNAVEAAD
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LSLDRGEDESNLAFASRLADAIRR
LPAARIDEVERQLTAQGHGLPLRTIAEALKNPTG
PEAARIVAYLEIVRYKDRDLAARA
VVRSYRQNDASPMRTEARPEIQLHEDNRPAATR
QLAEKVPVLVAPLTEAAALLTAE
FLIAETVEAADPETFPQEEAPAPVAAAEVAA
EESLPQELEAQQLSTDLKDIEDT
QEAVEQS AVQPRIVSKADPVIPRNWAGIVASMT
EEASEMIATLIREQEIETVLEDVP
VEAAVEIDTILDEAVISEATGSLTKQPMELAAPD
VRQTAALRPSQPDIPPLVVETROP
REVSAQAE MIPVPETIESPYVPLAARMPEGLAYT
QLPYQFAKDILSNEKAGETHHQHQ
HHRDGA PQDQNDQEQQAQSGGEDAE PDGEETDAA
FARRTPRMIDAEFVAHQFAGAAAAD
PVYALYQRMVGWE"
/gene="rpsA"

gene      complement(135131..1368
34)

CDS      complement(135131..1368
34)

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/locus-tag="RL0106"
/inference="similar to
sequence:INSDC:AE009341"
/inference="similar to
sequence:INSDC:SME591783"
/note="similarity:fasta;
with=UniProt:RS1-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; rpsA; 30S ribosomal
protein S1.; length=568; id
92.908; 564 aa overlap; query
1-564; subject 1-564
similarity:fasta;
with=UniProt:Q8U8I8
(EMBL:AE009341); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; rpsA; 30S ribosomal
protein S1.; length=572; id
95.398; 565 aa overlap; query
1-565; subject 7-571"
/codon-start=1
/transl-table=11
/product="putative 30S ribosomal
protein S1"
/protein-id="CAK05594.1"
/db-xref="GI:115254520"
/db-xref="GOA:Q1MN58"
/db-xref="UniProtKB/TrEMBL:Q1MN58"

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/translation="MSVATPSREDFAALLEESFA  
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DVGLKVEGRIALKEFGARAKDGLLKVGVDEVVYV  
ERENALGEAVLSREKARREESWV  
KLEAKFEAGERVEGVIFNQVKGFTVDLDGAIAF  
LPRSQVDIRPIRDVITPLMHNPPQF  
EILKMDKRRGNIVVSRRTVLEESRAEQRSEIVQN  
LEEQQVVDGVVKNITDYGAFVDLG  
GIDGLLHVTDMAWRRVNHPSSEILNIGQQVKVQII  
RINQETHRISLGMKQLESDDPWGI  
QAKYPEGKKISGTVNITDYGAFVELEPGIEGLI  
HISEMSWTKKNVHPGKILSTSQEV  
EVVVLEVDPSKRRISLGLKQTLNPNAAFARSH  
AGTEVEGEVKNKTEFGLFIGLDGD  
VDGMVHLSOLDWNRPEQVIEEFNKGDDVVKAVVL  
DVDVEKERISLGIKQLGKDAVGDA  
AASGDLRKNNAVVSCEVIANDGGVEVKLVNHEDI  
TSFIRRADLARDRDEQRPERFSVG  
QVFDARVTNFSKKDRKIMLSIKALEIAEEKEAVA  
QFGSSDSGASLDILGAALKNRGG E"

misc-feature complement(135245..135472)

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/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"

misc-feature complement(135515..135739)

/gene="rpsA"  
  
/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"  
/gene="rpsA"

misc-feature complement(135776..136000)

/gene="rpsA"  
  
/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"  
/gene="rpsA"

misc-feature complement(136037..136255)

/gene="rpsA"  
  
/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"  
/gene="rpsA"

misc-feature complement(136304..136516)

/gene="rpsA"  
  
/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"  
/gene="rpsA"

misc-feature complement(136556..136768)

/gene="rpsA"  
  
/locus-tag="RL0106"  
/inference="protein  
motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"

gene complement(137011..1376 /locus-tag="RL0107"  
58)

CDS complement(137011..1376 /locus-tag="RL0107"  
58)

/inference="similar to  
sequence:INSDC:A04448"  
/note="similarity:fasta;  
with=UniProt:KCY-ECOLI  
(EMBL:A04448); Escherichia coli  
O157:H7.; cmk; Cytidylate kinase  
(EC 2.7.4.14) (CK) (Cytidine  
monophosphate kinase) (CMP kinase)  
(Mssa protein) (P25).; length=EC  
2.7.4.14; id 41.475; 217 aa  
overlap; query 1-203; subject  
1-216 similarity:fasta;  
with=UniProt:KCY-RHIME  
(EMBL:SME591783); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; cmk; Cytidylate kinase  
(EC 2.7.4.14) (CK) (Cytidine  
monophosphate kinase) (CMP  
kinase).; length=EC 2.7.4.14; id  
83.092; 207 aa overlap; query  
5-211; subject 2-208"  
/codon-start=1  
/transl-table=11  
/product="putative cytidylate  
kinase"  
/protein-id="CAK05595.1"  
/db-xref="GI:115254521"  
/db-xref="GOA:Q1MN57"  
/db-xref="UniProtKB/TrEMBL:Q1MN57"  
/translation="MTNETFTIAIDGPAAGKGT  
LSRRIADQYGFHLLDTGLTYRATA  
KALLDAGLPLDDAEVAEKIAREVELAGLDRDILS  
KHEIGEASRIAVMPFAVRRLVEA  
QRRFSTKAPGTVLDGRDIGTVVCPNAAVKFYVTA  
SPEVRRARRRYDEILGKGLTADFDA  
IFEDVKKRRDERDMGRADSPKPADDAHLLDTSEM  
SIEAAFQAAQSIIDAVLSRNA"

misc-feature complement(137023..1374 /locus-tag="RL0107"  
81)

/inference="protein  
motif:Pfam:PF02224.5"  
/note="Pfam match to entry  
PF02224.5 Cytidylate-kin"

misc-feature complement(137548..1376 /locus-tag="RL0107"  
31)

/inference="protein  
motif:Pfam:PF00406.10"  
/note="Pfam match to entry  
PF00406.10 ADK"

gene complement(137731..1390 /gene="aroA"  
89)

/locus-tag="RL0108"

CDS complement(137731..1390 /gene="aroA"  
89)

/locus-tag="RL0108"  
/EC-number="2.5.1.19"

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/inference="similar to
sequence:INSDC:AF326475"
/note="similarity:fasta;
with=UniProt:ARO-A-BRUAB
(EMBL:AF326475); Brucella
abortus.; aroA; 3-phosphoshikimate
1-carboxyvinyltransferase (EC
2.5.1.19) (5-
enolpyruvylshikimate-3-phosphate
synthase) (EPSP synthase)
(EPSPS).; length=450; id 79.418;
447 aa overlap; query 1-447;
subject 1-444 similarity:fasta;
with=UniProt:AAL67577; length=455;
id 86.637; 449 aa overlap; query
1-449; subject 1-449"
/codon-start=1
/transl-table=11
/product="putative
3-phosphoshikimate
1-carboxyvinyltransferase
(5-enolpyruvylshikimate-3-phosphat
e synthase) (EPSP synthase)"
/protein-id="CAK05596.1"
/db-xref="GI:115254522"
/db-xref="GOA:Q1MN56"
/db-xref="UniProtKE/TREMBL:Q1MN56"
/translation="MLNGSASKPATARKSAGLTG
SVRIPGDKSISHSFMIIGGLASGE
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VRLTMGLVGTYDFHSTFIGDASLSKRPMPGRVLNP
LREMGVQVSASEGRDLPTVTLRPGP
TPSPIRYRVPMSAQVKSAVLLAGLNTPGVTTVI
EPVMTDRDHTKMLQGFGAALSVET
DGDGVRITIRLEGRGKLAGQVIDVPGDPSSTAFPL
VAALIVPGSDITIVNVLNPNTRIG
LILTLQEMGADIEVVNARLAGGEDVADLRVRHSE
LKGVTVPEDRAPSMIDEYPILAVA
ACFAEGATVMKGLEELRVKESDRLSAVADGLKLN
GVDCDEGEDFLIVRGRPDGKGLGN
AADGRVSTHLDHRIAMSFLVLGLASEHAVTIDDA
AMIAISFPEFMQLMTGLGAKIELV AE"
misc-feature complement(137770..1390
50) /gene="aroA"
/locus-tag="RL0108"
/inference="protein
motif: Pfam:PF00275.8"
/note="Pfam match to entry
PF00275.8 EPSP-synthase"
gene 139366..139749 /locus-tag="RL0109"
CDS 139366..139749 /locus-tag="RL0109"
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sequence:INSDC:AE008273"
/note="similarity:fasta;
with=UniProt:Q8U4Y6
(EMBL:AE008273); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-L-1500p.; length=129;
id 77.344; 128 aa overlap; query
1-126; subject 1-128"
/codon-start=1

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gene	139901..139976	
tRNA	139901..139976	
gene	140098..140430	
CDS	140098..140430	
misc-feature	140098..140340	
gene	140531..141253	
CDS	140531..141253	

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SFMTGNTRRAALAL$EGNLYHAAVLICAIVFVL
GNAAGIVISHISQRRIFVVLGCVG
LVLALASMMTVQNMLFARFYMIVFSMGMVNAAVE
HIEGLPIGLTYVTGALS$RFRGGIG
RWIIGDRRVEWTIQIVPWG$MVLGAIAGAVLTRL
TGAHALWLVS$LFAMV$ALAAMLIP
RPLQRRENQKVAPSG$AITRAK"
/locus-tag="RL0111"

misc-feature    order(140573..140641,
140723..140791,
140810..140869,
140927..140995,
141053..141106,
141116..141184)

misc-feature    140585..141175

gene            141322..142110
CDS             141322..142110

/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted at aa 31-53,
81-103, 110-129, 149-171,191-208
and 212-234"
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/inference="protein
motif:Pfam:PF06912.1"
/note="Pfam match to entry
PF06912.1 DUF1275"
/locus-tag="RL0112"
/locus-tag="RL0112"
/inference="similar to
sequence:INSDC:SME591783"
/note="similarity:fasta;
with=UniProt:Q92KS9
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; HYPOTHETICAL
TRANSMEMBRANE PROTEIN.;
length=335; id 60.377; 265 aa
overlap; query 1-261; subject
74-334"
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protein"
/protein-id="CAK05600.1"
/db-xref="GI:115254526"
/db-xref="GOA:Q1MN52"
/db-xref="UniProtKB/TrEMBL:Q1MN52"
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LVFLALLAGLLRWRTL$ILGAAGS
ALILFVTLTYTAGNLLMQGLEQRF$AKPADPD$
QCMIVLGGGFENEVNTARHGIEFN
GGADRFIEALRLAQKFQ$SRILVSGDGSISGIY
EGDAAASERFFPLFGVGRDRLIEE
RQSRRTTFENAVNTKEFLASQGL$NCLLITSGFHM
PR$VGIFRKL$GIDIVPWPTDYRTD
GQVRLGLDFTQPSLNAQNLATAIREWYGLVGYYL
AGRTSELYPS"
/locus-tag="RL0112"

misc-feature    order(141349..141414,
141433..141501)

/inference="protein

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		/note="2 probable transmembrane helices predicted at aa 10-31 and 38-60"
misc-feature	141550..142062	/locus-tag="RL0112"
		/inference="protein
		motif:Pfam:PF02698.5"
		/note="Pfam match to entry PF02698.5 DUF218"
gene	142264..142677	/locus-tag="RL0113"
CDS	142264..142677	/locus-tag="RL0113"
		/inference="similar to sequence:INSDC:AE008990"
		/note="similarity:fasta; with=UniProt:Q8UIY6 (EMBL:AE008990); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0155.; length=150; id 43.443; 122 aa overlap; query 5-124; subject 25-144"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAK05601.1"
		/db-xref="GI:115254527"
		/db-xref="UniProtKB/TrEMBL:Q1MN51"
		/translation="MRRRDHEITAFGNLQVEIIG TAVVIALRPLLFPVAGQLALVDHRV DQAVIVDVLPPDETIGKFGRLALLLEMFLLVDLR VGDQRLLTGDSRHGKQDDIQNG EHQRFGHFLLDKGSVAQCMSPKVCSGSRTTTCI T"
gene	142765..143400	/locus-tag="RL0114"
CDS	142765..143400	/locus-tag="RL0114"
		/inference="similar to sequence:INSDC:AE008990"
		/note="similarity:fasta; with=UniProt:Q8UIY7 (EMBL:AE008990); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0154.; length=229; id 73.460; 211 aa overlap; query 1-211; subject 18-228"
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		/transl-table=11
		/product="putative transmembrane protein"
		/protein-id="CAK05602.1"
		/db-xref="GI:115254528"
		/db-xref="GOA:Q1MN50"
		/db-xref="UniProtKB/TrEMBL:Q1MN50"
		/translation="MSLLVLYDYAGIALFAATGA LAASRKQLDLIGFLFFAMVGTGG GTVRDIDLGRVPVFWVLNPAYILVCCIVGVVMVF TAHLLSRYRLLIWDLAIGLAAYC VIGAAKGLAATGSPTIAIVTGTLATFGGILRDL MANEPSVLLRPEIYVTAALIGAV FTLANGLGMQLYASACGVVAAFVVRGALWFGW TFPTYRHKPGRHPDDVM"

sig-peptide	142765..142828	/locus-tag="RL0114" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0114 by SignalP 2.0 HMM (Signal peptide probability 0.910) with cleavage site probability 0.839 between residues 22 and 23"
misc-feature	order(142774..142833, 142852..142920, 142930..142998, 143032..143085, 143095..143163, 143197..143265, 143278..143346)	/locus-tag="RL0114"
misc-feature	142774..143031	/inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted at aa 4-23, 30-52, 56-78, 90-107,111-133, 145-167 and 172-194"
misc-feature	143032..143301	/locus-tag="RL0114" /inference="protein motif:Pfam:PF03458.3" /note="Pfam match to entry PF03458.3 UPF0126"
gene	complement(143477..1438 99)	/locus-tag="RL0115" /gene="irr"
CDS	complement(143477..1438 99)	/locus-tag="RL0115" /inference="similar to sequence:INSDC:AF073772" /inference="similar to sequence:INSDC:RLE492871" /note="similarity:fasta; with=UniProt:O85719 (EMBL:AF073772); Bradyrhizobium japonicum.; irr; Iron response regulator.; length=163; id 61.111; 126 aa overlap; query 14-139; subject 38-163 similarity:fasta; with=UniProt:Q8KLU1 (EMBL:RLE492871); Rhizobium leguminosarum (biovar viciae).; irr; Iron response regulator protein.; length=139; id 98.561; 139 aa overlap; query 2-140; subject 1-139" /codon-start=1 /transl-table=11 /product="iron response regulator" /protein-id="CAK05603.1" /db-xref="GI:115254529" /db-xref="GOA:Q1MN49" /db-xref="UniProtKB/TrEMBL:Q1MN49"

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VESAKTYFDTNVDHMHFFVEGDN
EVLDDIPVSNLTIANLPEPPPEGMEIAHVDVVIRLR
AKQG"
misc-feature complement(143498..1438
54) /gene="irr"
/locus-tag="RL0115"
/inference="protein
motif: Pfam:PF01475.6"
/note="Pfam match to entry
PF01475.6_FUR"
gene 144197..144712 /gene="fabA"
/locus-tag="RL0116"
CDS 144197..144712 /gene="fabA"
/locus-tag="RL0116"
/EC-number="4.2.1.60"
/inference="similar to
sequence: INSDC: C97377"
/inference="similar to
sequence: INSDC: HSDD9B1D"
/note="similarity: fasta;
with=UniProt: FABA-ECOLI
(EMBL: HSDD9B1D); Shigella
flexneri.; fabA;
3-hydroxydecanoyl-[acyl-carrier-pr
otein] dehydratase (EC 4.2.1.60)
(Beta-hydroxydecanoyl thioester
dehydratase).; length=171; id
55.952; 168 aa overlap; query
4-171; subject 3-170
similarity: fasta;
with=UniProt: Q8UIZ0 (EMBL: C97377);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; fabA;
D-3-hydroxydecanoyl-(Acyl
carrier-protein) dehydratase.;
length=acyl carrier-p ( 185; id
88.889; 171 aa overlap; query
1-171; subject 15-185"
/codon-start=1
/transl-table=11
/product="putative
3-hydroxydecanoyl-[acyl-carrier-pr
otein] dehydratase
(Beta-hydroxydecanoyl thioester
dehydratase)"
/protein-id="CAK05604.1"
/db-xref="GI:115254530"
/db-xref="GOA:Q1MN48"
/db-xref="UniProtKB/TrEMBL:Q1MN48"
/translation="MTTRQSSFSYEELIACAHGE
LFGPGNAQLPLPPLMLVHRITEIS
ETGGTFDKGYLRAEYDVRPDWYFFCHFEGNPIM
PGCLGLDGMWQLTGFFLGWLGEEG
RGMALSTGEVKFKGMVRPQTKLIEYGIDFKRVMR
GRLVLGTADGWLKADGETIYQAAD
LRVGLSKDKTA"
gene 144791..145990 /gene="fabB"
/locus-tag="RL0117"
CDS 144791..145990 /gene="fabB"

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/EC-number="2.3.1.41"
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sequence:INSDC:AE016764"
/note="similarity:fasta;
with=UniProt:FABB-ECOLI
(EMBL:AE016764); Escherichia coli
06.; fabB;
3-oxoacyl-[acyl-carrier-protein]
synthase I (EC 2.3.1.41) (Beta-
ketoacyl-ACP synthase I) (KAS I).;
length=406; id 59.091; 396 aa
overlap; query 1-396; subject
12-403 similarity:fasta;
with=UniProt:Q8UIZ1
(EMBL:AE008989); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; fabB;
3-oxoacyl-(Acyl-carrier-protein)
synthase I.;
length=acyl-carrier-protein; id
90.226; 399 aa overlap; query
1-399; subject 12-407; putative
3-oxoacyl-[acyl-carrier-protein]
synthase I"
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/product="3-oxoacyl-[acyl-carrier-
protein] synthase I
(Beta-ketoacyl-ACP synthase I)
(KAS I)."
/protein-id="CAK05605.1"
/db-xref="GI:115254531"
/db-xref="GOA:Q1MN47"
/db-xref="UniProtKB/TREMBL:Q1MN47"
/translation="MSSIGNDAAEVTESLRQAKS
GISFSSDFAEHGFKCQVWGSPKLG
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GLEEKDYAQNERTGIMGSGGSPST
RTLIEAAEITIKNNSPKRIGFPAVKAMSSTASA
TLATWFKIHGVNYSISSACSTSAH
CIGNAAEMIQWGKQDVMFAGGHEDLDWTMSNLF
DAMGAMSSKYNDTPDSASRAYDVNR
DGFVIAGGAGVLVLEELERAKARGAKIYAEIVGY
GATSDGYDMVAPSGEGAIRCMRQA
LATVKGDDVDYVNTHTGSTPTVGDSEIGAIREVFG
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/inference="protein
motif:Pfam:PF00109.11"
/note="Pfam match to entry
PF00109.11 ketoacyl-synt"
/misc-feature 145526..145984
/gene="fabB"
/locus-tag="RL0117"
/inference="protein
motif:Pfam:PF02801.7"
/note="Pfam match to entry

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gene	145998..146804	PF02801.7 Ketoacyl-synt-C"
CDS	145998..146804	/gene="fabI" /locus-tag="RL0118" /gene="fabI" /locus-tag="RL0118" /EC-number="1.3.1.9" /inference="similar to sequence:INSDC:HS757242" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:FABI-ECOLI (EMBL:HS757242); Shigella flexneri.; fabI; Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH- dependent enoyl-ACP reductase).; length=261; id 52.510; 259 aa overlap; query 3-260; subject 1-259 similarity:fasta; with=UniProt:FAI2-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; fabI2; Enoyl-[acyl-carrier-protein] reductase [NADH] 2 (EC 1.3.1.9) (NADH- dependent enoyl-ACP reductase 2).; length=268; id 85.448; 268 aa overlap; query 1-268; subject 1-268" /codon-start=1 /transl-table=11 /product="putative Enoyl-[acyl-carrier-protein] reductase [NADH] (NADH-dependent enoyl-ACP reductase)" /protein-id="CAK05606.1" /db-xref="GI:115254532" /db-xref="GOA:Q1MN46" /db-xref="UniProtKB/TrEMBL:Q1MN46" /translation="MTGIMQGKRGGLVMGVANNHS IAWGISKALAAQGAELAFITYQGDA LGKRVKPLAAEVNSDFVLPDVEDIASVDAVVDA ISERWGKLDIVHAIGFSDKNELK GLYADTTRENFRTMVISCSFTEIAKRCAPLME DGGAMLTLTYNGSTRVIPNYVMG VAKAALEASVRYLAADYGPRGIRVNAISAGPIRT LAGAGISDARAILSWNQRNAPLRK TVTIDQVGSSALYLLSDLSSGVTGEVHFVDAGFN VTSMTPLETLRKADVE" /gene="fabI" /locus-tag="RL0118" /inference="protein motif:Pfam:PF00106.11" /note="Pfam match to entry PF00106.11 adh-short" /locus-tag="RL0119"
misc-feature	146058..146750	
gene	complement(146893..147909)	
CDS	complement(146893..147909)	/locus-tag="RL0119" /EC-number="2.1.1.52"

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sequence:INSDC:SME591783"
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sequence:INSDC:U00096"
/note="similarity:fasta;
with=UniProt:RSMC-ECOLI
(EMBL:U00096); Escherichia coli.;
rsmC; Ribosomal RNA small subunit
methyltransferase C (EC 2.1.1.52)
(rRNA
(guanine-N(2)-)-methyltransferase)
(16S rRNA m2G1207
methyltransferase).; length=342;
id 31.366; 322 aa overlap; query
23-336; subject 18-333
similarity:fasta;
with=UniProt:Q92KT0
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc00325.; length=338; id 70.710;
338 aa overlap; query 1-338;
subject 1-338"
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/product="putative ribosomal RNA
small subunit methyltransferase"
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/db-xref="UniProtKB/TrEMBL:Q1MN45"
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LVLCTKHKGENEANLAAAIARTRL
GGLIVVAGAKEDGIQPLRKRMEGFNLAVDYPKY
HGVAFWFGRPADADEIISKAKAP
VRVDGRFNATAGMFSHDRIDAGSELLTSLRPEDF
TGDVADFAGAGYGLSVEMARKSVG
LTRLDLYEADHAALEAARDNLAKNCFNAPARFFW
HDLAGEPVKDKYDLIMNPPFHG
HAAEPALGOAMIKTAASALRGGGRLMLVANRGLP
YEPVLAANFRESGETCRNARFKVL WAKK"

misc-feature    complement(146896..1470
48)              /locus-tag="RL0119"

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motif:Pfam:PF05175.2"
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PF05175.2 MTS"

gene            complement(147985..1501
23)              /gene="pnp"

                  /locus-tag="RL0120"

CDS             complement(147985..1501
23)              /gene="pnp"

                  /locus-tag="RL0120"
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sequence:INSDC:AE007950"
                  /inference="similar to
sequence:INSDC:HS106228"
                  /note="similarity:fasta;
with=UniProt:PNP-ECOLI

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(EMBL:HS106228); Escherichia coli.; pnp; Polynucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase).; length=711; id 56.802; 713 aa overlap; query 1-712; subject 1-708 similarity:fasta; with=UniProt:Q8UJ56 (EMBL:AE007950); Agrobacterium tumefaciens (strain C58/ATCC 33970).; pnpA; Polynucleotide nucleotidyltransferase (AGR-C-124p).; length=713; id 92.546; 711 aa overlap; query 1-711; subject 1-711" /codon-start=1 /transl-table=11 /product="putative Polynucleotide nucleotidyltransferase (Polynucleotide phosphorylase) (PNPase)" /protein-id="CAK05608.1" /db-xref="GI:115254534" /db-xref="GOA:Q1MN44" /db-xref="UniProtKB/TrEMBL:Q1MN44" /translation="MFDTHTEIEWAGRPLKLET GKIAQADGAVLATYGETVVLATV VSAKAPKAGQDFPLTVNYQKTYAAGKIPGGYF KREGRPSEKETLVSRLIDRPIRPL FPEGYKNDTQVVTVIQHDLENDPDLVSMVATSA ALTISGVPFMGVGGARVGYINGE YVLNPHLDDESSLDLVVAGTYDAVLMVESEAK ELNEDVMLGAVMFGHKGFQPVLDA IIKLAEEVAKEPRDFQPADYSALESEMLGLAEGE LRNAYKITQKADRYAAVDVAKKV KAHFLPEEGEAKYTAEEVGAIKFHLQAKIVRWNI LDTKSRIIDGRNLETVRPIVSEVGL LPRTHGSALFTRGETQAIIVVATLGTGEDEQYVDS LTGMYSKERFLLHYNFPYSVGETG RMGSPGRREIGHGKLAWRAIRPMLPTPEQFPYTL RVVSEITENSGSSMATVCGTSLA LMDAGVPLAKPVAGIAMGLILEGDRFAVLSDILG DEDHLGDMDFKVAGTADGITSLQM DIKITGITEIMKVVALGQAQGGRVHILGEMSKAI TESRGQLGEFAPRIEVMNIPVDKI REVIGSGGKVIREIVEKTGAKINIEDDGTVKIAS SSGKEIEAARKWIHSIVAEPEIGQ VYEGTVVKTADFGAFVNFVGARDGLVHISQLASE RVAKTQDVVKEGDKVWVKLLGFDE RGKVRLSMKVVDQATGQEIIPNEKKKEEAAE"

misc-feature complement(148051..148259)

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motif:Pfam:PF00575.9"  
/note="Pfam match to entry  
PF00575.9 S1"

misc-feature complement(148285..148458)

/gene="pnp"  
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		/inference="protein motif:Pfam:PF00013.12" /note="Pfam match to entry PF00013.12 KH-1"
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misc-feature	complement(148753..149154)	/gene="pnp"  /locus-tag="RL0120" /inference="protein motif:Pfam:PF01138.10" /note="Pfam match to entry PF01138.10 RNase-PH"
misc-feature	complement(149161..149403)	/gene="pnp"  /locus-tag="RL0120" /inference="protein motif:Pfam:PF03726.3" /note="Pfam match to entry PF03726.3 PNPase"
misc-feature	complement(149491..149685)	/gene="pnp"  /locus-tag="RL0120" /inference="protein motif:Pfam:PF03725.4" /note="Pfam match to entry PF03725.4 RNase-PH-C"
misc-feature	complement(149692..150090)	/gene="pnp"  /locus-tag="RL0120" /inference="protein motif:Pfam:PF01138.10" /note="Pfam match to entry PF01138.10 RNase-PH"
gene	complement(150472..150741)	/gene="rpsO"
CDS	complement(150472..150741)	/locus-tag="RL0121" /gene="rpsO"  /locus-tag="RL0121" /inference="similar to sequence:INSDC:BS29668" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:RS15-BACSU (EMBL:BS29668); Bacillus subtilis.; rpsO; 30S ribosomal protein S15 (BS18).; length=BS18 (88; id 64.773; 88 aa overlap; query 2-89; subject 1-88 similarity:fasta; with=UniProt:Q92SW1 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; PROBABLE 30S RIBOSOMAL PROTEIN S15.; length=89; id

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87.640; 89 aa overlap; query 1-89;
subject 1-89"
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protein S15"
/protein-id="CAK05609.1"
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/db-xref="GOA:Q1MN43"
/db-xref="UniProtKB/TrEMBL:Q1MN43"
/translation="MSITAERKSA LIKEYATVEG
DTGSPEVQVAILTERINNLT EHFK
DHKKDNHSRRGLLTMVSSRRSLDYLKKKDEGRY
SKLITSLGIRR"
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/inference="protein
motif:Pfam:PF00312.9"
/note="Pfam match to entry
PF00312.9 Ribosomal-S15"
gene complement(150895..1518 /locus-tag="RL0122"
33)
CDS complement(150895..1518 /locus-tag="RL0122"
33)
/inference="similar to
sequence:INSDC:AP005961"
/note="similarity:fasta;
with=UniProt:Q89EE1
(EMBL:AP005961); Bradyrhizobium
japonicum.; Oxidoreductase.;
length=308; id 51.399; 286 aa
overlap; query 22-306; subject
12-294"
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/transl-table=11
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/protein-id="CAK05610.1"
/db-xref="GI:115254536"
/db-xref="UniProtKB/TrEMBL:Q1MN42"
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HGGPTEGKIMRGTAIGILTFFSMF
LAAAGARSAERWAE LPAFPMPVAKTSGMAEVND
IKMYAEYEGEGDPI LFHGG LGNA
DVWGHGVADFAKDLHVI VADSRGHGRSTRSQPF
GYDLMTSDYVALLDYLKIDKVTLV
GWSGGIGIDMAMKNPEKLTRVIAQAANVITDG
VKADV MNKTFNDYINVAGEYYRK
LSPTPNEYEAFTQISHMWETQPAWTAADLGKIA
VPVTLAIGDHDEAVKLDHTEMMAK
DIPGAKLVILKDASHFAM LQDPTGYDAMIRDAMA
GR"
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88)
/inference="protein
motif:Pfam:PF00561.8"
/note="Pfam match to entry
PF00561.8 Abhydrolase-1"
gene complement(151863..1527 /gene="truB"
95)
/locus-tag="RL0123"
CDS complement(151863..1527 /gene="truB"

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/EC-number="4.2.1.70"
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/inference="similar to
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/note="similarity:fasta;
with=UniProt:TRUB-ECOLI
(EMBL:S79856); Escherichia coli.;
truB; tRNA pseudouridine synthase
B (EC 4.2.1.70) (tRNA
pseudouridine 55 synthase) (Psi55
synthase) (Pseudouridylate
synthase) (Uracil hydrolyase)
(Protein p35).; length=314; id
37.460; 315 aa overlap; query
1-308; subject 1-308
similarity:fasta;
with=UniProt:TRUB-AGRT5
(EMBL:HS368258); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; truB; tRNA pseudouridine
synthase B (EC 4.2.1.70) (tRNA
pseudouridine 55 synthase) (Psi55
synthase) (Pseudouridylate
synthase) (Uracil hydrolyase).;
length=315; id 82.803; 314 aa
overlap; query 1-309; subject
1-314"
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/transl-table=11
/product="putative tRNA
pseudouridine synthase B (tRNA
pseudouridine 55 synthase) (Psi55
synthase) (Pseudouridylate
synthase) (Uracil hydrolyase)"
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/db-xref="GI:115254537"
/db-xref="GOA:Q1MN41"
/db-xref="UniProtKB/TrEMBL:Q1MN41"
/translation="MSKPRKPKGRISGWLILDK
PVDFGSTAENVSKIKWLYKAEKAGH
AGTLDPASGMLFIALGDATKTVPYVMDGRKIYE
FTVSWGEERATDDLEGDVTKSSDK
RPSEQQIRDILPGYIGTISQVPPQFSAIKIAGER
AYDLAREGETIEIPSEVDIFRLT
LLACPDADSAHFEVECGKGYVRALARDFGRELG
CYGHVSGLRRTFVAPFAEGAMVPL
ADLVALEAIEDMDERLAALDALLIDTCEALSSLP
HLVINDDAQHRLKMGNPILVRGRD
APVAESEAYATARGKLIAGEIGQGEFRPKRVFA
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misc-feature complement(152250..1527 /gene="truB"
05)

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/locus-tag="RL0123"
/inference="protein
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/note="Pfam match to entry
PF01509.7 TruB-N"

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gene complement(152809..1532 /gene="rbfA"
13)

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CDS	complement(152809..153213)	/locus-tag="RL0124" /gene="rbfA"  /locus-tag="RL0124" /inference="similar to sequence:INSDC:HS134244" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:RBFA-ECOLI (EMBL:HS134244); Shigella flexneri.; rbfA; Ribosome-binding factor A (P15B protein).; length=132; id 33.929; 112 aa overlap; query 12-120; subject 6-114 similarity:fasta; with=UniProt:RBFA-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; rbfA; Ribosome-binding factor A.; length=135; id 84.328; 134 aa overlap; query 1-134; subject 1-134" /codon-start=1 /transl-table=11 /product="putative ribosome-binding factor protein" /protein-id="CAK05612.1" /db-xref="GI:115254538" /db-xref="GOA:Q1MN40" /db-xref="UniProtKB/TrEMBL:Q1MN40" /translation="MTRPTSSAPSQRMRLRIGEV RAAITQVLQRGVDDVIEATVIS VSEVRMSPLDKIATAYVTPLGVSDHSIVIEALNR HARFIRGRGLGQLRQMKYMEPVRF RDDTSFDNYKKIDELLSPEVSRDLGDNDNQ" /gene="rbfA"
misc-feature	complement(152860..153180)	/locus-tag="RL0124" /inference="protein motif:Pfam:PF02033.5" /note="Pfam match to entry PF02033.5 RBFA"
gene	complement(153364..156117)	/gene="infB"
CDS	complement(153364..156117)	/locus-tag="RL0125" /gene="infB"  /locus-tag="RL0125" /inference="similar to sequence:UniProtKB:Q8UJ51" /inference="similar to sequence:UniProtKB:Q9ZF31" /note="similarity:fasta; SWALL:IF2-SALTY (SWALL:Q9ZF31); Salmonella typhimurium; translation initiation factor if-2; infB; length 892 aa; 909 aa overlap; query 11-917 aa; subject 53-891 aa similarity:fasta; SWALL:IF2-AGRT5 (SWALL:Q8UJ51); Agrobacterium tumefaciens;



translation initiation factor  
 if-2; infB; length 913 aa; 935 aa  
 overlap; query 1-917 aa; subject  
 1-913 aa"  
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 /transl-table=11  
 /product="putative translation  
 initiation factor IF-2"  
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 /db-xref="GI:115254539"  
 /db-xref="GOA:Q1MN39"  
 /db-xref="UniProtKB/TrEMBL:Q1MN39"  
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 VQARFPQOPTAPAPRVQGGNNNTNQ  
 RFPQQSHQPPFRQNDPRFPVVLNHLSPPEMDARRR  
 ALADSQARDAQDAIRRAEEERKRA  
 AEEVIRKAAEAEEAARRAAEEAIRQAEAPAVAEP  
 AAAEPAPAEARTDAPPPQPASSA  
 PAARRPDAAAGAPAAPAPGAAVPGAVRGRDEKE  
 EDDRGAARGGPGVRGVVRPEPAKP  
 VTTRPKTDEERRRGKLTITTANVDGEDNARGRSL  
 SAMRRRQEKFRRGQMQETREKISR  
 EVVLPETITITIELSORMSERAVDVIKYLMEGQM  
 MKPGDVIDADLAEIIAGEFGHTVR  
 RVSESDELGVIFNVSDDEGLVSRPPVVTIMGHV  
 DHGKTSLLDAIRHANVVSGEAGGI  
 TQHIGAYQVEQNGQKITFIDTPGHAFTAMRARG  
 AQATDIAILVVAAADDSVMPQIES  
 INHAKAAGVP IIVAINKVDKHEADPKVRNQLLQ  
 HEVFVESMGGEVLVDVEVSAKTGN  
 LDKLLEAILLQAEILDLKANANRTAEGTVIEAQL  
 DRGRGSVATVLVQKGLTRPGQIIV  
 AGDVMGRVRLVIDKGDHVKEAGPATPVEVLGLS  
 GTPQAGDKFAVVESESAREISEY  
 RQRLARDKAAARQSGQRGSLEQMMMQRQSVGIKE  
 FPLVIKGDVQGSIEAIAGALEKLG  
 TDEVRARIVHSGAGGITESDISLAESNAAIIGF  
 NVRANTQARQFAEREGIEIRYYNI  
 IYDLVDDVKAAMSGLLSPERRETFIGNAEILEVF  
 NITKVGKVAGCRVVEGKVERGAGV  
 RLIRNDVVVHEGKLTLLKRFKDEVSEVPMGQECG  
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misc-feature complement(153400..1536  
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/locus-tag="RL0125"  
 /inference="protein  
 motif:Pfam:PF03144.8"  
 /note="Pfam match to entry  
 PF03144.8 GTP-EFTU-D2"  
 /gene="infB"

misc-feature complement(154114..1543  
 05)

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 motif:Pfam:PF03144.8"  
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 /gene="infB"

misc-feature complement(154372..1548  
 75)

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 /inference="protein"

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		/note="Pfam match to entry
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misc-feature	complement(154948..155103)	/gene="infB"
		/locus-tag="RL0125"
		/inference="protein
		motif:Pfam:PF04760.3"
		/note="Pfam match to entry
		PF04760.3 IF2-N"
gene	complement(156219..156911)	/locus-tag="RL0126"
CDS	complement(156219..156911)	/locus-tag="RL0126"
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		sequence:INSDC:C97369"
		/note="similarity:fasta;
		with=UniProt:Q8UJ50 (EMBL:C97369);
		Agrobacterium tumefaciens (strain
		C58/ATCC 33970).; Hypothetical
		protein Atu0088 (AGR-C-134p).;
		length=233; id 71.304; 230 aa
		overlap; query 4-230; subject
		5-233"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical
		protein"
		/protein-id="CAK05614.1"
		/db-xref="GI:115254540"
		/db-xref="UniProtKB/TrEMBL:Q1MN38"
		/translation="MMTAHEPDAPLEDDLAGYD
		VNGRMCIVTRESGSPHEELIRFVA
		PDGTVVADLKRELPGRGCWVKIDRSLVDRAVAKK
		LFARALKTDVKAADDLGESVDRLL
		AAQLMQMNMNMARKAGQFVSGSSKVDAAVRS
		GAALAVFHSTGAADDGVRKIDQARKAWH
		LGMETEEIIPSFRLFSESEMGLMGQNAFIHA
		AAVLAGQAGEGVVKRAKMLEQYRIGGQ
		SRAAGGAGRLKQ"
misc-feature	complement(156606..156851)	/locus-tag="RL0126"
		/inference="protein
		motif:Pfam:PF04296.2"
		/note="Pfam match to entry
		PF04296.2 DUF448"
gene	complement(156908..158509)	/gene="nusaA"
		/locus-tag="RL0127"
CDS	complement(156908..158509)	/gene="nusaA"
		/locus-tag="RL0127"
		/inference="similar to
		sequence:INSDC:AE007950"
		/inference="similar to
		sequence:INSDC:B91135"
		/note="similarity:fasta;
		with=UniProt:NUSA-ECOLI
		(EMBL:B91135); Shigella flexneri.;
		nusaA; Transcription elongation
		protein nusaA (N utilization
		substance protein A) (L factor).;

length=495; id 43.697; 476 aa  
 overlap; query 9-480; subject  
 4-479 similarity:fasta;  
 with=UniProt:Q8UJ49  
 (EMBL:AE007950); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; nusA; N-utilization  
 substance protein A (AGR-C-136p).;  
 length=538; id 91.011; 534 aa  
 overlap; query 1-533; subject  
 1-532"  
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 substance protein A) (L factor)"  
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 PPMDFGRIAAQSAQVIVQKVREAERDRQFDEFK  
 DRVGEIVNGIVKRVEYGNVIVDLG  
 RGEGIIRDEMIPRENVRIGDRVRAYVYDVRRREQ  
 RGPQIFLSRTHPQFMVKLFTMEVP  
 EIYDGI IQVKS VARDPGSRAKIAVISNDSSIDPV  
 GACVGMGRSRVQAVVGELQGEKID  
 IIPWSQDPATFVVNALQPAEVAKVVLDEDAERIE  
 VVVPDEQLSLAIGRRGQNVRLASQ  
 LTGWIDIDIMTEAEESERRQKEFNERNINLFMDSLD  
 VDEMVGQVLASEGFAAVEELAYVD  
 LDEISSIDGFDEETAQEIQQRAREFLERLEAEMD  
 EKRAKALGVQDELREINGMTAQMMV  
 ALGEDGIKSIEDFAGCAADDLVGWSERKNGETKK  
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 /note="Pfam match to entry  
 PF00013.12 KH-1"  
 /gene="nusA"  
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 /note="Pfam match to entry  
 PF00575.9 S1"  
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 /inference="similar to  
 sequence:INSDC:SME591783"  
 /note="similarity:fasta;  
 with=UniProt:Y236-RHIME  
 (EMBL:SME591783); Rhizobium

misc-feature complement (157442..1575  
88)

misc-feature complement (157904..1581  
04)

gene complement (158569..1591  
74)

CDS complement (158569..1591  
74)

meliloti (Sinorhizobium  
 meliloti).; Hypothetical UPF0090  
 protein R00236.; length=205; id  
 77.612; 201 aa overlap; query  
 1-200; subject 1-201"  
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 protein"  
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 MVRKSDFVRWQGHVLCETSIILIDNRKFRGKIV  
 EAGTDGFTLERDQIAYGEEQKVTI  
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 NEADDEE"

misc-feature complement(158665..1590  
 93)

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 PF02576.5 DUF150"

gene 159373..161052  
 CDS 159373..161052

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 with=UniProt:Q8UJ47  
 (EMBL:AE007951); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; MFS permease  
 (AGR-C-139p).; length=542; id  
 73.371; 537 aa overlap; query  
 22-558; subject 6-542"  
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 /transl-table=11  
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 transport protein"  
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 /db-xref="UniProtKB/TrEMBL:Q1MN35"  
 /translation="MRIYCRWRAITKAGEIVAYT  
 SSTLAPLRHDTYRTIWFASLSSNF  
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 CMLTLVSALLTASALLGWITPWLLEFFTFLIGCG  
 TALNNPSWQASVGDMPVPRADLPAA  
 VILNSMGFNITRSVGAIGGVIVAAAGAAAAFAV  
 NTLSYLALIYALLRWRPAAPVSTL  
 PREALGSAIFAGLRVYSMSPNLEKVLVRGLLFGI  
 GASSILALLPVVALDLVAGPLTY  
 GFMLGAFGIGAIGGAVLNARLRQVLSSEMIVRLS  
 FAGFALSAVIAALSPSAVLTSAGL  
 LVSGACWVSALSLFNTIVQLSTPRWVVRGRLSLY  
 QTVTFGGIAGGSWLWGIAADRYGV  
 ADALLMSVVMLLGIAIGLRFSPAFASLNLDP  
 LNRFTIEPALSLDITPRSGPIVIQVD

		YEIADEDLAEFMELMGERRRIRIRDGARNWALMR DLENPSLWTETYHTPTWVEYIRHN QRRQADAENTDRLRALHRGEGPLHVHRMIERQA IPPDNDVFHKAPIDLHH" /locus-tag="RL0129" /inference="protein motif:Pfam:PF05977.1" /note="Pfam match to entry PF05977.1 DUF894" /locus-tag="RL0129"
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misc-feature	order(159475..159543, 159571..159639, 159700..159768, 159913..159981, 160102..160170, 160183..160251, 160288..160356, 160369..160428, 160465..160533, 160543..160611)	
gene	161049..161531	/inference="protein motif:TMHMM:2.0" /note="10 probable transmembrane helices predicted at aa 35-57, 67-89, 110-132, 181-203,244-266, 271-293, 306-328, 333-352, 365-387 and 391-413" /locus-tag="RL0130" /locus-tag="RL0130" /inference="similar to sequence:INSDC:BX640432" /inference="similar to sequence:INSDC:SGPHNOL" /note="similarity:fasta; with=UniProt:Q54244 (EMBL:SGPHNOL); Streptomyces griseus.; phnO-like; Regulatory protein for C-P lyase.; length=150; id 55.102; 147 aa overlap; query 14-160; subject 7-150 similarity:fasta; with=UniProt:Q7W6J0 (EMBL:BX640432); Bordetella parapertussis.; Putative acetyltransferase.; length=154; id 61.486; 148 aa overlap; query 13-160; subject 7-153" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator/acetyltransferase" /protein-id="CAK05618.1" /db-xref="GI:115254544" /db-xref="GOA:Q1MN34" /db-xref="UniProtKB/TrEMBL:Q1MN34" /translation="MRPAMQSRSGIYRFLARQSD LAAIVRLADDNLGGTREIVSDPV DARYLSAFAAIEADANQLLAVANDATDRVVGCLQ LSFVPLSLRTGMWRGQIESVRVAS DLRGSGLSGHFIEWAIAQCAERGGLVQLTPDKT RGDAIRFYERLGFVASHEGLKRNL /locus-tag="RL0130" /inference="protein"
CDS	161049..161531	
misc-feature	161241..161498	

		motif:Pfam:PF00583.9" /note="Pfam match to entry PF00583.9 Acetyltransf-1" /locus-tag="RL0131"
gene	complement(161538..1628 12)	
CDS	complement(161538..1628 12)	/inference="similar to sequence:INSDC:AF458045" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q8RP11 (EMBL:AF458045); Pseudomonas syringae (pv. maculicola).; Type III effector HopPmaG.; length=413; id 35.782; 422 aa overlap; query 14-424; subject 10-412 similarity:fasta; with=UniProt:Q92SW8 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSGLYCOSYLASE TRANSMEMBRANE PROTEIN.; length=412; id 69.343; 411 aa overlap; query 14-424; subject 2-412" /codon-start=1 /transl-table=11 /product="conserved hypothetical exported protein" /protein-id="CAK05619.1" /db-xref="GI:115254545" /db-xref="GOA:Q1MN33" /db-xref="UniProtKB/TrEMBL:Q1MN33" /translation="MRGLHMLKDGPRRLRIFALA LAAALLPLSCYAAPSKADVEVQFE KWWQADLWPEAKANGISEKVFQAAFSGITLNNWL PDLAPPGFPPPKQKQQTQAEFSSP APYFNEDQLKKLAATGRGFAAQYGSTLKRIEKTY GVPGSIVLAIWGRETFGGAAKIPN SAIEVLATKAFMSTRKEMFTELVAALHILDGGD VTPANFKGSWAGALGQPOFMPTSY LKYAVDFDGDGHRNIWTSVPDILASIANYLVKKG WQRNRDWGFVSIPEAVSCAQEGP DLAKPLSHWTS LGIDRISGKGFPSPGEMKAEGMML VPAGRDGPEFIVTPNFYIIKEYNN SDLYALYIGNLADRIAYNGGAFQKGWGDVGMKMLR SDVAAMQKALERQGYDVGGSDGLP GYKTRRSIGQWQAKNGMKPTCTCFEATMKGKLG"
misc-feature	complement(162708..1627 76)	/locus-tag="RL0131"  /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 13-35"
sig-peptide	complement(162713..1628 12)	/locus-tag="RL0131"  /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0131 by SignalP 2.0 HMM

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(Signal peptide probability 1.000)
with cleavage site probability
0.980 between residues 32 and 33"
gene      complement(162809..1634 /gene="recR"
14)
CDS      complement(162809..1634 /locus-tag="RL0131A"
14) /gene="recR"
/locus-tag="RL0131A"
/inference="similar to
sequence:INSDC:HST35386"
/inference="similar to
sequence:INSDC:SME591783"
/note="similarity:fasta;
with=UniProt:RECR-STRCO
(EMBL:HST35386); Streptomyces
coelicolor.; recR; Recombination
protein recR.; length=199; id
44.271; 192 aa overlap; query
10-201; subject 6-197
similarity:fasta;
with=UniProt:RECR-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; recR; Recombination
protein recR.; length=201; id
89.055; 201 aa overlap; query
1-201; subject 1-201"
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/product="putative recombination
protein"
/protein-id="CAK05620.1"
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/db-xref="UniProtKB/TrEMBL:Q1MN32"
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PGLGPR SARRAALHLIKKKDQLLG
PLSHAMGEAYDKVKICSRGNVDITVDPICIVCTDV
QRDQSVIIVVEDVSDLWALERAGA
MNAAYHVLGGLTSLPLDGVGPDLLNIRGLIDRVGE
GGIRELI IAVNATVEGQTTAHYIT
DQLQGLDVKITRLAHGVFVGELDYLDDEGLTAAA
LRARTVI"
gene      163433..164101 /locus-tag="RL0132"
CDS      163433..164101 /locus-tag="RL0132"
/inference="similar to
sequence:INSDC:A97370"
/note="similarity:fasta;
with=UniProt:Q8UJ44 (EMBL:A97370);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Hypothetical
protein Atu0094 (AGR-C-144p).;
length=AGR-C ( 229; id 52.657; 207
aa overlap; query 11-216; subject
23-229"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05621.1"
/db-xref="GI:115254547"

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/db-xref="UniProtKB/TrEMBL:Q1MN31"
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VMIDAEGLVGDAICNRKHHGGVDQAVYVEGSLTL
DWWSRLELRPYEPGTGFENMVISD
LDNRDVAVGDRFLTGDVLVLEVTSCRMPCATFAAR
MADPKFVKRYTAAARPGIYCRVIR
GGVVEPGMPMEYTSFSGDKITMFELMEAFGRRLP
GADRTRYLAAPIHXYKLRLAMEAQ DEAR"
/misc-feature 163580..163948 /locus-tag="RL0132"
/inference="protein
motif:Pfam:PF03473.5"
/notes="Pfam match to entry
PF03473.5 MOSC"
gene complement(164124..1644 /locus-tag="RL0133"
47)
CDS complement(164124..1644 /locus-tag="RL0133"
47)
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sequence:INSDC:SME591783"
/notes="similarity:fasta;
with=UniProt:Y231-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical UPF0133
protein R00231.; length=107; id
83.178; 107 aa overlap; query
1-107; subject 1-107"
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/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05622.1"
/db-xref="GI:115254548"
/db-xref="GOA:Q1MN30"
/db-xref="UniProtKB/TrEMBL:Q1MN30"
/translation="MRDIMGMGKVKEMQAKMEQ
MQAEIAELTAEGKAGGLVTVLIS
GKGDLKSLKIDPSLKFEDDVLEDLIVAHHKDA
KDKAEALAAEKTALTAGLPIPPG FKLPF"
/misc-feature complement(164148..1644 /locus-tag="RL0133"
26)
/inference="protein
motif:Pfam:PF02575.4"
/notes="Pfam match to entry
PF02575.4 DUF149"
gene complement(164470..1663 /gene="dnaX"
47)
/locus-tag="RL0134"
CDS complement(164470..1663 /gene="dnaX"
47)
/locus-tag="RL0134"
/EC-number="2.7.7.7"
/inference="similar to
sequence:INSDC:C97370"
/inference="similar to
sequence:INSDC:U00096"
/notes="similarity:fasta;
with=UniProt:DP3X-ECOLI
(EMBL:U00096); Escherichia coli.;
dnaX; DNA polymerase III subunit

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tau (EC 2.7.7.7) [Contains: DNA polymerase III subunit gamma].; length=643; id 36.170; 564 aa overlap; query 18-560; subject 3-540 similarity:fasta; with=UniProt:Q8UJ42 (EMBL:C97370); Agrobacterium tumefaciens (strain C58/ATCC 33970).; DNA polymerase III, tau subunit (AGR-C-147p).; length=624; id 76.874; 627 aa overlap; query 1-625; subject 1-624"

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/transl-table=11  
/product="putative DNA polymerase III"  
/protein-id="CAK05623.1"  
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/db-xref="GOA:Q1MN29"  
/db-xref="UniProtKB/TrEMBL:Q1MN29"  
/translation="MSDTERQSKDAASTGTGYRV LARKYRPFKDFDTLMVGQEPVMRTL NAFETGRIAQAYMLTGVGVGKTTTARILARAL NYKTSEIDKPTIDLRAPGEHCQAI MEGRHVDVVIEMDAASHTGIDDIIEIIEQVRYRPV SARVKVYIIDEVHMLSTQAFNGLL KTLLEPPFEHVKEIFATTEIRKVPITVLSRCQRFDRRISASDLVGLFTTIAAKEGIEA EPDALAMIAAAEGSARDGLSLDQAIHAGAGVV QAEAVRGMGLGLADRARIVDLFQHI VKGDVAAALGEFQNOYEAGANPVVVLTDLADFTH LVTRLKYVPDAANDPSLSEVERTK AAEFAKCAVATTLRIWQMLLKGIPETEGSSRTA GAAEMVILRLAHAAHLPAPEDAAR RLAEFSGDNTGPRPSSSPSGNGGSGTRVPYQSS VAAAAEETAPSQPPSSAPVAMLRA VPSSQSETHAVGRIEKPFAEAPKPLVPVNSVNDI VNLATEKRDPKPKAMVRTFLRPVR IEAGRLDVS LAPGAPTTLNLA VKLKEWTGIHV IVSLSRDEGQPTLVEAEARTREQH VIDARQDPDVAAILAHFFGAKIIDVRVRAPEPEE EGEATPPAAAESEEGDILPGDDIE F"

/gene="dnaX"  
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/inference="protein  
motif:Pfam:PF00004.12"  
/note="Pfam match to entry PF00004.12 AAA"  
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/inference="similar to sequence:INSDC:AE007951"  
/note="similarity:fasta; with=UniProt:Q8UJ41 (EMBL:AE007951); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0097 (AGR-C-148p).; length=174; id 62.069; 174 aa overlap; query 1-174; subject 1-174"  
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misc-feature complement(165595..166182)

gene 166459..166989  
CDS 166459..166989

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protein"
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KSKPTCEKTASRRKRQEECLKGF
ALDPRLENDSVSIMVTGLCDLRLSKDARWPWLIL
VPRRADITEIFELTFLDQVLLAFE
TELVAKALKKITGATKINIGALGNIVRQLHVHVI
ARFEGDANWPGPVWGFGRAPEDYD
GKRDEFTAKLREALSS"
misc-feature 166582..166881
/locus-tag="RL0135"
/inference="protein
motif:Pfam:PF01230.10"
/notes="Pfam match to entry
PF01230.10 HIT"
gene 166986..167945
CDS 166986..167945
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/inference="similar to
sequence:INSDC:AE007951"
/notes="similarity:fasta;
with=UniProt:Q8UJ40
(EMBL:AE007951); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; MutT/nudix family protein
(AGR-C-150p).; length=320; id
69.085; 317 aa overlap; query
1-317; subject 2-318"
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/product="putative MutT/nudix
family protein"
/protein-id="CAK05625.1"
/db-xref="GI:115254551"
/db-xref="UniProtKB/TrEMBL:Q1MN27"
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FAANDLNRDSEHRDEQSVKALAK
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GIDVDDLTSQYKPADGRTLIFREMLIDEVLLGEFA
QAASLIRWNGDNRFCGRCGSAMEI
HIGGYKRVCAACEHVIFFRIDPVPVIMLTVDEQRD
LCLLGRSPHFAPGMYSCLAGFLEP
GETIENAVRRETLEESGIRTGRIRYHASQWPMP
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DCRWFTREETIEMLERPSATGRASPFGAIAHRL
MRDWVEWKR"
misc-feature 167523..167906
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/inference="protein
motif:Pfam:PF00293.12"
/notes="Pfam match to entry
PF00293.12 NUDIX"
gene 167950..168645
CDS 167950..168645
/locus-tag="RL0137"
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/inference="similar to
sequence:INSDC:SME591782"
/notes="similarity:fasta;
with=UniProt:Q92SX3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium

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meliloti).; PUTATIVE TRANSCRIPTION
REGULATOR PROTEIN.; length=230; id
67.111; 225 aa overlap; query
3-227; subject 1-225"
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regulator"
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/db-xref="UniProtKB/TrEMBL:Q1MN26"
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LEALVLGSRWRVARAAEPRLAGAGA
DALAKIAAVLPADMREMIDSAALFVGPKRRDEK
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sequence:INSDC:SME591782"
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with=UniProt:Q8GPH6
(EMBL:AF451953); Pantoea
agglomerans.; EhpR.; length=129;
id 33.333; 123 aa overlap; query
3-121; subject 10-129
similarity:fasta;
with=UniProt:Q92KT5
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02901.; length=122; id 63.115;
122 aa overlap; query 1-122;
subject 1-122"
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glyoxalase/dioxygenase"
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/db-xref="GOA:Q1MN25"
/db-xref="UniProtKB/TrEMBL:Q1MN25"
/translation="MTSPNLIILYVKDPGESASF
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/inference="protein
motif:Pfam:PF00903.11"
/note="Pfam match to entry
PF00903.11 Glyoxalase"

gene 169172..169540 /locus-tag="RL0139"
CDS 169172..169540

misc-feature 169178..169522

gene complement(169654..1705
08)
CDS complement(169654..1705 /locus-tag="RL0139"
08)

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sequence:INSDC:AE007951"
/note="similarity:fasta;
with=UniProt:PHEA-ECOLI
(EMBL:A30261); Shigella flexneri.;
pheA; P-protein [Includes:
Chorismate mutase (EC 5.4.99.5)
(CM); Prephenate dehydratase (EC
4.2.1.51) (PDT)].; length=386; id
32.143; 280 aa overlap; query
1-275; subject 99-375
similarity:fasta;
with=UniProt:Q7D273
(EMBL:AE007951); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-151p.; length=287;
id 87.324; 284 aa overlap; query
1-284; subject 1-284"
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/transl-table=11
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[includes: chorismate mutase and
prephenate dehydrogenase]"
/protein-id="CAK05628.1"
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/db-xref="UniProtKB/TrEMBL:Q1MN24"
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IGFYFMPIRFQLMVLPGVTKDEIR
TVHSHIHALGQCRKIVRANGWKPIAGDTAGAAK
LVQETGDRSMAALAPRLAADLYGL
EIIAENVEDTENNVTFRVVLRSDEEWAQRNSAEE
KVVITTFVFNVRNIPAAALYKALGGF
ATNNINMTKLESYQLGGKFVATQFYADIEGHPND
PNVRRALEELRFFSEKVRILGVYK GHAMRGLL"
misc-feature complement(169693..1699
17) /locus-tag="RL0139"
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motif:Pfam:PF01842.8"
/note="Pfam match to entry
PF01842.8 ACT"
misc-feature complement(169954..1704
87) /locus-tag="RL0139"
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motif:Pfam:PF00800.8"
/note="Pfam match to entry
PF00800.8 PDT"
gene complement(170519..1712
74) /gene="kdsB"
/locus-tag="RL0140"
CDS complement(170519..1712
74) /gene="kdsB"
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sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:KDSB-ECOLI
(EMBL:A26322); Escherichia coli.;
kdsB; 3-deoxy-manno-octulosonate
cytidyltransferase (EC 2.7.7.38)
(CMP-KDO synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase) (CKS).;
length=247; id 45.122; 246 aa
overlap; query 10-243; subject
3-243 similarity:fasta;
with=UniProt:Q92SX6
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PROBABLE
3-DEOXY-MANNO-OCTULOSONATE
CYTIDYLTRANSFERASE (CMP-KDO
SYNTHETASE) PROTEIN (EC
2.7.7.38).; length=250; id 77.500;
240 aa overlap; query 10-249;
subject 10-249; putative
3-deoxy-manno-octulosonate
cytidyltransferase (CMP-KDO
synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase)"
/codon-start=1
/transl-table=11
/product="3-deoxy-manno-octulosa
te cytidyltransferase (CMP-KDO
synthetase)
(CMP-2-keto-3-deoxyoctulosonic
acid synthetase) (CKS).;"
/protein-id="CAK05629.1"
/db-xref="GI:115254555"
/db-xref="GOA:Q1MN23"
/db-xref="UniProtKB/TrEMBL:Q1MN23"
/translation="MSDSNLDGVLVLIIPARMAST
RLPGKPLADICGLPMIVQVAMRAR
EAAIGRVVVAVDETRVFDAAAGFEVVMTRVDH
QSGSDRIFEALTKVDPEGKAKIIV
NIQGDLPITIDPETVRAALRPLENEAVDIGTLTTE
IDNEEDKTAPHIVKIIIGSPISGNR
LHALYFTRATAPYGGQPLYHHIGLYAYRRAALER
FVSLGPSTLEKRESLEQLRALEAG
MRIDAENVVDTPVLGVDTPADLEKARRILSAKSN"
/misc-feature complement(170612..1712
47)
/gene="kdsB"
/locus-tag="RL0140"
/inference="protein
motif;Pfam:PF02348.6"
/note="Pfam match to entry
PF02348.6 CTP-transf-3"
/gene="cycM"
/locus-tag="RL0141"
/gene="cycM"
/locus-tag="RL0141"
/inference="similar to
sequence:INSDC:AP005940"
/inference="similar to
sequence:INSDC:HS370249"

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misc-feature	complement(170612..171247)
gene	171429..171992
CDS	171429..171992

		<pre> /note="similarity:fasta; with=UniProt:CYCM-BRAJA (EMBL:AP005940); Bradyrhizobium japonicum.; cycM; Cytochrome c homolog.; length=184; id 48.913; 184 aa overlap; query 1-180; subject 1-180 similarity:fasta; with=UniProt:CYCM-AGRT5 (EMBL:HS370249); Agrobacterium tumefaciens (strain C58/ATCC 33970).; cycM; Cytochrome c homolog.; length=192; id 70.213; 188 aa overlap; query 1-185; subject 1-187" /codon-start=1 /transl-table=11 /product="putative cytochrome c" /protein-id="CAK05630.1" /db-xref="GI:115254556" /db-xref="GOA:Q1MN22" /db-xref="UniProtKB/TrEMBL:Q1MN22" /translation="MNSYVNTAVGALLGTIFVLM SVSIASEGIFHSEAPEKEGFAIVA EEAPAAGGAAAPAVAVPIAQLLASADAKAGETVF KKCQACHDGTGGPNKVGPNFLGV VDRPIASHAGFAYSAPMKDFSGKSEKWTFEYLN KFLAPKKDIPGTAMGFAGLAKDQ ERANVILYLHTLADSPGFLPDPNAATQ" /gene="cycM" /locus-tag="RL0141" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0141 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.974 between residues 25 and 26" </pre>
sig-peptide	171429..171501	
misc-feature	171447..171515	<pre> /gene="cycM" /locus-tag="RL0141" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 7-29" </pre>
misc-feature	171642..171947	<pre> /gene="cycM" /locus-tag="RL0141" /inference="protein motif:Pfam:PF00034.8" /note="Pfam match to entry PF00034.8 Cytochrom-C" </pre>
gene	complement(172062..173015)	/locus-tag="RL0142"
CDS	complement(172062..173009)	<pre> /inference="similar to sequence:INSDC:AE007950" /note="similarity:fasta; with=UniProt:Q8UJ58 (EMBL:AE007950); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Permease (AGR-C-121p).; length=AGR-C-121p; id 65.815; 313 aa overlap; query 1-313; subject </pre>

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1-313"
/codon-start=1
/transl-table=11
/product="putative transmembrane
permease protein"
/protein-id="CAK05631.1"
/db-xref="GI:115254557"
/db-xref="GOA:Q1MN21"
/db-xref="UniProtKB/TrEMBL:Q1MN21"
/translation="MSAIIIFDVLPVFILILIGWV
IVRSGLMASNVGEALSEFVFKIAV
PLLLFRTIAEADFHGASPPRLWIVYFSGVAITWT
AGHIAATRLFGDRDIGVLAVGVS
AFANNIFIGLPLVERTVGDEGLVALSILLAVHLP
VMMVAGTVLMEHAERKIAGKSDRS
MVLVLRQIAVNLVRNPLVIGLAAGMAMHLSGLTM
PTTLATVVVQIAGIAGPAALISLG
MALERYGVSGNLGIASVTSSLKLLLPGCVWAAS
RLGLSPWNTAAIVLTSSVPTGVN
AWLIANRFGVGHSLAASTITVTALGAIIVSLWA
YFLGA"
misc-feature complement(join(172077..172145,172164..172232,
172260..172328,
172347..172415,
172443..172511,
172572..172640,
172668..172727,
172746..172814,
172947..173015)) /locus-tag="RL0142"

/inference="protein
motif:TMHMM:2.0"
/notes="9 probable transmembrane
helices predicted at aa 21-43,
88-110, 117-136, 146-168,189-211,
221-243, 250-272, 282-304 and
311-333"
misc-feature complement(172080..173003) /locus-tag="RL0142"

/inference="protein
motif:Pfam:PF03547.6"
/notes="Pfam match to entry
PF03547.6 Auxin-eff"
gene 173497..174489 /locus-tag="RL0143"
CDS 173497..174489 /locus-tag="RL0143"

/inference="similar to
sequence:INSDC:B97368"
/inference="similar to
sequence:INSDC:BCAJ3322"
/notes="similarity:fasta;
with=UniProt:O44015
(EMBL:BCAJ3322); Babesia canis.;
adk; Adenosine kinase.;
length=368; id 29.338; 317 aa
overlap; query 6-313; subject
36-346 similarity:fasta;
with=UniProt:Q8U5P4 (EMBL:B97368);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; AGR-C-118p.;
length=330; id 82.121; 330 aa
overlap; query 1-330; subject
1-330"

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/codon-start=1
/transl-table=11
/product="putative Pfk family
kinase"
/protein-id="CAK05632.1"
/db-xref="GI:115254558"
/db-xref="GOA:Q1MN20"
/db-xref="UniProtKB/TrEMBL:Q1MN20"
/translation="MTRFDVLTVGNAIVDIIARC
DDQFLIDNQITKAAMNLIDAEAE
LLYSRMGPALEASGGSGAGTAAGVASLGGKAAFY
GNVAQDQLGDIFAHDIRAQGVHYQ
TRPKGTFFPTARSMIFVTEDGERSMNTYLGACVE
LGPEDVETDVVADAKVTYFEGYLW
DPPRAKEAILDCARIAHENGREMSMTLSDSFCVD
RYRGEFLDLMRSGKVDIVFANRQE
ALSLYETDDFEALNRIAADCKIAAVTMSDGA
ILKGRERFYVDIAIRREVVDITGA
GDLFASGFLYGYTQGRSLEDCKGLGCLAAGIVIQ
QIGPRPMTLSLSEAAKRAGL"
/locus-tag="RL0143"
/inference="protein
motif:Pfam:PF00294.10"
/note="Pfam match to entry
PF00294.10 PfkB"
misc-feature 173581..174456
gene complement(174482..1750
21) /locus-tag="RL0144"
CDS complement(174482..1750
21) /locus-tag="RL0144"
/inference="similar to
sequence:INSDC:A97368"
/note="similarity:fasta;
with=UniProt:Q8UJ60 (EMBL:A97368);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; Hypothetical
protein Atu0078.; length=200; id
73.889; 180 aa overlap; query
1-179; subject 24-200 Similar, but
truncated at the N-terminus, to
Agrobacterium tumefaciens (strain
C58/ATCC 33970) Hypothetical
protein Atu0078 (200 aa)"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05633.1"
/db-xref="GI:115254559"
/db-xref="UniProtKB/TrEMBL:Q1MN19"
/translation="MRSKVLKSCALALALAAAM
GSVEFAHAQAAKGPSGLPLPRFVT
LKSKRVNLRIQGTDDYAVSVMYKSGLPVEIIQE
YDNRWRIRDADGTGEGVNVQSLLSG
QRAALAAPWMKTKGKIYVNLRRQAQPSASIVAK
LEPGVMLTIGECNGDWCAESDGA
SGWVAQSEIWGAYPGEAFK"
/locus-tag="RL0144"
misc-feature complement(174485..1749
10)
/inference="protein
motif:Pfam:PF06347.1"
/note="Pfam match to entry
PF06347.1 DUF1058"

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sig-peptide	complement(174934..175021)	/locus-tag="RL0144" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0144 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.446 between residues 28 and 29"
gene	175207..176208	/gene="gyaR" /locus-tag="RL0145"
CDS	175207..176208	/gene="gyaR" /locus-tag="RL0145" /EC-number="1.1.1.26" /inference="similar to sequence:INSDC:AB033995" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:GYAR-THELI (EMBL:AB033995); Thermococcus litoralis.; gyaR; Glyoxylate reductase (EC 1.1.1.26) (Glycolate reductase).; length=331; id 46.364; 330 aa overlap; query 6-329; subject 2-321 similarity:fasta; with=UniProt:Q92T15 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE HYDROXYACID DEHYDROGENASE PROTEIN (EC 1.1.1.-).; length=334; id 86.787; 333 aa overlap; query 1-333; subject 1-333" /codon-start=1 /transl-table=11 /product="putative glyoxylate reductase" /protein-id="CAK05634.1" /db-xref="GI:115254560" /db-xref="GOA:Q1MN18" /db-xref="UniProtKB/TrEMBL:Q1MN18" /translation="MTAKKKPKVYITRKLPDAVE TRMRELFDAELNIDDAPRSVPELI AAVKTADVLVPTVTDRIIDAAALIEQAGPQMGLIAS FSNGTDHIDVEAAARKGITVTNTPT NVLTEDTADMTMALILAVPRRLGEGARVLTDKPG EWAGWSPTWMLGRIHGRIGIVG MGRIGTAVARRAKAFGLSIHYHNRKRVNPAVEDE LEATYWESLDQMLARVDIVSVNCP STPATPHLISARRLALLQPTAYLVNTARGDVVDE AALIKCLREGRIAGAGLDVFENEP AVNPRLIKLANEGKVLLPHMSSATIEGRIDMGD KVIINIRTFIDGHRPPNVRVLPGR"
misc-feature	175225..175515	/gene="gyaR" /locus-tag="RL0145" /inference="protein motif:Pfam:PF00389.14" /note="Pfam match to entry PF00389.14 2-Hacid-dh"
misc-feature	175531..176094	/gene="gyaR"

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/locus-tag="RL0145"
/inference="protein
motif: Pfam:PF02826.5"
/note="Pfam match to entry
PF02826.5 2-Hacid-dh-C"
gene      complement(176222..1767 /locus-tag="RL0146"
10)
CDS       complement(176222..1767 /locus-tag="RL0146"
10)
/locus-tag="RL0146"
/inference="similar to
sequence: INSDC: SME591782"
/note="similarity: fasta;
with=UniProt: Q92T05
(EMBL: SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
ACETYLTRANSFERASE PROTEIN (EC
2.3.1.-).; length=156; id 62.821;
156 aa overlap; query 1-156;
subject 1-156"
/codon-start=1
/transl-table=11
/product="putative
acetyltransferase"
/protein-id="CAK05635.1"
/db-xref="GI:115254561"
/db-xref="GOA: Q1MN17"
/db-xref="UniProtKB/TrEMBL: Q1MN17"
/translation="MRIVPLDQTFTTRWDELLALI
LSAFASMNGRIDPPSSALKLTTAS
LAEKAGTEIGHVAIDGEKLGICFLRPEADCLYV
GKLAVLPEVQGGKLGKRLALAE
TAAALDLPALRLTRIETLDNHAFFAANGFCRTA
EKAHGFGARTTFVEMRKVLAPPIC VA"
misc-feature complement(176312..1765 /locus-tag="RL0146"
48)
/inference="protein
motif: Pfam:PF00583.9"
/note="Pfam match to entry
PF00583.9 Acetyltransf-1"
gene      complement(176707..1775 /locus-tag="RL0147"
31)
CDS       complement(176707..1775 /locus-tag="RL0147"
31)
/inference="similar to
sequence: INSDC: AE007949"
/inference="similar to
sequence: INSDC: HS53223"
/note="similarity: fasta;
with=UniProt: O54307
(EMBL: HS53223); Synechococcus sp.
(strain PCC 7942) (Anacystis
nidulans R2).; moeB; MPT-synthase
sulfurylase.; length=391; id
48.770; 244 aa overlap; query
21-264; subject 11-247
similarity: fasta;
with=UniProt: Q7D290
(EMBL: AE007949); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-11lp.; length=285;
id 75.836; 269 aa overlap; query

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2-266; subject 13-281"
/codon-start=1
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/product="putative molybdopterine
synthase sulfurylase"
/protein-id="CAK05636.1"
/db-xref="GI:115254562"
/db-xref="GOA:Q1MN16"
/db-xref="UniProtKB/TrEMBL:Q1MN16"
/translation="MTEAAGPGVGRHNDIGAMEP
LSPEETIARYHRHILLPEIGAGAGQ
KLKAARVLVIGAGGLGAPVLQYLAAGVGLGIV
DDDRVLSLNLQROVIHDSGTIGEL
KTESAAFAIARLNPVRLIRFEERFSPEAARRQL
SGFDLLIDGSDNFDTRYAADAAD
EARIPLVTVGAVGRFDGSLTLVKPYETAEDGTIPN
RYRDLFPPEAPPAGLIPACAEAGII
GALTGVIGTMMAMEAIKLVGTGIGEPVGRLLLYD
ALSARFDTIRYKRRRTTORQAG"
misc-feature complement(176713..1769 /locus-tag="RL0147"
61)
/inference="protein
motif:Pfam:PF05237.1"
/note="Pfam match to entry
PF05237.1 MoeZ-MoeB"
misc-feature complement(176989..1773 /locus-tag="RL0147"
93)
/inference="protein
motif:Pfam:PF00899.8"
/note="Pfam match to entry
PF00899.8 ThiF"
gene complement(177528..1786 /gene="recF"
52)
/locus-tag="RL0148"
CDS complement(177528..1786 /gene="recF"
52)
/locus-tag="RL0148"
/inference="similar to
sequence:INSDC:AF008187"
/note="similarity:fasta;
with=UniProt:RECF-RHIME
(EMBL:AF008187); Rhizobium
meliloti (Sinorhizobium
meliloti).; recF; DNA replication
and repair protein recF.;
length=374; id 75.000; 372 aa
overlap; query 1-372; subject
1-372"
/codon-start=1
/transl-table=11
/product="putative DNA replication
and repair protein"
/protein-id="CAK05637.1"
/db-xref="GI:115254563"
/db-xref="GOA:Q1MN15"
/db-xref="UniProtKB/TrEMBL:Q1MN15"
/translation="MPHKVLSRLKLTDFRNYAA
AALALDGRHAVLTGDNGAGKTNLM
EAVLLSPGRGLRRAAYGDITRVGAAGGFSIFAA
LDGMEGDVEIGTGIETGETTARK
LRINGTTAKTADLTDLHLLWLTPAMDGLFTGA
SSDRRRFLDRLVLSLDPAGHRRAS

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DFERAMRSRNKLLDEGRFDPSSLAGIEEQMASLG
IAMALARQEMGLGLTRLIEETRET
SPFSPASLQLSGFMDGGQFSRPSVDLEDDYAAMLA
ESRYRDAGAGRTLEGPHRADLIVH
HREKAMEAERCSTGEQKALLVGLVAHARLVGNL
TGHAPILLDEIAAHLDEGRRAL
FDLIDGLGGQAFMTGTRAMFSALGDKAQFFTV
DGRVFE"
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40) /locus-tag="RL0148"
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motif:Pfam:PF02463.6"
/notes="Pfam match to entry
PF02463.6 SMC-N"
gene 179034..179399 /locus-tag="RL0149"
CDS 179034..179399 /locus-tag="RL0149"
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sequence:INSDC:AP005937"
/inference="similar to
sequence:INSDC:SME591783"
/notes="similarity:fasta;
with=UniProt:Y410-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative HTH-type
transcriptional regulator R00410.;
length=139; id 42.609; 115 aa
overlap; query 2-111; subject
8-116 similarity:fasta;
with=UniProt:Q89WA2
(EMBL:AP005937); Bradyrhizobium
japonicum.; B110790 protein.;
length=137; id 56.977; 86 aa
overlap; query 2-84; subject 5-90"
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transcriptional regulator"
/protein-id="CAK05638.1"
/db-xref="GI:115254564"
/db-xref="GOA:Q1MN14"
/db-xref="UniProtKB/TrEMBL:Q1MN14"
/translation="MPDPVDIIIVGRNVRQFRALR
RVSQLELGEALGLTFQIQIYKYGK
ANRVSASKLHQIAVFLDVIDISALFEGAGMSPFGS
RVELSPDAYALALS YDKLNSPAGK
EAVKTIIVTLMTGESAETTA"
/misc-feature 179070..179234 /locus-tag="RL0149"
/inference="protein
motif:Pfam:PF01381.9"
/notes="Pfam match to entry
PF01381.9 HTH-3"
gene complement(179558..1797 /locus-tag="RL0150"
58)
CDS complement(179558..1797 /locus-tag="RL0150"
58)
/inference="similar to
sequence:INSDC:SME591784"
/notes="similarity:fasta;
with=UniProt:Q92S48
(EMBL:SME591784); Rhizobium

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meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02277.; length=70; id 33.333;
60 aa overlap; query 1-60; subject
1-58; hypothetical protein
smc02277"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05639.1"
/db-xref="GI:115254565"
/db-xref="UniProtKB/TrEMBL:Q1MN13"
/translation="MAPAFSSQSEDVDVLAGAIY
TWCAERNIKLRSSQGLSIAISIAID
LYHAGHOTQDDLLMALHECEHLH"
gene      complement(180070..1811
97)      /gene="dnaJ"
CDS      complement(180070..1811
97)      /locus-tag="RL0151"
          /gene="dnaJ"
          /locus-tag="RL0151"
          /inference="similar to
sequence:INSDC:I39586"
          /note="similarity:fasta;
with=UniProt:DNAJ-AGRT5
(EMBL:I39586); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; dnaJ; Chaperone protein
dnaJ.; length=377; id 91.534; 378
aa overlap; query 1-375; subject
1-377"
          /codon-start=1
          /transl-table=11
          /product="putative chaperone
protein"
          /protein-id="CAK05640.1"
          /db-xref="GI:115254566"
          /db-xref="GOA:Q1MN12"
          /db-xref="UniProtKB/TrEMBL:Q1MN12"
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LKSAFRKLAMKYHPDKNPDKDDAE
RKFKINEAYEMLKDPQKRAAYDRYGHAAFEHGG
MGGGGGGFAGGGFSDIFEDIFGEM
MGGGRARQRSSGGRERGADLRYNMEITLESFSG
KTAQIRVPTSITCDVCSGSGAKFG
TQPKNCGTCQGTGRVRAAQGFPSIERTCPTCHGR
GQIIPDPCPKCHGQGRVTEERSLS
VNIPAGIEDGTRIRLQGEAGARGGPAGDLYIF
LSVKPHEFYQRDGADLYCAVPIISM
TTAALGGTFDVAITLDGTSKRVITVPEGTQVGKQFR
LKGGMPVLRSVQTDGLYIQIQIE
TPQKLTKRQRELLQEFELSSKENNPSTGFFAR
MKEFFEG"
misc-feature complement(180145..1805
13)      /gene="dnaJ"
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          /inference="protein
motif:Pfam:PF01556.7"
          /note="Pfam match to entry
PF01556.7 DnaJ-C"
misc-feature complement(180550..1807
          /gene="dnaJ"

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92)                                     /locus-tag="RL0151"
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motif:Pfam:PF00684.8"
                                     /note="Pfam match to entry
PF00684.8 DnaJ-CXKCXG"
misc-feature complement(180988..1811 /gene="dnaJ"
85)
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                                     /inference="protein
motif:Pfam:PF00226.13"
                                     /note="Pfam match to entry
PF00226.13 DnaJ"
gene complement(181283..1831 /gene="dnaK"
99)
CDS complement(181283..1831 /locus-tag="RL0152"
99) /gene="dnaK"
                                     /locus-tag="RL0152"
                                     /inference="similar to
sequence:INSDC:I39585"
                                     /inference="similar to
sequence:INSDC:RLDNAKJ"
                                     /note="similarity:fasta;
with=UniProt:DNAK-AGRT5
(EMBL:I39585); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; dnaK; Chaperone protein
dnaK (Heat shock protein 70) (Heat
shock 70 kDa protein) (HSP70).;
length=Heat sh ( 633; id 93.103;
638 aa overlap; query 1-638;
subject 1-633 similarity:fasta;
with=UniProt:DNAK-RHILE
(EMBL:RLDNAKJ); Rhizobium
leguminosarum.; dnaK; Chaperone
protein dnaK (Heat shock protein
70) (Heat shock 70 kDa protein)
(HSP70).; length=Heat sh ( 638; id
96.708; 638 aa overlap; query
1-638; subject 1-638"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative heat shock
chaperone protein"
                                     /protein-id="CAK05641.1"
                                     /db-xref="GI:115254567"
                                     /db-xref="GOA:Q1MN11"
                                     /db-xref="UniProtKB/TrEMBL:Q1MN11"
                                     /translation="MAKVIIGIDLGTNSCVAVM
DKDAKVIENAEAGARTTPSMVAFSD
DGERLVGQPAKRQAVTNPTNTLFAVKRLIGRRYE
DPTVEKDKHLVPFTIIVKGDNGDAW
VEANGKGYSPAQISAMILQKMKETAESYLGEKVE
KAVITVPAYFNDAQRQATKDAGRI
AGLEVLRIINEPTAAALAYGLDKKEGKTIIVYDL
GGGTFFDISILEIGDGVFEVKSNG
DTFLGGEDFDMRLVEYLVGEFGRDNGIDLKNDKL
ALQRLKEAAEKAKIELSSSQOTEI
NLPFITADASGPKHLTLKLTRAKLESIVDDLQVR
TIAPSKAALKDAGVTAAEIDEVVL
VGGMSRMPKVQEVVKQLFGKEPKHGVNPDVVVL

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GAAIQAGVLQGDVVKDVLLEDVDTPL
SLGIETLGGVFTRLIERNTTIPTKKSQTFSTAED
NQQAVTIRVSQGEREMAADNKLGL
QFDVLVLPPSPRGMPQIEVTFDIDANGIVQVSAC
DKGTGKEQQIRIQASGGLSDADIE
KMWKDAEAHATEDKKRREAVEARNQAESLIHSSE
KSLKDYGDVSEADRTAISDAIAA
LKTASEASEPDADDIKAKTQTLMEVSMKLGQAIY
EAQQAEGGAAGDASAESGDNVVDA
DYEIEIKDDDRKKSA"
misc-feature complement(181397..1831 /gene="dnaK"
90) /locus-tag="RL0152"
/inference="protein
motif:Pfam:PF00012.7"
/note="Pfam match to entry
PF00012.7 HSP70"
gene complement(183536..1858 /locus-tag="RL0153"
72)
CDS complement(183536..1858 /locus-tag="RL0153"
72)
/inference="similar to
sequence:INSDC:BSPBPF"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:PBPB-BACSU
(EMBL:BSPBPF); Bacillus subtilis.;
pbpF; Penicillin-binding protein
1F (PBP-1F).; length=( 714; id
33.333; 585 aa overlap; query
117-679; subject 50-616
similarity:fasta;
with=UniProt:Q92T08
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
PENICILLIN-BINDING PROTEIN.;
length=767; id 67.602; 784 aa
overlap; query 5-777; subject
18-766"
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/transl-table=11
/product="putative
penicillin-binding
transpeptidase/transglycosylase
protein"
/protein-id="CAK05642.1"
/db-xref="GI:115254568"
/db-xref="GOA:Q1MN10"
/db-xref="UniProtKB/TrEMBL:Q1MN10"
/translation="MAGRGRSGDRIEPSFSGRPA
RDDDEFSLDADDRIAGGRSQRRGG
SKPPPPRAAPRRRREPPEREGGGFFGMRRRIYW
CVVFLIWAGIGVAGLVVYYSRMP
SASTWAIPEPPPNVKITAVDGSVIANRGATGGEA
LSLENMSPYIPEAVIAIEDRRFYS
HFGVDPLGLGRAIVTNLTAGHVMQGGSTLTQQLA
KNLFLSPERTLERKVQEVLLSLWL
EQKYTKDQILAMYNLRVFFGSNAYGVEAASRRYF
NKSARDVNLGEAAVLGGLKAPSR
LSPARDAEAAANARQLVLAAMREQGFIIDSEVKT

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AMSQTPASAKSYWSGAGHYVADMV
MDELPGLIGDVKEDVIVDTTIDKSLEKKAESLV
DILDKEGGKLDASQAALVSDGTG
AIRALVGGRDYATSQFNRAVKAKRQPGSSFKPFV
YAAALEKGLTPYSVFNDAPIRIGD
WTPENYEKKYNGEVTLATALAKSLNTVAAQLVMY
DGPDQVIKLAHRLGIESELOFNAS
IALGTSEVSLMELTASYAFAFMNGGYKATPHVIRR
VTTAEGKVLIENTYDSPPRVLSEQ
IAAEMDAMMMGVINDGTGKSAKIPGWQAAGKTGT
TQNSRDALFVGFTSNLTGTVWFGN
DDGKPMKKVTGGGLPAKAWKEFMIAAHKGLSPAP
LFGNGQLIADPNNGQPMAEAFNGG
QLGSGQPMTAEAPPSTIGGIISGVFGGNDNANRY
PQAPVRQQAATSGSGPVPPADIAE
GGSGYEGMVPPGDVGAQTTSVQPRRTLLDL
IMGQ"

misc-feature      complement(183929..1847 /locus-tag="RL0153"
29)

                        /inference="protein
                        motif:Pfam:PF00905.8"
                        /note="Pfam match to entry
                        PF00905.8 Transpeptidase"

misc-feature      complement(185024..1855 /locus-tag="RL0153"
27)

                        /inference="protein
                        motif:Pfam:PF00912.8"
                        /note="Pfam match to entry
                        PF00912.8 Transgly"

misc-feature      complement(185582..1856 /locus-tag="RL0153"
50)

                        /inference="protein
                        motif:TMHMM:2.0"
                        /note="1 probable transmembrane
                        helix predicted at aa 82-104"

gene              complement(186083..1863 /locus-tag="RL0154"
04)

CDS               complement(186083..1863 /locus-tag="RL0154"
04)

                        /note="no significant database
                        hits"
                        /codon-start=1
                        /transl-table=11
                        /product="hypothetical protein"
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                        /db-xref="GI:115254569"
                        /db-xref="UniProtKB/TrEMBL:Q1MN09"
                        /translation="MTQDYLAFLGLFAPRAAAID
                        VTVVHKHNPILPVRLTDGANLNPS
                        GQIWRRFHLGEWEYKQDPETLDDYEARQF"

sig-peptide       complement(186247..1863 /locus-tag="RL0154"
04)

                        /inference="protein
                        motif:SignalP-HMM:2.0"
                        /note="Signal peptide predicted
                        for RL0154 by SignalP 2.0 HMM
                        (Signal peptide probability 0.751)
                        with cleavage site probability
                        0.712 between residues 18 and 19"

gene              complement(186908..1875 /locus-tag="RL0155"
58)

CDS               complement(186908..1875 /locus-tag="RL0155"

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58)

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/inference="similar to
sequence:INSDC:AE007308"
/note="similarity:fasta;
with=UniProt:Q92KK7
(EMBL:AE007308); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein.;
length=283; id 58.706; 201 aa
overlap; query 1-200; subject
14-204"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05644.1"
/db-xref="GI:115254570"
/db-xref="UniProtKB/TrEMBL:Q1MN08"
/translation="MKNLIVKVAAMVLAPAI
AQAAEGYSTANVNMRRAGPSTRYPA
VAVVPAGSSVEIRGCLSNVNWCDVEFYGGRGWVS
GQYVQAVYQQRVYVGPQYYRPLG
IPMVSVSGNYWDRYRNRDFYRERDRWSRGPDY
YYRDRVYRDRDRDWSDDKRRDDRR
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sig-peptide

complement(187486..1875  
58)

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motif:SignalP-HMM:2.0"
/note="Signal peptide predicted
for RL0155 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability
0.995 between residues 23 and 24"
/locus-tag="RL0156"
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gene

complement(187564..1878  
21)

CDS

complement(187564..1878  
21)

/locus-tag="RL0156"

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/note="no significant database
hits"
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/transl-table=11
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/db-xref="GI:115254571"
/db-xref="UniProtKB/TrEMBL:Q1MN07"
/translation="MESHGPTALKVHAFATISQGL
SRTRYCVTKFPFFKLRSPPPEYKL
LKDNENSGALTNASDRSMFCRWHMFRKRSQALL
EKRANEE"
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gene

complement(187987..1894  
44)

CDS

complement(187987..1894  
44)

/locus-tag="RL0157"

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sequence:INSDC:AE007952"
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sequence:INSDC:AP006627"
/note="Similar to Bacillus clausii
KSM-K16. Deacylase. Q5WDJ9
(EMBL:AP006627) (432), and to
```

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Agrobacterium tumefaciens (strain
C58/ATCC 33970). AGR-C-165p.
Q7D266 (EMBL:AE007952) (507)
similarity:fasta;
with=UniProt:Q5WDJ9
(EMBL:AP006627); Bacillus clausii
KSM-K16.; Deacylase.; length=432;
id 33.183; 443 aa overlap; query
45-483; subject 4-429
similarity:fasta;
with=UniProt:Q7D266
(EMBL:AE007952); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-165p.; length=507;
id 82.062; 485 aa overlap; query
2-485; subject 22-506"
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/transl-table=11
/product="putative peptidase"
/protein-id="CAK05646.1"
/db-xref="GI:115254572"
/db-xref="GOA:Q1MN06"
/db-xref="UniProtKB/TrEMBL:Q1MN06"
/translation="MFFRLACL SGLVYRPAEFQK
ESKMTD VNQVLARADQNLSSSLDK
LFELLRIQSI STDPAYKAECKAAEWLVAYLEGL
GFTASVRDTPGHPMVVAHHAGASA
DAPHVLFGHYDVQFVDPIELWENDPFEPISKDV
GEGRKILTGRGTSDDKQQLMTFVE
ACRAYKEINGALPCRVTILFEGEEESGSPSLKPF
LEANATELKADYALVCDTGMWDRD
TPAIAAALRGLVGEEVIVTAADRDLSGLFGGA
ANPIHILVKALAGLHDETGRITLD
GFYEGVEETPDNIKASWETLGKTAESFLGEVGLS
IPSGEKGRSVLELTWARPTAEING
IWGGYTIGEGFKTVIAAKASAKVSFRLVGTQDPAA
IREAFRSYISSKIPADCSVEFHPH
GGSPAHLSDYSPVLTKAKNALSDEWPKPAIVIG
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GLSDDRIHSPNEKVELVSYHKGIRSWVRILEALA
A"
misc-feature      complement(187990..1893
12)                /locus-tag="RL0157"
                    /inference="protein
motif:Pfam:PF01546.12"
                    /note="Pfam match to entry
PF01546.12 Peptidase-M20"
gene              189588..191972
CDS                189588..191972
                    /locus-tag="RL0158"
                    /locus-tag="RL0158"
                    /inference="similar to
sequence:INSDC:AY323811"
                    /inference="similar to
sequence:INSDC:HS161255"
                    /note="Codons 260 to the
C-terminus are similar to codons
740 to the C-terminus of
Pseudomonas putida. morA Q7WYW5
(EMBL:AY323811) ( MorA.), and to
Agrobacterium tumefaciens (strain
C58/ATCC 33970). GGDEF family
protein. Q8U728 (EMBL:HS161255)
(779) similarity:fasta;

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with=UniProt:Q7WYW5  
 (EMBL:AY323811); Pseudomonas  
 putida.; MorA.; length=1282; id  
 38.889; 522 aa overlap; query  
 261-760; subject 742-1263  
 similarity:fasta;  
 with=UniProt:Q8U728  
 (EMBL:HS161255); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; GGDEF family protein.;  
 length=779; id 49.935; 773 aa  
 overlap; query 1-765; subject  
 1-766"  
 /codon-start=1  
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 /product="putative GGDEF/EAL  
 domain transcriptional regulator"  
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 /db-xref="GI:115254573"  
 /db-xref="GOA:Q1MN05"  
 /db-xref="UniProtKB/TrEMBL:Q1MN05"  
 /translation="MFSVITCIRDNDWRLVLA  
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 GYQLGLTALSFLLSVVGSWAAILV  
 ASESRRFRFSRIRGGVLMALGIASMHLTGMQAIET  
 QAAILYDFPMTLSAVLAGALLSSA  
 AFHAFQSKGLRRLASSITFVLAICALHFISMA  
 SITLVPDPGKEVPATVLDAALLAA  
 IVVVAATLILIALAVFIESHLTDLKGLANASQ  
 EGLLILREGRIIDANERFQGLSGW  
 KLAGLSGKAPSAVLTAVOGTGQNRPSSETVLNTRD  
 GREIAVEVTASRIVYRGHNCEVLA  
 VRDLTERRQAEEMIEHLAHDVLTDLPNRSLFDT  
 RIRQALQMAERKNSEVALFYLDLD  
 RFKAVNDIFGHAEGDRILRKVASILRRVADESIT  
 VARLGGDEFIILAGQQPAAQK  
 LAADILGEFAAEMDTARDPTAVGVSVGIALYPTD  
 GAAAEELCNNADTALYRVKHDGRG  
 KICFFDAEMDKAARNRRQIESELRHAIIRNQIHV  
 SYQPIILDALSIGEIGGYEALMRWRN  
 PGHGLTEPDIFISIAEESGSIVOLGEWLVQQACR  
 EAVRWPLPLMIAVNLSPVQFMLEN  
 LCERIEAILAETGLAPSRLEITEAALIRDRDR  
 VMTLLRLHKLGVHIVMDDFTGTF  
 SSLNLRSPFPDKIKVDRSFTGVLEHDAGARSIV  
 RAIIGLGHSLGMPVVTGVEVETEMQ  
 RRIIVVEGCAQVQGLLLGKPDIEPSIKLAAHENV  
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misc-feature      order(189630..189692,  
                     189729..189797,  
                     189825..189893,  
                     189930..189989,  
                     190017..190085,  
                     190119..190187,  
                     190230..190298)

/inference="protein  
 motif:TMHMM:2.0"  
 /note="7 probable transmembrane  
 helices predicted at aa 15-35,  
 48-70, 80-102, 115-134,144-166,  
 178-200 and 215-237"

misc-feature	189759..189944	/locus-tag="RL0158" /inference="protein motif:Pfam:PF03707.5" /note="Pfam match to entry PF03707.5 MHYT"
misc-feature	189945..190130	/locus-tag="RL0158" /inference="protein motif:Pfam:PF03707.5" /note="Pfam match to entry PF03707.5 MHYT"
misc-feature	190629..191114	/locus-tag="RL0158" /inference="protein motif:Pfam:PF00990.8" /note="Pfam match to entry PF00990.8 GGDEF"
misc-feature	191154..191867	/locus-tag="RL0158" /inference="protein motif:Pfam:PF00563.9" /note="Pfam match to entry PF00563.9 EAL"
gene	complement(192083..192499)	/locus-tag="RL0159"
CDS	complement(192083..192499)	/locus-tag="RL0159"  /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T13 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.; length=147; id 64.925; 134 aa overlap; query 1-134; subject 6-139" /codon-start=1 /transl-table=11 /product="putative MarR family transcriptional regulator protein" /protein-id="CAK05648.1" /db-xref="GI:115254574" /db-xref="GOA:Q1MN04" /db-xref="UniProtKB/TrEMBL:Q1MN04" /translation="MSGAYLASQLAKGFARSLH QRAVGLGFSFGQFPILLELWAEDG LTQKQLLERVDIEQATMANTLSRMVRDGLIERRP HPSDKRAQLLFLTPRAMEAEAI ETAREADLALFKGFRVFERELTLEYIRRLLENAK AL"
misc-feature	complement(192107..192418)	/locus-tag="RL0159"  /inference="protein motif:Pfam:PF01047.8" /note="Pfam match to entry PF01047.8 MarR"
gene	192994..196044	/gene="polA" /locus-tag="RL0160"
CDS	192994..196044	/gene="polA" /locus-tag="RL0160" /EC-number="2.7.7.7" /inference="similar to sequence:INSDC:U86403" /note="similarity:fasta;

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with=UniProt:DPO1-RHILE
(EMBL:U86403); Rhizobium
leguminosarum.; polA; DNA
polymerase I (EC 2.7.7.7) (POL
I).; length=EC 2.7.7.7; id 98.524;
1016 aa overlap; query 1-1016;
subject 1-1016"
/codon-start=1
/transl-table=11
/product="putative DNA polymerase
I"
/protein-id="CAK05649.1"
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/db-xref="GOA:Q1MN03"
/db-xref="UniProtKB/TrEMBL:Q1MN03"
/translation="MPNSINTSSHARAIHARMKK
GDHLFLVDGSGFIFRAFHALLPLT
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P
THLAVIFDYSARTFRKDLDAYKA
NRSAPPEELIPQFGLIREATRAFNLPFCIETEGFE
ADDIIATYARQAEATGADVTVSS
DKDMLQVLSPNVHMYDSMKDKQIGIPDVVEKMGV
PPEKMIDLQAMTGDSVDNVPGIPG
IGPKTAAQLLEEYGLDITLLERATEIKQVKRRET
ILANIDMARLSRDLVRLRTDVPID
LDLDALVLEPQNGPKLIGFLKTMFTTLTRRVAE
ACDCDASAIEPAIVRIEWGEKARG
PDLDAAEPEPVAGGIPDVSGESVPVPRAKAKTA
VEGAFSPADLAKARAEAFATLPFD
HSAYVTIRDLATLDRWIADARATGLVAFDTEETS
LDAMQAEVLVGFSLAIDANTADPTG
TKIRAAVYPLVHKNGVGDLLGGGLAENQIPMGDA
LARLKALLEDESILKVAQNLKYDY
LLMKRYGIETRSFDDTMLISYVLDA GTGAHGMDF
LSEKFLGHTPIPYKDVAGSGKANV
TFDLVDIRATHYAAEDADVTLLRLWLKPRLAA
AGLTSVYERLERPLLPVLARMEAR
GITVDQRQILSRSLGELAQAARLEDEIYVLAGER
FNIGSPKQLGDILFGKMGSLSGGSK
TKTGQWSTSAQVLEDLAAAGFELPRKIVDWRQVT
KLKSTYTDALPGYVHPETKRVHTS
YSLASTTTGRLSSSEPNLQNIQVPTAEGRKIRTA
FISTPGHKLISADYSQIELRVLAH
VAEIPQLTKAFEDGVDIHAMTASEMFGVPVEGMP
GEVRRRAKAINFGIYIGISAFGLA
NQLSIERSEAGDYIKKYFERFPGIRDYMESRKAM
ARDKGYVETIFGRRINYPEIRSSN
PSVRAFNERAAINAFIQGSAADVIRRAMIKIEPA
LVEVGLADRVRLMLQVHDELIFEV
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RAATNWEAH"
/gene="polA"
/locus-tag="RL0160"
/inference="protein
motif:Pfam:PF02739.5"
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PF02739.5 5-3-exonuc-N"

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misc-feature 193057..193569

misc-feature 193573..193875

misc-feature	194179..194790	PF01367.9 5-3-exonuc" /gene="polA" /locus-tag="RL0160" /inference="protein motif:Pfam:PF01612.10" /note="Pfam match to entry PF01612.10 3-5-exonuc"
misc-feature	194875..196038	/gene="polA" /locus-tag="RL0160" /inference="protein motif:Pfam:PF00476.9" /note="Pfam match to entry PF00476.9 DNA-pol-A"
gene	196319..198664	/locus-tag="RL0161"
CDS	196319..198664	/locus-tag="RL0161" /inference="similar to sequence:INSDC:A64828" /inference="similar to sequence:INSDC:C96030" /note="Codons 60 to the C-terminus are similar to codons 650 to the C-terminus of Escherichia coli. ftsK FTSK-ECOLI (EMBL:A64828) ( DNA translocase ftsK.), and codons 180 to the C-terminus are similar to Rhizobium meliloti (Sinorhizobium meliloti). Putative cell division protein FtsK like protein. Q92TK5 (EMBL:C96030) (611) similarity:fasta; with=UniProt:FTSK-ECOLI (EMBL:A64828); Escherichia coli.; ftsK; DNA translocase ftsK.; length=1329; id 43.490; 722 aa overlap; query 63-775; subject 649-1324 similarity:fasta; with=UniProt:Q92TK5 (EMBL:C96030); Rhizobium meliloti (Sinorhizobium meliloti).; Putative cell division protein FtsK like protein.; length=611; id 79.500; 600 aa overlap; query 187-779; subject 6-600" /codon-start=1 /transl-table=11 /product="putative cell division DNA translocase protein" /protein-id="CAK05650.1" /db-xref="GI:115254576" /db-xref="GOA:Q1MN02" /db-xref="UniProtKB/TrEMBL:Q1MN02" /translation="MRFPRTNLTDAGDFSSEIET DLPEENPGEKPAAPIWQSNFSLAP NVRFRTRIPETLISRRRAPNEFVRDSSQIGQQAIR IEPVAVDVFPDIYLPPEPDEISAAP QRIELQQSPDLLDEAAAPAFRASAEISSLISDFAFW EVMAFEAEAPVRAPPLISFPKTET SPESITSLFRIMEWRPGRPAQVVSRRPAPQPA VSAKVAVRPAAAIISLEKPRRIAVE APVMLAPQAAPTQLAPAPHIASAPQAAPAPQRT PPVAAVLPSRLAARPEKIDASGY EFFPRALLQEPERLGEIMSQETLEQNAGLESV

		<p>LEDGFIGKEIIHVRPGPVVTLYEF  EPAPGVKSSRVIGLADDIARMSALSARVAVVPG  RNVIGIELPNVTRRETVYFREMIES  QDFEKSQYKLALGLKGTIGGEPVIAELAKMPHLL  VAGTTGSGKSVAINTMILSLLYRM  TPEQCRLIMVDPKMLELSVYDGI PHLLTPVVTDP  KKAVMALKAVAVREMEERYRKMSRL  GVRNIDGYNDRVAQAREKGETIHMVQVGFDKGT  GTPIEESQALDLTFMPYIVVIVDE  MADLMMVAGKDIEGAIQRLAQMARAAGIHLIMAT  QRPVSDVITGITKANFPFTRISFQV  TSKIDSTRITLGEQGAQQLLGQDMLHMQGGGRIS  RVHGFPFVSDVEVEKVV AHLKTQGR  PEYLDTVTADEEEEEEEEAGAVDKSAMASEDG  NELYEQAQVVMVRDKKCSYSIQR  RLGIGYNRAASLVERMEKEGLVGPANHVGKREIV  SGRGDGE"</p>
misc-feature	197471..198133	<p>/locus-tag="RL0161"  /inference="protein  motif:Pfam:PF01580.8"  /note="Pfam match to entry  PF01580.8 FtsK-SpoIIIE"</p>
gene	complement(198700..199203)	/locus-tag="RL0162"
CDS	complement(198700..199203)	<p>/locus-tag="RL0162"  /inference="similar to  sequence:INSDC:AE011062"  /inference="similar to  sequence:INSDC:BF39410"  /note="similarity:fasta;  with=UniProt:GRPB-BACPF  (EMBL:BF39410); Bacillus  pseudofirmus.; grpB;  Glutamate-rich protein grpB.;  length=174; id 28.395; 162 aa  overlap; query 4-158; subject  9-169 similarity:fasta;  with=UniProt:Q8TK81  (EMBL:AE011062); Methanosarcina  acetivorans.; Hypothetical protein  MA3535.; length=186; id 38.509;  161 aa overlap; query 4-161;  subject 21-181"  /codon-start=1  /translation-table=11  /product="conserved hypothetical  protein"  /protein-id="CAK05651.1"  /db-xref="GI:115254577"  /db-xref="UniProtKB/TrEMBL:Q1MN01"  /translation="MRAIKVVVDYDPSWPRLFAEII  SAEVSALLGDRLLSIDHIGSTSV  GLAAKPKIDLAAVMISDAFLPAAIEIVRAADFV  HGDGTGEQRWAFTRDHGQYGFRLYL  CGPDNRAHRGRILFRDYLRNHPERAKAYADLKR  RLAAEADDWDFYITGGKIDFVSETV RLAAALKT"  /locus-tag="RL0162"</p>
misc-feature	complement(198715..199203)	<p>/inference="protein  motif:Pfam:PF04229.3"  /note="Pfam match to entry</p>

		PF04229.3 UPF0157"
gene	complement(199223..199819)	/gene="phnN"
		/locus-tag="RL0163"
CDS	complement(199223..199819)	/gene="phnN"
		/locus-tag="RL0163"
		/inference="similar to sequence:INSDC:B97379"
		/inference="similar to sequence:INSDC:HSPD32662"
		/note="similarity:fasta; with=UniProt:PHNN-ECOLI (EMBL:HSPD32662); Escherichia coli.; phnN; ATP-binding protein phnN.; length=185; id 35.955; 178 aa overlap; query 15-191; subject 3-176 similarity:fasta; with=UniProt:Q8UIX3 (EMBL:B97379); Agrobacterium tumefaciens (strain C58/ATCC 33970).; gmk; Guanylate kinase (AGR-C-277p).; length=199; id 57.955; 176 aa overlap; query 15-190; subject 15-190"
		/codon-start=1
		/transl-table=11
		/product="putative ATP-binding phosphate metabolism protein"
		/protein-id="CAK05652.1"
		/db-xref="GI:115254578"
		/db-xref="GOA:Q1MN00"
		/db-xref="UniProtKB/TrEMBL:Q1MN00"
		/translation="MMSHEPHAGAGAERGTMVVV VGPSGAGKDTLMNLAARRFKGRD VHFVRRVITRHRDAGGEDHLSVSLQGFAAMEQSG SFAVWWEAHLKYGIPAEISVALS KGHIVVANGSRSAALHRFQAAPRLKVINVTARPE VLAGRLETRGRETHEDIMARLARG PLTVRGEYDVVELDNSGSLEEAEQKMIEILNGLL TKTP"
gene	complement(199816..200988)	/gene="phnM"
		/locus-tag="RL0164"
CDS	complement(199816..200988)	/gene="phnM"
		/locus-tag="RL0164"
		/inference="similar to sequence:INSDC:ECPHN"
		/inference="similar to sequence:INSDC:RME591985"
		/note="similarity:fasta; with=UniProt:PHNM-ECOLI (EMBL:ECPHN); Escherichia coli.; phnM; PhnM protein.; length=378; id 47.340; 376 aa overlap; query 17-389; subject 2-377 similarity:fasta; with=UniProt:Q92V74 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative enzyme protein.; length=379; id 76.781;



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379 aa overlap; query 12-390;
subject 1-379"
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metabolism protein"
/protein-id="CAK05653.1"
/db-xref="GI:115254579"
/db-xref="UniProtKB/TrEMBL:Q1MMZ9"
/translation="MPAPKAERPDAMSKETVFSN
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SEGNVAGEDFEGDYMIPGLVELHTDHLLEGHYQP
RPGIRWNKTAAVQAHDAQIVTSGI
TTVFDCLRMGADEGGFEHGEMREMADAIQSAET
EGRRLAEHLIHLRCEVSADNVLEH
FADFESDRHVRVLVSLMDHAPGQRQFQTMDQYIFY
YQKKRGLSDEAFARFVAKRQAES
RNSTPHRNAIAKVCAERGITVASHDDATLSHVDE
AIDNGVRLAEFFTSFDAARASHEH
GMSVLMGAPNIVRGKSHSGNIAARDLAEMGVLDV
LSSDYVPLSLLHAPFILADEVESI
SLPKAIAMVTSTPARTVSLDDRGRIATGLRADLV
RVHRSHGVPTVTRSVWRQGRRA"
/misc-feature complement(199876..2008
14) /gene="phnM"
/locus-tag="RL0164"
/inference="protein
motif:Pfam:PF01979.7"
/note="Pfam match to entry
PF01979.7 Amidohydro-1"
gene complement(200969..2016
64) /locus-tag="RL0165"
CDS complement(200969..2016
64) /locus-tag="RL0165"
/inference="similar to
sequence:INSDC:AE008991"
/note="similarity:fasta;
with=UniProt:Q8UIX1
(EMBL:AE008991); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu0170.; length=232; id 59.292;
226 aa overlap; query 1-226;
subject 4-222"
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protein"
/protein-id="CAK05654.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMZ8"
/translation="MRYALYFSPPKDDPLTGAAS
LWLGRNAFTGETYPAPEHEQLGAA
EQFELTADPRRYGFHATIKAPFLASSVTEKDL
TV AEDFARRTQAFEIPELVLGQLG
RFFALVPGSLHQPLQDFAAKVRSFEPFRAALSE
TDMARRNPEKLSDSQRAHLKRWGY
PYVMEDFGFHMTLSGQVPETRAEVMKAILTERFA
NFTGRPLSISGLAVFIEETRGAF
KVHSWLPLAGAKS"
/misc-feature complement(200975..2016
64) /locus-tag="RL0165"

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/note="Pfam match to entry
PF06299.1 DUF1045"
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38)      /gene="phoT"
CDS       complement(201786..2031
38)      /locus-tag="RL0166"
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         /locus-tag="RL0166"
         /inference="similar to
sequence:INSDC:AE007958"
         /inference="similar to
sequence:INSDC:HSH95946"
         /note="similarity:fasta;
with=UniProt:Q52909
(EMBL:HSH95946); Rhizobium
meliloti (Sinorhizobium
meliloti).; phoT; PhoT (Phosphate
uptake ABC transporter permease
protein).; length=Phosphate uptake
ABC transpor ( 505; id 49.105; 503
aa overlap; query 1-447; subject
1-503 similarity:fasta;
with=UniProt:Q8UIX0
(EMBL:AE007958); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; phnE; ABC transporter,
membrane spanning protein
(AGR-C-284p).; length=449; id
70.667; 450 aa overlap; query
1-450; subject 1-449"
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         /transl-table=11
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component of phosphate uptake ABC
transporter protein"
         /protein-id="CAK05655.1"
         /db-xref="GI:115254581"
         /db-xref="GOA:Q1MMZ7"
         /db-xref="UniProtKB/TrEMBL:Q1MMZ7"
         /translation="MSSVPTINAAERERLLSAYP
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AFCFAFFNVIPTFVNGNWDRAAIYVQDNYSWRAQ
PRLRFQNDQVVPQWTSRRQYPEGA
DINWLKPNADGSRYYTVFGSDGDRMEVTPSRVDV
YIDGKLYPVTITHDRA SLPSDAPA
RMQQDDNKVNVVYGFAGQAEI RTNQVYIQRFLG
WANFFFDTHSPFWGRSLPEVVGLM
FSGERLDPNQSNASLALDNFLNNAWQHGDILSK
LMQTLVMAFVGTILFGLVAFPLAF
IAARNIMRSRAANWGTRKRLDFDLRSIDMLIWALE
FTRAFGPGPLPGIAAIFFTDTGAL
GKVVAAEALENIDDKQREGVRSVGAAPVAVQRYGV
IPQVLPVFISQSLYFWESNTRSAT
AIGAVGAGGIGLKLLESMTNSDWDKVAYMVLII
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misc-feature complement(201801..2023
82)      /gene="phoT"
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motif:Pfam:PF00528.10"

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                                /locus-tag="RL0166"
                                /inference="protein
                                motif:TMHMM:2.0"
                                /note="4 probable transmembrane
                                helices predicted at aa 32-54,
                                257-279, 306-328 and 419-441"
gene              complement(203138..2041
                                18)
                                /gene="phoE"

                                /locus-tag="RL0167"
CDS               complement(203138..2041
                                18)
                                /gene="phoE"

                                /locus-tag="RL0167"
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                                sequence:INSDC:A95947"
                                /inference="similar to
                                sequence:INSDC:AE008991"
                                /note="similarity:fasta;
                                with=UniProt:Q52908 (EMBL:A95947);
                                Rhizobium meliloti (Sinorhizobium
                                meliloti).; phoE; PhoE (Phosphate
                                uptake ABC transporter permease
                                protein).; length=Phosphate uptake
                                ABC transpor ( 320; id 59.683; 315
                                aa overlap; query 9-323; subject
                                6-320 similarity:fasta;
                                with=UniProt:Q8UIW9
                                (EMBL:AE008991); Agrobacterium
                                tumefaciens (strain C58/ATCC
                                33970).; phnE; ABC transporter,
                                membrane spanning protein.;
                                length=328; id 81.620; 321 aa
                                overlap; query 6-326; subject
                                8-328"
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                                /transl-table=11
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                                component of phosphate uptake ABC
                                transporter"
                                /protein-id="CAK05656.1"
                                /db-xref="GI:115254582"
                                /db-xref="GOA:Q1MMZ6"
                                /db-xref="UniProtKB/TrEMBL:Q1MMZ6"
                                /translation="MAHSAGADSLSGLQEGSRTI
                                LDHYQSQVRRRIYTVVSIVVFLI
                                ILGASLDFANSANGSKFFERLPYFFDFMKSFPVD
                                SPLEIFRAMFDLPSPFSDGSIKYD
                                YTSRVRWITDSFYIPNFFYQLAITLNIAIVSTIL
                                GASGAFLLCFFASTINLVGAGVTRW
                                VVRRIMEIMRAFPEIVVAGLLAAILSIGPISAI
                                AVVWHTVGALGLKFFEVVENADMK
                                PDEGLRAAGAWLERVRFALLPQVLNPNFVSYTLL
                                RTEINVRASTIIGAVGGGGIGEVF
                                SLSIGRDHAAKTYAIIILLITVICVDQFSAWLR
                                RRLIGKQSFEFGQAA"
                                /gene="phoE"
misc-feature      complement(203174..2037
                                52)

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HQMVTKGLLDMDDIVVEVWKSPLIPNGPLMVSQKL
PADLQKKVTTYFAELPKTDKSCFE
SFTGGGYVDWVVPVQSFYQTIIDARKAVIGG"
gene      complement(205369..2064 /locus-tag="RL0169"
36)
CDS       complement(205369..2064 /locus-tag="RL0169"
36)
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          sequence:INSDC:AE016960"
          /inference="similar to
          sequence:INSDC:OCA82447"
          /note="similarity:fasta;
          with=UniProt:TRAI-COXB
          (EMBL:AE016960); Coxiella
          burnetii.; Transposase for
          insertion sequence element
          IS1111A.; length=339; id
          26.706;
          337 aa overlap; query
          9-337;
          subject 7-335
          similarity:fasta;
          with=UniProt:Q6LB66
          (EMBL:OCA82447);
          Oligotropha
          carboxidovorans
          (Pseudomonas
          carboxydovorans.);
          Transposase
          ISC1190.; length=300;
          id 87.667;
          300 aa overlap; query
          57-355;
          subject 1-300;
          transposase for
          insertion sequence
          element
          is1111a"
          /codon-start=1
          /transl-table=11
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          transposase for
          insertion element
          family protein"
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          /db-xref="UniProtKB/TrEMBL:Q1M490"
          /translation="MTASYEYHIGVDYHKSYSHL
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          WLDLDDICDDVV
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          LAHLLRADLVPEAWAPSERDRLR
          VALRERMFYV
          RLRTMTKNRIVTVFDRYPEQTAQL
          KKLGDLFQKAGRVQLAQVNVSEIDRIQIDRGLAF
          IGDIDMRKQSEATIRAMTKANAN
          VKLLKTIPGIGEFAFLIDAEIDDISRFRH
          SKKL
          AAYAGLVPSHTHSGGKTFHGKIIK
          QGNKWLRFVFAVPAIAISDPQLRAQY
          EHLKIK
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          RAYEPRGESTMEGASTISRLS"
misc-feature complement(205525..2058 /locus-tag="RL0169"
54)
          /inference="protein
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          /note="Pfam match to
          entry
          PF02371.5 Transposase-20"
gene      complement(206639..2074 /gene="phoC"
84)
          /locus-tag="RL0170"
CDS       complement(206639..2074 /gene="phoC"
84)
          /locus-tag="RL0170"

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/inference="similar to
sequence:INSDC:RM59229"
/note="similarity:fasta;
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(EMBL:RM59229); Rhizobium meliloti
(Sinorhizobium meliloti).; phoC;
PhoC.; length=270; id 80.695; 259
aa overlap; query 2-260; subject
1-256 similarity:fasta;
with=UniProt:Q8UIW7 (EMBL:A97380);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; phnC; ABC
transporter, nucleotide
binding/ATPase protein.;
length=290; id 83.846; 260 aa
overlap; query 1-260; subject
5-264"
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/transl-table=11
/product="putative ATP-binding
component of phosphate uptake ABC
transporter"
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/db-xref="UniProtKB/TREMBL:Q1MMZ3"
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RDCAMIFQQFNLVPRLDVLTNVM
GRLNHRSTLMSLLNIFTEERVHAIAALERLGIE
QTALQAAGTSLSGGQQQRVAIARAL
MQNPKMVLADEPIASLDPLNAKIVMDALRDINER
EGITVITNLHTLDTARNYCERIVG
MAGGRVVF DGKPSSELTAEAVKEIYGTDKDGAGID
ETMTSTSLSKRRAEDVSSGRVAK AA AVH"
misc-feature complement(206819..2074
03) /gene="phoC"
/locus-tag="RL0170"
/inference="protein
motif;Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
gene complement(207600..2082
17) /locus-tag="RL0171"
CDS complement(207600..2082
17) /locus-tag="RL0171"
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sequence:INSDC:AF047479"
/inference="similar to
sequence:INSDC:B97380"
/note="similarity:fasta;
with=UniProt:CAT4-ECOLI
(EMBL:AF047479); Escherichia
coli.; catB2; Chloramphenicol
acetyltransferase (EC 2.3.1.28).;
length=210; id 39.053; 169 aa
overlap; query 23-188; subject
26-190 similarity:fasta;
with=UniProt:Q8UIW6 (EMBL:B97380);

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Agrobacterium tumefaciens (strain
C58/ATCC 33970).;
Acetyltransferase (AGR-C-291p).;
length=205; id 76.585; 205 aa
overlap; query 1-205; subject
1-205"
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acetyltransferase"
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WRRANRVITIGNDVWIGHGATILPGVSVNGAVIG
AGAVVSKDVAPYITVGGVPAKLIR
ERFPREVGERMDRLSWWDWEHDLRQALEDFRNL
DAEDFLSRYGG"
misc-feature      complement(207789..2078
42)               /locus-tag="RL0171"
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motif:Pfam:PF00132.9"
                  /note="Pfam match to entry
PF00132.9 Hexapepl"
misc-feature      complement(207843..2078
96)               /locus-tag="RL0171"
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motif:Pfam:PF00132.9"
                  /note="Pfam match to entry
PF00132.9 Hexapep"
misc-feature      complement(208008..2080
61)               /locus-tag="RL0171"
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motif:Pfam:PF00132.9"
                  /note="Pfam match to entry
PF00132.9 Hexapep"
misc-feature      complement(208110..2081
63)               /locus-tag="RL0171"
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motif:Pfam:PF00132.9"
                  /note="Pfam match to entry
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21)               /locus-tag="RL0172"
CDS               complement(208214..2089
21)               /locus-tag="RL0172"
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sequence:INSDC:HSH96023"
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with=UniProt:AAR91740; length=234;
id 56.828; 227 aa overlap; query
1-227; subject 1-227
similarity:fasta;
with=UniProt:Q92TQ1
(EMBL:HSH96023); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative phosphonate
uptake ABC transporter ATP-binding

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protein.; length=235; id 77.872;
235 aa overlap; query 1-235;
subject 1-235"
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component of phosphate uptake ABC
transporter"
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/db-xref="UniProtKB/TrEMBL:Q1MMZ1"
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RTVPRVAIDVVAEPLVARGEDAVTAREKAGALL
ARLNLPELTLWLPPATFSGGQQOR
VNIARGFITEHTILLDEPTASLDARNRAVVVGM
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ADRLIDVQQQFSRKIAA"
misc-feature complement(208238..2088 /locus-tag="RL0172"
13)
/inference="protein
motif:Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
gene complement(208948..2097 /gene="phnK"
24)
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CDS complement(208948..2097 /gene="phnK"
24)
/locus-tag="RL0173"
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sequence:INSDC:ECPHN"
/inference="similar to
sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:PHNK-ECOLI
(EMBL:ECPHN); Escherichia coli.;
phnK; Phosphonates transport
ATP-binding protein phnK.;
length=252; id 68.235; 255 aa
overlap; query 3-257; subject
2-251 similarity:fasta;
with=UniProt:Q52988
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; phnK; PhnK protein
(Putative phosphonate uptake ABC
transporter ATP-binding protein).;
length=Putative phosphonate ( 258;
id 89.535; 258 aa overlap; query
1-258; subject 1-258"
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component of phosphate uptake ABC
transporter"
/protein-id="CAK05662.1"
/db-xref="GI:115254588"
/db-xref="GOA:Q1MMZ0"

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/db-xref="UniProtKB/TrEMBL:Q1MMZ0"
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NEAERRFLMRTDWGFVHQNPDGL
RMTVSAGANVGERLMTATGDRHYGKIRASAI DWLE
RVEIDADRIDDQFRAFSGGMRQRL
QIARNLVTGPRLVFMEPTGGLDVSVQARLLDLV
RGLVNDLGLSAIIVTHDLAVARLL
SHRMMVMKDGVIIEHGLTDRVLDDPREPYTQLLV
SSILQV"
misc-feature      complement(209041..2096
31)                /gene="phnK"

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/inference="protein
motif:Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
gene              complement(209721..2105
96)                /gene="phnJ"

/locus-tag="RL0174"
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CDS                complement(209721..2105
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/inference="similar to
sequence:INSDC:RME591985"
/ note="similarity:fasta;
with=UniProt:PHNJ-RHIME
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; phnJ; PhnJ protein.;
length=297; id 90.722; 291 aa
overlap; query 1-291; subject
1-291"
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metabolism protein"
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/db-xref="UniProtKB/TrEMBL:Q1MMY9"
/translation="MTDLASYNFAYLDEQTKRMI
RRAILKAIAIPGYQVPFASREMPM
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AVSIRAFFQKVAVAVTTHTKDAT
IIQTRHRIPEEKLGVGQVLVYQVPIPEPLRFLEP
RETETRKMHALEEYGLMHVKLYED
IAHNGRISRTIYAPVKVHGRYVMDPSPTPKFDNP
KMHMSDALQLFGAGREKRIYAVPP
YTDVVSLDFEDYPFDIQRFKPKALCGAEDVYLD
EVLVDDKGRMFVCSDDTHCEDRR
AHGHAGEMLAREAAE"
misc-feature      complement(209754..2105
90)                /gene="phnJ"

/locus-tag="RL0174"
/inference="protein
motif:Pfam:PF06007.1"
/ note="Pfam match to entry
PF06007.1 PhnJ"
gene              complement(210593..2116
99)                /gene="phnI"

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CDS	complement(210593..211699)	/locus-tag="RL0175" /gene="phnI"  /locus-tag="RL0175" /inference="similar to sequence:INSDC:AE007959" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:PHNI-RHIME (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; phnI; PhnI protein.; length=368; id 81.351; 370 aa overlap; query 1-368; subject 1-368 similarity:fasta; with=UniProt:Q8UIW2 (EMBL:AE007959); Agrobacterium tumefaciens (strain C58/ATCC 33970).; phnI; Hypothetical protein phnI (AGR-C-299p).; length=369; id 82.656; 369 aa overlap; query 1-368; subject 1-369" /codon-start=1 /transl-table=11 /product="putative phosphonate metabolism protein" /protein-id="CAK05664.1" /db-xref="GI:115254590" /db-xref="GOA:Q1MMY8" /db-xref="UniProtKB/TrEMBL:Q1MMY8" /translation="MYVAVKGGETAIANAHRLLA DRRRGDRSLPAIGIDQIVAQIALA VDRVMAEASLFDRTLAALAIRQSRGDMIEAIFLL RAYRTILPRFGYSRPLDTADMTIE RRI SATYKDLPGGQLLGPTFDYTHRLDPSLLSD EAVETPAQRAAETGRVMRVSEILG EEGLIEADGMPEDHEIGDLTREPMEFFPMTRDLR LQALARGDEGFFLLALGYSTQRGYG RNHPFTGEIRIGDVEVEFDVPELGFVSLGTIQI TECQMVNQFKGSAKAPQOFTRGYG LVFGQSERKAMAMSLVDRLRAEELGEDITAPAQ DEEFVISHSDNVQATGFEVHLKLP HYVDFQAE LDLVRRMRREFEAA RRGEDMK EAAE "
misc-feature	complement(210632..211699)	/gene="phnI"  /locus-tag="RL0175" /inference="protein motif:Pfam:PF05861.1" /note="Pfam match to entry PF05861.1 PhnI"
gene	complement(211704..212312)	/gene="phnH"  /locus-tag="RL0176"
CDS	complement(211704..212312)	/gene="phnH"  /locus-tag="RL0176" /inference="similar to sequence:INSDC:AE007959" /inference="similar to

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sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:PHNH-RHIME
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; phnH; PhnH protein.;
length=200; id 58.883; 197 aa
overlap; query 1-197; subject
1-197 similarity:fasta;
with=UniProt:Q8UIW1
(EMBL:AE007959); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; phnH; Hypothetical
protein phnH (AGR-C-302p).;
length=203; id 64.677; 201 aa
overlap; query 1-201; subject
2-202"
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utilisation protein"
/protein-id="CAK05665.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMY7"
/translation="MGLKTEALTGGEVPEVFHAQ
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PEWLGFHTGAPLTTEKAEARFAFT
EAGTALSSFGLFASGTQEYPDRSTTLIELAELE
GRRRLALMGPGIQSVAEIAPIGLP
ETFLRLWTENRALFPRGVDIVLTAGKRFLCLPRT
TKITATEI"
misc-feature complement(211716..2122 /gene="phnH"
97) /locus-tag="RL0176"
/inference="protein
motif:Pfam:PF05845.1"
/note="Pfam match to entry
PF05845.1 PhnH"
gene complement(212312..2127 /gene="phnG"
88) /locus-tag="RL0177"
CDS complement(212312..2127 /gene="phnG"
88) /locus-tag="RL0177"
/inference="similar to
sequence:INSDC:C96023"
/inference="similar to
sequence:INSDC:HS380249"
/note="similarity:fasta;
with=UniProt:PHNG-RHIME
(EMBL:C96023); Rhizobium meliloti
(Sinorhizobium meliloti).; phnG;
PhnG protein.; length=156; id
60.127; 158 aa overlap; query
1-158; subject 1-156
similarity:fasta;
with=UniProt:Q8UIW0
(EMBL:HS380249); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; phnG; Hypothetical

```

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protein phnG (AGR-C-303p).;
length=153; id 61.589; 151 aa
overlap; query 8-158; subject
3-153"
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/product="putative phosphonate
utilisation protein"
/protein-id="CAK05666.1"
/db-xref="GI:115254592"
/db-xref="GOA:Q1MMY6"
/db-xref="UniProtKB/TrEMBL:Q1MMY6"
/translation="MISADRTDAASQTASGRKRA
ADLLARAERSELLAAFDALPEKPV
AHQVRGPEITGLVMVRGRIGGGGAPFNLGEVTVTR
ATVRLDSGSVGHQAQALGTDREKAR
LAAIFDALWQEATKDFVEQALLLPVTERIADAE
RRKADETAATRVDFFTMVRGDN"
/misc-feature complement (212315..2127
55) /gene="phnG"
/locus-tag="RL0177"
/inference="protein
motif:Pfam:PF06754.1"
/note="Pfam match to entry
PF06754.1 PhnG"
gene 212906..213643
CDS 212906..213643
/locus-tag="RL0178"
/locus-tag="RL0178"
/inference="similar to
sequence:INSDC:AE007959"
/note="similarity:fasta;
with=UniProt:Q8UIV9
(EMBL:AE007959); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Transcriptional
regulator, GntR family
(AGR-C-306p).; length=245; id
64.490; 245 aa overlap; query
1-245; subject 1-245"
/codon-start=1
/transl-table=11
/product="putative GntR family
transcriptional regulator"
/protein-id="CAK05667.1"
/db-xref="GI:115254593"
/db-xref="GOA:Q1MMY5"
/db-xref="UniProtKB/TrEMBL:Q1MMY5"
/translation="MSGLKQVQRQTGVALWRQIA
DRIREAISNGAYDETMVPPETML
ALQFGVNRHTVRSALAAQEGIVRAVQGRGTLI
ERKERLNFPIITRRTRFTAGIGDQA
REMRGRLLEEAKEEASAEIARWLGLKPGEEVIRL
ETLRQADKRFPVSRATSNWFPKRF
GIGEAYRTEESITKFAELGLPDYVRATTEVTAA
HASAADMADELTPGAILLIAKAM
NTDLEGVPVQYISIRFAADRVQFTIEN"
/misc-feature 212948..213139
/locus-tag="RL0178"
/inference="protein
motif:Pfam:PF00392.9"
/note="Pfam match to entry
PF00392.9 GntR"
gene complement (213683..2143
18) /gene="gpmA"

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CDS      complement(213683..214318) /locus-tag="RL0179"
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                                              /locus-tag="RL0179"
                                              /EC-number="5.4.2.1"
                                              /inference="similar to
sequence:INSDC:AY074773"
                                              /inference="similar to
sequence:INSDC:SME591782"
                                              /note="similarity:fasta;
with=UniProt:GPMA-BARHE
(EMBL:AY074773); Bartonella
henselae (Rochalimaea henselae).;
gpmA;
2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase (EC
5.4.2.1) (Phosphoglyceromutase)
(PGAM) (BPG-dependent PGAM)
(dPGM).; length=206; id 62.745;
204 aa overlap; query 1-204;
subject 1-204 similarity:fasta;
with=UniProt:GPMA-RHIME
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; gpmA;
2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase (EC
5.4.2.1) (Phosphoglyceromutase)
(PGAM) (BPG-dependent PGAM)
(dPGM).; length=211; id 88.152;
211 aa overlap; query 1-211;
subject 1-211; putative
2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase
(Phosphoglyceromutase) (PGAM)
(BPG-dependent PGAM) (dPGM)"
/codon-start=1
/transl-table=11
/product="2,3-bisphosphoglycerate-
dependent phosphoglycerate mutase
(phosphoglyceromutase) (pgam)
(bpg-dependent pgam) (dpgm)"
/protein-id="CAK05668.1"
/db-xref="GI:115254594"
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/db-xref="UniProtKB/TrEMBL:Q1MMY4"
/translation="MSGTLVLVRHGQSDWNLNKL
FTGWKDPDLTELGIQEANTGGAAL
AEYGIKFDVAYTSVLVRAQHTLKLILDKVGQPD
LTIRDQALNERDYGDL SGLNKDDA
RAKWGEQVHIWRRSYDVP PPGGESLRDTGARVN
PYYLTEILPRVLRGEKVLVAAHGN
SLRSLVMVLDKLSREGVLALNLTGVP M VYKLKA
DSTVASKEVLGDMSGAH"
/misc-feature complement(213713..214312) /gene="gpmA"

                                              /locus-tag="RL0179"
                                              /inference="protein
motif:Pfam:PF00300.9"
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PF00300.9 PGAM"
gene      complement(214340..2151) /gene="dapB"

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64) /locus-tag="RL0180"  
CDS complement(214340..2151 /gene="dapB"  
64) /locus-tag="RL0180"  
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/inference="similar to  
sequence:INSDC:ECAPAH02"  
/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:DAPB-ECOLI  
(EMBL:ECAPAH02); Escherichia  
coli.; dapB; Dihydropicolinate  
reductase (EC 1.3.1.26) (DHPR).;  
length=273; id 46.350; 274 aa  
overlap; query 1-273; subject  
1-272 similarity:fasta;  
with=UniProt:DAB1-RHIME  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; dapB;  
Dihydropicolinate reductase (EC  
1.3.1.26) (DHPR).; length=272; id  
80.074; 271 aa overlap; query  
1-271; subject 1-271"  
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/transl-table=11  
/product="putative  
dihydropicolinate reductase"  
/protein-id="CAK05669.1"  
/db-xref="GI:115254595"  
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/db-xref="UniProtKB/TrEMBL:Q1MMY3"  
/translation="MSDAAMKLVVVGAAAGRMGGT  
LIRLIHSIEGVRLHAAVERAGSFF  
VGKDAGEIAGLGPTGVIIGDDPLNAFLDAEGVLD  
FTSPAATVEFSGLAQAQIRIVHVVG  
TTGCSADDNTKIAAAARHARIVKSGNMSLGVNLL  
SVLAEQAARALDPDDWDIEILEMH  
HKHKVDAPSGTALLIGEAAAKRGIDLASQSVRV  
RDGHTGAREAGTIGFATLRGGSVI  
GEHSVLFAGEGETVTLSHSAADRSIFARGAIKAA  
LWARDKKPGLYSMLDVLGLSSS"  
misc-feature complement(214355..2147 /gene="dapB"  
71) /locus-tag="RL0180"  
/inference="protein  
motif:Pfam:PF05173.2"  
/note="Pfam match to entry  
PF05173.2 DapB-C"  
misc-feature complement(214778..2151 /gene="dapB"  
49) /locus-tag="RL0180"  
/inference="protein  
motif:Pfam:PF01113.9"  
/note="Pfam match to entry  
PF01113.9 DapB-N"  
gene complement(215180..2169 /locus-tag="RL0181"  
67)  
CDS complement(215180..2169 /locus-tag="RL0181"  
67)

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sequence:INSDC:C85617"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:MSBA-ECOLI
(EMBL:C85617); Escherichia coli.;
msbA; Lipid A export
ATP-binding/permease protein
msbA.; length=582; id 36.380; 558
aa overlap; query 34-587; subject
26-579 similarity:fasta;
with=UniProt:Q92T26
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE ATP-BINDING
ABC TRANSPORTER PROTEIN.;
length=601; id 75.966; 595 aa
overlap; query 1-594; subject
1-594"
/codon-start=1
/transl-table=11
/product="putative transmembrane
component of ABC transporter"
/protein-id="CAK05670.1"
/db-xref="GI:115254596"
/db-xref="GOA:Q1MMY2"
/db-xref="UniProtKB/TREMBL:Q1MMY2"
/translation="MEAAESRTQSVSSDVTGIL
KRIIAENGRDHLGWYVFAIACLIV
VALSTAFTAWIMRAIIDEAFANRRADVVMICLS
IFIAFVLRGFASYGQAVALSVRGN
DIVARYQRRLYAHMLTSLGVGFSEARSAHIAAQV
SQNVSGIRDVLNLTTITSTVRDLT
FVSL LAVMIIQDPLLSLAVFIMAPLLLYALRYVS
KRLRSATREAVHLNSHVLGAMQET
IQGIAIVKFTMEELERKVNKLKGAESRANRI
ARLSERTSPLTESFAGFAVASVLA
YAAYSRIYFNVPPGAFFSFVTALLLAYDPARRLA
RLQVQMERAVVNARMYIELLDMEP
RQRDLDPARPLTVTQARIEFRNVSFAYGESVLS
GVSFIAEGGGTTALVPGSGAGKST
VISLIPRFYDPREGEILIDGQDIAHITKSLRQQ
LAYVSQQPYLFEGTIRDNIRYGRF
EATDAEVEEAARLAYAHDFISAQPPQGYETPVGEN
GVTLSGGQRQLSIARALVRNAPI
LLLDEATSA LDTESEAAVQKALDEAMSGRVTVVII
AHRSLTVVRADKIVVMQGRVVEE
GNHETLAKVSDGLYARLNNLQRPSSADSN"
misc-feature complement(215285..2158 /locus-tag="RL0181"
39) /inference="protein
motif:Pfam:PF00005.11"
/note="Pfam match to entry
PF00005.11 ABC-tran"
misc-feature complement(216050..2168 /locus-tag="RL0181"
65) /inference="protein
motif:Pfam:PF00664.9"
/note="Pfam match to entry
PF00664.9 ABC-membrane"
misc-feature complement(join(216062. /locus-tag="RL0181"

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.216121,216398..216466,
216566..216634,
216695..216763,
216806..216874))

/inference="protein
motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted at aa 32-54,
69-91, 112-134, 168-190 and
283-302"
gene      complement(217115..2181 /gene="glk"
40)
CDS       complement(217115..2181 /locus-tag="RL0182"
40)       /gene="glk"

/locus-tag="RL0182"
/EC-number="2.7.1.2"
/inference="similar to
sequence:INSDC:AE005470"
/inference="similar to
sequence:INSDC:C97381"
/note="similarity:fasta;
with=UniProt:GLK-ECOLI
(EMBL:AE005470); Escherichia coli
O157:H7.; glk; Glucokinase (EC
2.7.1.2) (Glucose kinase).;
length=EC 2.7.1.2; id 37.097; 310
aa overlap; query 16-325; subject
6-314 similarity:fasta;
with=UniProt:GLK-AGRT5
(EMBL:C97381); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; glk; Glucokinase (EC
2.7.1.2) (Glucose kinase).;
length=EC 2.7.1.2; id 72.189; 338
aa overlap; query 4-340; subject
6-343"
/codon-start=1
/transl-table=11
/product="putative glucokinase"
/protein-id="CAK05671.1"
/db-xref="GI:115254597"
/db-xref="GOA:Q1MMY1"
/db-xref="UniProtKB/TrEMBL:Q1MMY1"
/translation="MSKPNNSTAPLPFPILIGDI
GGTNARFSILTDAYAEPKQFPNVR
TADFATIDEAIQQGVLDKTAQVQFRSAILAVAGPI
NDDEIPLTNCDWVVRPKMTIEGLG
MEDVLVVNDFEAQAALAAALSDENRERIGDATRD
MIASRVVLGPGTGLGVGLVHAQH
SWIPVPGEGGHVDLGPSCRKRDYDIFPHIETIEGR
VSAEQILCGRLVNLVHAICVVDG
IEPTMKDPADITSHALAGSDKAAVETVSLFATYL
GRVAGDLAMVFMARGGVYLSGGIS
QKIIPALKKPEFRIAFEDKAPHTALLRTIPTVYV
THPLAALAGLSSYARMPANFVGST EGRWRRR"
misc-feature complement(217160..2181 /gene="glk"
10)

/locus-tag="RL0182"
/inference="protein
motif:Pfam:PF02685.4"
/note="Pfam match to entry

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gene complement(218158..218538) /locus-tag="RL0183"  
 CDS complement(218158..218538) /locus-tag="RL0183"  
 /EC-number="4.2.3.3"  
 /inference="similar to  
 sequence:INSDC:AE005286"  
 /inference="similar to  
 sequence:INSDC:SME591782"  
 /note="similarity:fasta;  
 with=UniProt:MGSA-ECOLI  
 (EMBL:AE005286); Shigella  
 flexneri.; mgsA; Methylglyoxal  
 synthase (EC 4.2.3.3) (MGS).;  
 length=152; id 50.442; 113 aa  
 overlap; query 5-117; subject  
 12-123 similarity:fasta;  
 with=UniProt:MGSA-RHIME  
 (EMBL:SME591782); Rhizobium  
 meliloti (Sinorhizobium  
 meliloti).; mgsA; Methylglyoxal  
 synthase (EC 4.2.3.3) (MGS).;  
 length=126; id 83.471; 121 aa  
 overlap; query 1-121; subject  
 1-121; putative methylglyoxal  
 synthase"  
 /codon-start=1  
 /transl-table=11  
 /product="methylglyoxal synthase  
 (mgs)"  
 /protein-id="CAK05672.1"  
 /db-xref="GI:115254598"  
 /db-xref="GOA:Q1MMY0"  
 /db-xref="UniProtKB/TrEMBL:Q1MMY0"  
 /translation="MAGGKCLALIAHDQKKDDMA  
 AFARANRDLRSWKIVATGTTGGR  
 VLDAAPDLDVVRLKSGPLGGDQIGALISTGEVD  
 ALIFFVDPLTPMPHDVDVKALMRL  
 AIVYDIPMALNHATAIKLLPTLEA"  
 misc-feature complement(218203..218487) /locus-tag="RL0183"  
 /inference="protein  
 motif:Pfam:PF02142.8"  
 /note="Pfam match to entry  
 PF02142.8 MGS"  
 gene complement(218624..219700) /locus-tag="RL0184"  
 CDS complement(218624..219700) /locus-tag="RL0184"  
 /inference="similar to  
 sequence:INSDC:AE015256"  
 /inference="similar to  
 sequence:INSDC:SME591782"  
 /note="Similar, but extended at  
 the N and C-termini, to Shigella  
 flexneri. mepA MEPA-ECOLI  
 (EMBL:AE015256)  
 (Penicillin-insensitive murein  
 endopeptidase precursor (EC  
 3.4.99.-)  
 (D-alanyl-D-alanine-endopeptidase)

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(DD-endopeptidase).), and to
entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
PUTATIVE MUREIN ENDOPEPTIDASE
TRANSMEMBRANE PROTEIN (EC 3.4.99.-
). Q92T29 (EMBL:SME591782) (355)
similarity:fasta;
with=UniProt:MEPA-ECOLI
(EMBL:AE015256); Shigella
flexneri.; mepA;
Penicillin-insensitive murein
endopeptidase precursor (EC
3.4.99.-)
(D-alanyl-D-alanine-endopeptidase)
(DD-endopeptidase).; length=274;
id 38.372; 258 aa overlap; query
52-307; subject 29-270
similarity:fasta;
with=UniProt:Q92T29
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE MUREIN
ENDOPEPTIDASE TRANSMEMBRANE
PROTEIN (EC 3.4.99.-).;
length=355; id 61.708; 363 aa
overlap; query 1-358; subject
1-355"
/codon-start=1
/transl-table=11
/product="putative murein
endopeptidase
(d-alanyl-d-alanine-endopeptidase)
"
/protein-id="CAK05673.1"
/db-xref="GI:115254599"
/db-xref="GOA:Q1MMX9"
/db-xref="UniProtKB/TREMBL:Q1MMX9"
/translation="MAFGFAQAFRTLGLTLAGA
IGAGLAVGVDVGAEQKTPSPGSAKA
LFGGAGLPTQGPAPQIGFYAKGCMAGAVALEPTDG
PTWQAMRLSRNRRWGNPAMIALLE
RFSQDAVRYAGWPGILVGDIAQPRGGPMLNGHSS
HQIGLDADIWFSMPARRMTAQER
EDLFFTSMLQKDKFLTVPNPKVWTESRARLLMLAA
SYPEVERIFVNPFAIKKKMCDTWGG
DRTNLGLKLRPIYGHDSHFHRIKCPFGAAGCTPQ
APVPAGDGCDSLAYWFTAPWAP
PKPKPGKAKPKPPPREMMVTDLPNACAAVLDAAS
VASMQAATYGGPSAASALAATPAA
ASADDTDGALPDVGPVNDKPAIQ"
/misc-feature complement(218768..219529) /locus-tag="RL0184"
/inference="protein
motif:Pfam:PF03411.3"
/notes="Pfam match to entry
PF03411.3 Peptidase-U6"
/sig-peptide complement(219613..219700) /locus-tag="RL0184"
/inference="protein
motif:SignalP-HMM:2.0"
/notes="Signal peptide predicted
for RL0184 by SignalP 2.0 HMM

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gene	219976..221808	(Signal peptide probability 0.937) with cleavage site probability 0.632 between residues 28 and 29"
CDS	219976..221808	/locus-tag="RL0185" /locus-tag="RL0185" /inference="similar to sequence:INSDC:RSAE104" /note="Similar, but truncated at the C-terminus, to Rhizobium sp. (strain NGR234). Hypothetical protein Y4WM precursor. Y4WM-RHISN (EMBL:RSAE104) (663) similarity:fasta; with=UniProt:Y4WM-RHISN (EMBL:RSAE104); Rhizobium sp. (strain NGR234).; Hypothetical protein Y4WM precursor.; length=663; id 67.833; 600 aa overlap; query 11-609; subject 16-614" /codon-start=1 /transl-table=11 /product="putative solute-binding component of ABC transporter" /protein-id="CAK05674.1" /db-xref="GI:115254600" /db-xref="GOA:Q1MMX8" /db-xref="UniProtKB/TREMBL:Q1MMX8" /translation="MAALWSKIGFLSLAGALAP MTATAQDQDPFLIGSSVISEMKYKP GFAHFQDYVNPDAFGGDLRLSASGAFDTFNPLLA KGQAAVGLTLVYDTLMKPADDELL VSYGLLAEGLSFPTDVSSATFRLRKEAKWSGQGP VTPEDVIFSLDKTKELNPLTANY RHHVAKAEKTGDRDVTFTFDEKNNRELPNILGQLV VVPKHWEGQGPDGKPRDISKTL EPVMGSGPYKIASFSPGATIRYELRDDYWGKDLN VNVGQNNFRNVIYTYFGDRDVEFE AFRAGNSDYQETTAARWATGYDFPAVKEGRVKK EEVANPLRATGIMQALVPNMRRDL FKDIRVREALNYGLDFEELNRTVAFNSYKRIDS YFWNTEASSGLPQGRELEILQGMK DKVPAEIFTTPYTNPVAGDPQKSRDNLKKAIAL KEAGWEIKGNRMVNSKTGQPMSE ILLSSPMLERWAVPYASNLRKIGIDARVRTVDAS QAVNRERSFDYDMIWNVWAETMNP GNEQADYWGSGSVNQGSRYAGIANPAVDELIR MVIFAPNRDEQIAAIKAMDRVLLA NHVYIPLFYRDTYNIAYWNTVTHPAEFPAYSGLF PDAWWSSTSAK" /locus-tag="RL0185" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0185 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 between residues 25 and 26"
sig-peptide	219976..220048	
misc-feature	220003..221790	/locus-tag="RL0185" /inference="protein motif:Pfam:PF00496.8" /note="Pfam match to entry

gene	221959..223047	PF00496.8 SBP-bac-5"
CDS	221959..223047	/locus-tag="RL0186" /locus-tag="RL0186" /inference="similar to sequence:INSDC:AE007959" /note="similarity:fasta; with=UniProt:Q8UIV3 (EMBL:AE007959); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, membrane spanning protein (AGR-C-318p).; length=364; id 87.637; 364 aa overlap; query 1-362; subject 1-364" /codon-start=1 /transl-table=11 /product="putative transmembrane component of ABC transporter" /protein-id="CAK05675.1" /db-xref="GI:115254601" /db-xref="GOA:Q1MMX7" /db-xref="UniProtKB/TrEMBL:Q1MMX7" /translation="MGAYILRLLLMIPTIVGIM AISFVVIQFAPGGPVEQVIAQLTG QADSADORLSGGDDLGGGSDEGSKYRGAQGLD PELIAKLEKQFGFDKPFPLTRFGEM MWNVIRFDFGESFFRNTSVLELIKELPVSISLG IWILIFSAYAISIPLGIRKAVKDGS TFDVTWTSGVIVVGAVSPFLFGILLIVLFAGGSF YDWFPLRGLVSDNFDQLAWWQKPL DYFVHLTLPLISLSLAFATTTLLTKNSFIEEIK KQYVVTARAKGLNERQVLYGHIFR NAMLIIIAGFPGAFISAFFTGSLLIENIFSLDGL GRLGYLSVINRDYPIVFATLIYFS LLGLVSVSLVSDLIYTWIDPRIDFERRDV" /locus-tag="RL0186"
misc-feature	order (221983..222051, 222343..222411, 222460..222528, 222619..222687, 222793..222861, 222931..222999)	
misc-feature	222343..223029	/inference="protein motif:TMHMM:2.0" /note="6 probable transmembrane helices predicted at aa 9-31, 129-151, 168-190, 221-243,279-301 and 325-347" /locus-tag="RL0186" /inference="protein motif:Pfam:PF00528.10" /note="Pfam match to entry PF00528.10 BFD-transp-1" /locus-tag="RL0187" /locus-tag="RL0187" /inference="similar to sequence:INSDC:HS381248" /note="similarity:fasta; with=UniProt:Q8UIV2 (EMBL:HS381248); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, membrane spanning protein.; length=395; id
gene	223047..224195	
CDS	223047..224195	

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84.656; 378 aa overlap; query
5-382; subject 18-395"
/codon-start=1
/transl-table=11
/product="putative transmembrane
component of ABC transporter"
/protein-id="CAK05676.1"
/db-xref="GI:115254602"
/db-xref="GOA:Q1MMX6"
/db-xref="UniProtKB/TrEMBL:Q1MMX6"
/translation="MDAAANPVITTFVKPPRKGL
LSPTNIRRWNNFKANGRGYWSLWL
FLVLFLVLSLFAEFLANDRPIIASYKGEVLFPVLI
DYPEEKFGGFLAETDYRSSVIAD
INANGWMIWPPIRYSYRSVNSNIPHSAPTAPFWL
MTNEERCAGYPQGVNDPDCTLGNL
NWLGTDDQARDVLARVIYGRISVLFGLVLTICS
AVIGVTAGAVQYFGGWTDLLQR
FIEIWSSMPVLYILLIAALLPPGFFVLLGIMLL
FSWGVGVGIVRAEFLRARNFEYVR
AARALGVNNRTIMWRHLLPNAMVATLTFLPFILS
GSTITLTSLDFLGFGMPPGSPSLG
EMIAQCKTNLQAPWLGLTAFFAMSLSLIFIG
EAVRDAFDPKRTFQ"
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223590..223658,
223728..223832,
223923..223991,
224082..224150)

/inference="protein
motif:TMHMM:2.0"
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helices predicted at aa 38-60,
182-204, 228-262, 293-315 and
346-368"

misc-feature      223584..224189
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/note="similarity:fasta;
with=UniProt:Q8UIV1 (EMBL:A97382);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; ABC transporter,
nucleotide binding/ATPase protein
(AGR-C-320p).; length=549; id
83.364; 541 aa overlap; query
5-545; subject 9-549"
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/product="putative ATP-binding
component of ABC transporter"
/protein-id="CAK05677.1"
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misc-feature	225134..225706	
gene	225838..226797	
CDS	225838..226797	
misc-feature	226141..226683	

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CDS	226886..227233	motif:Pfam:PF02826.5"
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		with=UniProt:Q92KE7
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		meliloti).; HYPOTHETICAL
		TRANSMEMBRANE PROTEIN.;
		length=117; id 33.333; 105 aa
		overlap; query 2-105; subject
		1-99"
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		/transl-table=11
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		/db-xref="UniProtKB/TrEMBL:Q1MMX3"
		/translation="MMAHQIDTRWEKSNGKLHKE
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		QPAPAPAPALQNGTAVPTETPNIT
		PAAPNVAPATPAQ"
misc-feature	226994..227062	/locus-tag="RL0190"
		/inference="protein
		motif:TMHMM:2.0"
		/note="1 probable transmembrane
		helix predicted at aa 37-59"
gene	227421..228725	/locus-tag="RL0191"
CDS	227421..228725	/locus-tag="RL0191"
		/EC-number="2.4.2.11"
		/inference="similar to
		sequence:INSDC:AE007962"
		/inference="similar to
		sequence:INSDC:ECD731"
		/note="similarity:fasta;
		with=UniProt:PNCB-ECOLI
		(EMBL:ECD731); Escherichia coli.;
		pncB; Nicotinate
		phosphoribosyltransferase (EC
		2.4.2.11) (NAPRTase).; length=399;
		id 35.135; 407 aa overlap; query
		19-420; subject 6-387
		similarity:fasta;
		with=UniProt:PNCB-AGRT5
		(EMBL:AE007962); Agrobacterium
		tumefaciens (strain C58/ATCC
		33970).; pncB; Nicotinate
		phosphoribosyltransferase (EC
		2.4.2.11) (NAPRTase).; length=434;
		id 85.253; 434 aa overlap; query
		1-434; subject 1-434; putative
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		phosphoribosyltransferase"
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(naprtase)"
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/db-xref="UniProtKB/TrEMBL:Q1MMX2"
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TTMWEIPALAIVNELRSRSAMKAL
GPFTLDVLYARAKAMWSKVERLKELPGLRISDF
GTRRRHSFLWQRCVEALKEGIGP
AFAGTSNVLLAMDSDEAVGTNAHELPMVAAAALA
ETDEQLRNAPYKILRDWNKLYGGN
LLIIVLPDAFGTAAFLRDAPEWVADWTGFRPDSAP
PIEGGEKIIDWKKMGRDPRQKLL
IFS DGLDQVDIAI IDTYRHFEGRVRMSFGWGTNLTN
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RIDQTVLV"
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motif:Pfam:PF04095.4"
/note="Pfam match to entry
PF04095.4 NAPRTase"
gene complement(229362..2297
60)
CDS complement(229362..2297 /locus-tag="RL0192"
60)
/inference="similar to
sequence:INSDC:AE012107"
/note="C-terminus from codon 60 is
similar to Xanthomonas campestris
(pv. campestris). Hypothetical
protein XCC0125. Q8PE56
(EMBL:AE012107) (85)
similarity:fasta;
with=UniProt:Q8PE56
(EMBL:AE012107); Xanthomonas
campestris (pv. campestris).;
Hypothetical protein XCC0125.;
length=85; id 32.836; 67 aa
overlap; query 62-128; subject
18-84"
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/translation="MCWIRARPNNEMARLPAYPR
GRRSDGAARFRRSKIPDFLPCSF
ASLHVWVYRLPKSKTEVKQVEELSVKSKIITVY
FSQEDGRLRICFKNGEERLFEQVP
SSEAHAMTVAPSPGHYYLDRIRTRFRLLAA"
gene complement(229806..2303
75) /locus-tag="RL0193"

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misc-feature	complement(229839..230348)	/locus-tag="RL0193"  /inference="protein motif:Pfam:PF06821.1" /note="Pfam match to entry PF06821.1 DUF1234"
gene	230468..230944	/locus-tag="RL0194"
CDS	230468..230944	/locus-tag="RL0194" /inference="similar to sequence:INSDC:AP002998" /note="similarity:fasta; with=UniProt:Q98JQ8 (EMBL:AP002998); Rhizobium loti (Mesorhizobium loti).; Probable transcriptional regulator.; length=160; id 77.483; 151 aa overlap; query 6-156; subject 5-155" /codon-start=1 /transl-table=11 /product="putative AsnC transcriptional regulator" /protein-id="CAK05683.1" /db-xref="GI:115254609" /db-xref="GOA:Q1MMW9" /db-xref="UniProtKB/TrEMBL:Q1MMW9" /translation="MAFQENNRVQLDPTDIAIIE AMQENGRIAVSELGRRRVGLSQPAA SERVKRLERDGIIVGYAARIDPTALGIGMTAVLR LRTTHEHIKPCCLKQFAEMPQVMEV LRLTGEDCFLLKVLVPAPGELETIVDTIARFGAV TTSVLRSSENPKPIGRALLQRP"
misc-feature	230570..230869	/locus-tag="RL0194" /inference="protein motif:Pfam:PF01037.8" /note="Pfam match to entry PF01037.8 AsnC-trans-reg"

gene	complement(231045..231134)	/gene="tRNA-Ser"
tRNA	complement(231045..231134)	/gene="tRNA-Ser"
		/product="tRNA-Ser"
		/note="anticodon GGA"
gene	231363..231680	/locus-tag="RL0195"
CDS	231363..231680	/locus-tag="RL0195"
		/inference="similar to sequence:INSDC:SME591782"
		/note="similarity:fasta; with=UniProt:Q92SY6 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; CONSERVED HYPOTHETICAL SIGNAL PEPTIDE PROTEIN.;
		length=105; id 52.381; 105 aa overlap; query 1-105; subject 1-105"
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		/transl-table=11
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		/db-xref="GI:115254610"
		/db-xref="GOA:Q1MMW8"
		/db-xref="UniProtKB/TrEMBL:Q1MMW8"
		/translation="MRFLRLASLVALAAAVIAG TIDSIQSVAAASVVMPTISDAWQD VSPPTLTSLQSSLSYYIHPRFYALIFQWLMLQPA FAVFLVIALLLWMIGYKKPSVAGR FTA"
misc-feature	order(231381..231449, 231576..231644)	/locus-tag="RL0195"
		/inference="protein motif:TMHMM:2.0"
		/note="2 probable transmembrane helices predicted at aa 7-29 and 72-94"
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CDS	231998..232990	/locus-tag="RL0196"
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		/note="similarity:fasta; with=UniProt:Q8UJ15 (EMBL:B97374); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Membrane lipoprotein (AGR-C-200p).;
		length=337; id 86.970; 330 aa overlap; query 1-330; subject 8-337"
		/codon-start=1
		/transl-table=11
		/product="putative outer membrane basic protein"
		/protein-id="CAK05685.1"
		/db-xref="GI:115254611"
		/db-xref="GOA:Q1MMW7"
		/db-xref="UniProtKB/TrEMBL:Q1MMW7"
		/translation="MKKSLLTLFAVAAMSTTALA ADVKPALVYGTGGKFDSFNEAAY NGAKKFKAETGIAYRDFEPTGDTQGEQAIRNFAS RGFNPVAVSVFATWSAIEKVAAEF"

sig-peptide 231998..232055

misc-feature 232001..232966

gene 233067..234590  
CDS 233067..234590

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AGMASKITGVGFVGGMDIPLIRKF  
ECGYEQGARSVKADIEVFQNMGTGTGAAWNDPVR  
GGELTKNQIDQGADVYAAAGATG  
LGVLTAAADNKKLSIGVDSNQNLHFGSVLTSMV  
KRVDLAVYNAYNDTKDKFTAGVQ  
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motif:SignalP-HMM:2.0"  
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for RL0196 by SignalP 2.0 HMM  
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with cleavage site probability  
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33970). ABC transporter,  
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Q8UJ14 (EMBL:C97374) (501)  
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with=UniProt:Q8UJ14 (EMBL:C97374);  
Agrobacterium tumefaciens (strain  
C58/ATCC 33970).; ABC transporter,  
nucleotide binding/ATPase  
protein.; length=501; id 87.976;  
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subject 3-501"  
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misc-feature	233931..234515	
gene	234598..235701	
CDS	234598..235701	
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misc-feature	234766..235638	335-353" /locus-tag="RL0198" /inference="protein motif:Pfam:PF02653.5" /note="Pfam match to entry PF02653.5 BPD-transp-2" /locus-tag="RL0199" /locus-tag="RL0199" /inference="similar to sequence:INSDC:AE007954" /note="similarity:fasta; with=UniProt:Q8UJ12 (EMBL:AE007954); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ABC transporter, membrane spanning protein (AGR-C-207p).; length=323; id 80.805; 323 aa overlap; query 1-323; subject 1-323" /codon-start=1 /transl-table=11 /product="putative transmembrane permease component of ABC transporter" /protein-id="CAK05688.1" /db-xref="GI:115254614" /db-xref="GOA:Q1MMW4" /db-xref="UniProtKB/TREMBL:Q1MMW4" /translation="MDYYDIFISVLASTIRLSIP LIFTALAGLFSERAGIFDIGLEK MLGSAAFAAACVAYLTDSAWLGLGAGILCSVALSL VHGFASITNRGNQIVSGVAINFFI AGITIVLQAWFGQGGRTPLADSRFAPILPG ADVARDIPIIGPLIYANVISGNIL TYLAFLAVPFSWVLYRTREGLRLRAVGENPGAV DIAGISVAVLRYRAVMCAGILCGF AGTYLAIAQSAAFIKDMSAGKGYIALAALVFAKW KPVVPMFACLLFGFLDALANFMQG KQVPLIGEVPVQVFQALPYVLTCLLAGFIGVAT PPKAGGVPTYKER" /locus-tag="RL0199"
gene	235712..236683	
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misc-feature	order(235730..235798, 235898..235966, 235985..236053, 236186..236239, 236333..236401, 236444..236512, 236570..236638)	/inference="protein motif:TMHMM:2.0" /note="7 probable transmembrane helices predicted at aa 7-29, 63-85, 92-114, 159-176,208-230, 245-267 and 287-309" /locus-tag="RL0199" /inference="protein motif:Pfam:PF02653.5" /note="Pfam match to entry PF02653.5 BPD-transp-2" /gene="cdd" /locus-tag="RL0200" /gene="cdd" /locus-tag="RL0200"
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subtilis.; cdd; Cytidine deaminase
(EC 3.5.4.5) (Cytidine
aminohydrolase) (CDA).; length=EC
3.5.4.5; id 44.000; 125 aa
overlap; query 3-127; subject
4-128 similarity:fasta;
with=UniProt:Q8UJ11
(EMBL:AE008987); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; cdd; Cytidine deaminase.;
length=145; id 84.252; 127 aa
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/db-xref="UniProtKB/TrEMBL:Q1MMW3"
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YLCDEAGVKKTMTMEELLPSFETELG"
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/inference="similar to
sequence:INSDC:AE007954"
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sequence:INSDC:BSJH6421"
/note="similarity:fasta;
with=UniProt:PUNA-BACSU
(EMBL:BSJH6421); Bacillus
subtilis.; punA; Purine nucleoside
phosphorylase I (EC 2.4.2.1) (PNP
I) (PU-NPASE I) (Inosine
phosphorylase).; length=271; id
46.586; 249 aa overlap; query
17-262; subject 20-268
similarity:fasta;
with=UniProt:Q8UJ10
(EMBL:AE007954); Agrobacterium

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tumefaciens (strain C58/ATCC
33970).; deoD; Purine nucleoside
phosphorylase (AGR-C-210p).;
length=266; id 75.769; 260 aa
overlap; query 5-264; subject
6-265; putative purine nucleoside
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i) (inosine phosphorylase)"
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IVLGSGGLGSLVGELDGAVRVPIYRD
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YYEKGDANAMRLPIEVLKALGVEA
LILNSAGSLRDDMPGVSVMQITDHINYSGMNPL
IGESDHRFVGMTNAYDAGLAAAM
ORAAKLEIELAQGVYMWFSGPSFETPAEIRMAR
ILGADAVGMSTVPEVVISRMLGLR
VAAASVITNYGAGMTGNLSHEETKDMAPIGGAR
LAAILKDMIAAGRG"
/misc-feature 237116..237865
/gene="punaA"
/locus-tag="RL0201"
/inference="protein
motif: Pfam:PF00896.9"
/note="Pfam match to entry
PF00896.9 Mtap-PNP"
/gene="deoC"
/gene="deoC"
/gene="deoC"
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/inference="similar to
sequence: INSDC:AE016772"
/inference="similar to
sequence: INSDC:HS374251"
/note="similarity: fasta;
with=UniProt:DEOC-ECOLI
(EMBL:AE016772); Escherichia coli
O6.; deoC; Deoxyribose-phosphate
aldolase (EC 4.1.2.4)
(Phosphodeoxyriboaldolase)
(Deoxyriboaldolase) (DERA).;
length=259; id 56.000; 250 aa
overlap; query 13-255; subject
11-258 similarity: fasta;
with=UniProt:DEOC-AGRT5
(EMBL:HS374251); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; deoC;
Deoxyribose-phosphate aldolase (EC
4.1.2.4)
(Phosphodeoxyriboaldolase)
(Deoxyriboaldolase) (DERA).;
length=259; id 71.705; 258 aa
overlap; query 1-258; subject
3-259"

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deoxyribose-phosphate aldolase"
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NLRDDCTEAQIDALCARAQTPYGT
SAAICIWPFVQAQRNILGTGHAVRIATVVNLP
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LVIPYRKLLAGNEKAVTDMKVAVRAECAGPVLLK
VIETGELKDAALIRHASELAIEA
GADFIKTSTGKVAVNATLEAADIMIRAIRESGRK
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AAASGY"
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/inference="protein
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/note="Pfam match to entry
PF01791.6 DeoC"
gene 238765..240072
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/gene="deoA"
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with=UniProt:TYPH-ECOLI
(EMBL:U00096); Escherichia coli.;
deoA; Thymidine phosphorylase (EC
2.4.2.4) (TdRPase).; length=EC 2.4
( 440; id 52.778; 432 aa overlap;
query 2-431; subject 3-434
similarity:fasta;
with=UniProt:Q8UJ08
(EMBL:AE007954); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; deoA; Thymidine
phosphorylase (AGR-C-214p).;
length=438; id 69.142; 431 aa
overlap; query 1-431; subject
3-433"
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phosphorylase"
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/db-xref="GOA:Q1MMW0"
/db-xref="UniProtKB/TrEMBL:Q1MMW0"
/translation="MIPQEIIRKRDGDELDAE
ISSFIAALAAGQLSEGGIGAFAMA
VWFKMSRSTETVALTLAMADSGDRLQWADVDRPI
ADKHSITGGVGDNVSLMLAPIAAAC
GLAVPMISGRGLGHTGGTLDKLESIPGYMITPDA

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		DLFHKKVKEAGCAIIGQTGTLAPA DGRLYAVRDVTATVDSIPLITASILSKKLAAGLE TLVLDVKVGNAGAFMVRGQQAETLA QSLVEVANGAGVKTSALITDMNQPLADSAGNAVE MRNCLDFLAGRKADTRLETVVLA AAEMLVKSGIAASSDEAEGMARRALSSGKAAEVF ARMVSMLGGPADLIENPDRYLARA PVAKFPVPAARSGWLAACDARGIGVSVIDLGGRR HPADRIDHRVGFSELLPLGTRVNA GEPIALVHAADDAEAERAVAALAAHYRITEKPE LTPVIAGLI"
misc-feature	238771..238965	/gene="deoA" /locus-tag="RL0203" /inference="protein motif:Pfam:PF02885.5" /note="Pfam match to entry PF02885.5 Glycos-trans-3N"
misc-feature	238987..239754	/gene="deoA" /locus-tag="RL0203" /inference="protein motif:Pfam:PF00591.9" /note="Pfam match to entry PF00591.9 Glycos-transf-3"
gene	complement(240079..240612)	/locus-tag="RL0204"
CDS	complement(240079..240612)	/locus-tag="RL0204"  /inference="similar to sequence:INSDC:B97375" /note="similarity:fasta; with=UniProt:Q8UJ07 (EMBL:B97375); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0134.; length=180; id 50.000; 176 aa overlap; query 1-175; subject 8-178" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05693.1" /db-xref="GI:115254619" /db-xref="UniProtKB/TrEMBL:Q1MMV9" /translation="MLVRTVLFASIAAVLATQVP SFFGGTSQQPAETLSANYVSAQTE QPVAEPFVYGSNAIRLQADAQGHYTGSPFKINGKP VQGLIDTGATYVALNETLARRLGF TANQLDFRYGVNTANGQTKAAHVTLDRVEIGGIR VREVEAFVLKDDALTTTLVGMFSFL QKLASYSVADGSLSLKQ"
sig-peptide	complement(240537..240612)	/locus-tag="RL0204"  /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0204 by SignalP 2.0 HMM (Signal peptide probability 0.991) with cleavage site probability 0.362 between residues 24 and 25"
gene	complement(240774..241403)	/gene="upp"  /locus-tag="RL0205"

CDS complement(240774..2414 /gene="upp"  
03)

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/EC-number="2.4.2.9"  
/inference="similar to  
sequence:INSDC:AE005479"  
/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:UPP-ECOLI  
(EMBL:AE005479); Shigella  
flexneri.; upp; Uracil  
phosphoribosyltransferase (EC  
2.4.2.9) (UMP pyrophosphorylase)  
(UPRTase).; length=208; id 52.427;  
206 aa overlap; query 4-209;  
subject 3-208 similarity:fasta;  
with=UniProt:UPP-RHIME  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; upp; Uracil  
phosphoribosyltransferase (EC  
2.4.2.9) (UMP pyrophosphorylase)  
(UPRTase).; length=209; id 86.124;  
209 aa overlap; query 1-209;  
subject 1-209"  
/codon-start=1  
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/product="putative uracil  
phosphoribosyltransferase (UMP  
pyrophosphorylase)"  
/protein-id="CAK05694.1"  
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/db-xref="UniProtKB/TrEMBL:Q1MMV8"  
/translation="MDGVTVIDHPLVQHKLIIMR  
RKETSTGSFRLLREISTLLCYEV  
TRDLELTMETIETPLQTMESPILEGKKLVFASIL  
RAGNGLLEGMLDLVPSARVSHIGV  
YRDHETLQPVVEYFKAPEDVAERLIIVVDPMLAT  
GNSSIAAIDKLKERGAHNIRFLCL  
LAAPEGIRNFRAAHPDVPVFTASIDSHLNEKGYI  
MPGLGDAGDRMYGTK"

misc-feature complement(240894..2412 /gene="upp"  
65)

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motif:Pfam:PF00156.11"  
/note="Pfam match to entry  
PF00156.11 Pribosyltran"

gene complement(241550..2425 /locus-tag="RL0206"  
18)

CDS complement(241550..2425 /locus-tag="RL0206"  
18)

/EC-number="3.5.4.4"  
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/inference="similar to  
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/note="similarity:fasta;  
with=UniProt:ADD-ECOLI  
(EMBL:A64919); Escherichia coli.;

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3.5.4.4) (Adenosine
aminohydrolase).; length=EC
3.5.4.4; id 28.916; 332 aa
overlap; query 1-322; subject
2-330 similarity:fasta;
with=UniProt:ADD-AGRT5
(EMBL:AE007955); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; add; Adenosine deaminase
(EC 3.5.4.4) (Adenosine
aminohydrolase).; length=EC
3.5.4.4; id 75.466; 322 aa
overlap; query 1-322; subject
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deaminase"
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WHDFASFLVCYDKVSEVYRTIEDYALLTETYLDE
LAGIDTIYSELIVSPDHGKRIGLG
ADAYISGICEGIRRAREKSGIEARLIVTGERHFG
PESVIGAAEYAAARAANPLITGFNL
AGEERMGRVADYARAFDIARDAGLGLTIHAGEVC
GAFSVADALDAVRPSRIGHGVRAI
EDLDLVTRLADLGTVLEICPGSNIALGVFPDFAS
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TSLKREYELAAGTFCFGDAEIDAMTRTAIEAAFV
DDETRKALLARI"
/misc-feature complement(241556..2425
09) /locus-tag="RL0206"
/inference="protein
motif:Pfam:PF00962.10"
/note="Pfam match to entry
PF00962.10 A-deaminase"
/gene complement(242515..2437
35) /gene="deoB"
/locus-tag="RL0207"
/CDS complement(242515..2437
35) /gene="deoB"
/locus-tag="RL0207"
/EC-number="5.4.2.7"
/inference="similar to
sequence:INSDC:AE007955"
/inference="similar to
sequence:INSDC:HS137240"
/note="similarity:fasta;
with=UniProt:DEOB-ECOLI
(EMBL:HS137240); Shigella
flexneri.; deoB;
Phosphopentomutase (EC 5.4.2.7)
(Phosphodeoxyribomutase).;
length=EC 5.4.2.7; id 55.746; 409
aa overlap; query 1-406; subject
1-407 similarity:fasta;
with=UniProt:DEOB-AGRT5

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(EMBL:AE007955); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; deoB; Phosphopentomutase
(EC 5.4.2.7)
(Phosphodeoxyribomutase).;
length=EC 5.4.2.7; id 78.818; 406
aa overlap; query 1-406; subject
1-406"
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phosphopentomutase
(phosphodeoxyribomutase)"
/protein-id="CAK05696.1"
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/db-xref="GOA:Q1MMV6"
/db-xref="UniProtKB/TrEMBL:Q1MMV6"
/translation="MARAFLFVLDSFGVGGAPDA
AAYGDEGADTLGHIAEFCAAGAAD
RAGLREGPLSLPNMSELGLMQIARSASGRFPAGM
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GHWEIAGTPVPSFDWGYFFIEGDAFFQEFIEALCR
EADVPGLGNCHASGTEIIARLGE
EHIRTGKPICTSSDSVFQVAAHEVHFGDLRLLA
FCGLARGLLDSYNIGRVIAFFIG
QSASTFQRTGNRRRDSVLPPEPTLLDLRIEQGRH
VHAVGKIGDIFAHQGISRVIKANG
NEALMDASLSAIDAEDGDLVFTNFVDFDMIYGH
RRDVPGYAAALEAFDARLPDVHKK
LKPGLDLVLTADHGCPTWRGTDHTRERVPVIAY
GPGIRSRSIGVRRGYADIGESIAR
HLGIPAGPHGRSFL"
/misc-feature complement(242584..2429
13) /gene="deoB"
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/inference="protein
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/note="Pfam match to entry
PF01676.6 Metalloenzyme"
/gene complement(243895..2444
76) /locus-tag="RL0208"
CDS complement(243895..2444
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sequence:INSDC:AE008989"
/note="similarity:fasta;
with=UniProt:Q8UIZ4
(EMBL:AE008989); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu0147.; length=197; id 43.243;
185 aa overlap; query 9-193;
subject 15-197"
/codon-start=1
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protein"
/protein-id="CAK05697.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMV5"
/translation="MALRNPFTRLVLTMRRLARD

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misc-feature	complement(244339..244407)	/locus-tag="RL0208"
		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 24-46"
gene	complement(244476..245111)	/locus-tag="RL0209"
CDS	complement(244476..245111)	/locus-tag="RL0209"
		/inference="similar to sequence:INSDC:AE007956" /note="similarity:fasta; with=UniProt:Q8U5N8 (EMBL:AE007956); Agrobacterium tumefaciens (strain C58/ATCC 33970).; AGR-C-240p.; length=211; id 53.299; 197 aa overlap; query 18-210; subject 15-205" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05698.1" /db-xref="GI:115254624" /db-xref="GOA:Q1MMV4" /db-xref="UniProtKB/TrEMBL:Q1MMV4" /translation="MTVIDQKTDKGRAPFRFL RFRFLARSREGAAAIEFALLAIPY FLVIFAILETFFVAFAAEELVSNVADTMSRRMRGT QITYNLGRITDMNQAFRQAFCD ISILIRCSASEVATPSKLYLDVQTFSTFSAIPTT IPKVSTDKYADINTAAFKFAPGGA GTINMVRAYYRWEIITDLVRPYITTIRPSDGSMP SQYLVATAAFAQNEQYP"
misc-feature	complement(244935..245003)	/locus-tag="RL0209"
		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 37-59"
gene	complement(245227..245637)	/gene="pilQ"
		/locus-tag="RL0210"
CDS	complement(245227..245637)	/gene="pilQ"
		/locus-tag="RL0210" /inference="similar to sequence:INSDC:AE007963" /inference="similar to sequence:INSDC:B97386" /note="putative alternative start site at codon 13 similarity:fasta; with=UniProt:Q8UIR6 (EMBL:B97386); Agrobacterium tumefaciens (strain C58/ATCC 33970).; PilQ.;

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length=124; id 73.387; 124 aa
overlap; query 14-136; subject
1-124 similarity:fasta;
with=UniProt:Q7D1X0
(EMBL:AE007963); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; AGR-C-384p.; length=136;
id 69.630; 135 aa overlap; query
3-136; subject 2-136"
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transmembrane protein"
/protein-id="CAK05699.1"
/db-xref="GI:115254625"
/db-xref="GOA:Q1MMV3"
/db-xref="UniProtKB/TrEMBL:Q1MMV3"
/translation="MSSSGKTIFFAGMIAVFGIS
GVSAAADDDMLRVYMDHARVLKLD
RPVSKVIVGNAAVADATVADAKTIVLTGRSFGTT
NLVLLDADGNAILDERILVSI DEG
NTVRVYRQTRQSVLSCTPNCEQHAQQAATATSSP
"
misc-feature complement(245560..2456
19) /gene="pilQ"
/locus-tag="RL0210"
/inference="protein
motif:TMHMM:2.0"
/note="1 probable transmembrane
helix predicted at aa 33-52"
gene 246017..246202 /gene="pila"
/locus-tag="RL0211"
CDS 246017..246202 /gene="pila"
/locus-tag="RL0211"
/inference="similar to
sequence:INSDC:AP003007"
/inference="similar to
sequence:INSDC:B87614"
/note="similarity:fasta;
with=UniProt:Q9L720 (EMBL:B87614);
Caulobacter crescentus.; pila;
Pilus subunit protein Pila.;
length=Pilus subunit protein Pila;
id 60.000; 55 aa overlap; query
1-55; subject 1-55
similarity:fasta;
with=UniProt:Q98BG0
(EMBL:AP003007); Rhizobium loti
(Mesorhizobium loti).; Fimbriae
associated protein.; length=58; id
65.455; 55 aa overlap; query 1-55;
subject 1-55"
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/transl-table=11
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protein"
/protein-id="CAK05700.1"
/db-xref="GI:115254626"
/db-xref="UniProtKB/TrEMBL:Q1MMV2"
/translation="MTKLFSRFLKDESGATAIEY
GLIAALISVALITGATTLGDRIGT
TFNNLGTGMNTGVTASN"

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misc-feature	246038..246178	/gene="pila" /locus-tag="RL0211" /inference="protein motif:Pfam:PF04964.3" /note="Pfam match to entry PF04964.3 Flp-Fap"
misc-feature	246074..246133	/gene="pila" /locus-tag="RL0211" /inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 20-39"
gene	246327..246839	/gene="cpaA"
CDS	246327..246839	/locus-tag="RL0212" /gene="cpaA" /locus-tag="RL0212" /inference="similar to sequence:INSDC:A87614" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q9L719 (EMBL:A87614); Caulobacter crescentus.; cpaA; Pilus assembly protein CpaA; length=Pilus assembly protein CpaA; id 35.583; 163 aa overlap; query 6-166; subject 8-169 similarity:fasta; with=UniProt:Q92T43 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE PILUS ASSEMBLY TRANSMEMBRANE PROTEIN.; length=174; id 56.805; 169 aa overlap; query 1-169; subject 5-173" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05701.1" /db-xref="GI:115254627" /db-xref="GOA:Q1MMV1" /db-xref="UniProtKB/TrEMBL:Q1MMV1" /translation="MIAAAVFVILPLCLAMAAFS DLFTMTIPNRISVILTASFFVLAP LSGLGLAEIGMHLAGAAIVFSACFALFAFNVGMG GDAKLMSAAALWFGLNESLLFLMT DVAMIGGLITLLILLVRGQSDTILAIGLPVPNSV LLAKKIPYGIAIAIGGFMAFPSPSP LFLAALESIK" /gene="cpaA" /locus-tag="RL0212" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0212 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.861 between residues 20 and 21"
sig-peptide	246327..246384	/gene="cpaA" /locus-tag="RL0212" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0212 by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.861 between residues 20 and 21"
misc-feature	order(246339..246407, 246417..246476,	/gene="cpaA"

	246495..246554, 246612..246680, 246756..246824)	/locus-tag="RL0212" /inference="protein motif:TMHMM:2.0" /note="5 probable transmembrane helices predicted at aa 5-27, 31-50, 57-76, 96-118 and 144-166" /gene="cpaA" /locus-tag="RL0212" /inference="protein motif:Pfam:PF01478.6" /note="Pfam match to entry PF01478.6 Peptidase-A24" /gene="cpaB" /locus-tag="RL0213" /gene="cpaB" /locus-tag="RL0213" /inference="similar to sequence:INSDC:AE007962" /inference="similar to sequence:INSDC:HS613241" /note="similarity:fasta; with=UniProt:Q9L718 (EMBL:HS613241); Caulobacter crescentus.; cpaB; Pilus assembly protein CpaB.; length=297; id 34.333; 300 aa overlap; query 1-264; subject 1-294 similarity:fasta; with=UniProt:Q8UIS0 (EMBL:AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpC; Components of type IV pilus (AGR-C-380p).; length=AGR-C- ( 268; id 66.914; 269 aa overlap; query 1-269; subject 1-268" /codon-start=1 /transl-table=11 /product="putative pilus assembly protein" /protein-id="CAK05702.1" /db-xref="GI:115254628" /db-xref="UniProtKB/TrEMBL:Q1MMV0" /translation="MKPARLIILAVAVVAGLAG LLAMQMAGSGGVVTQVRVVEKEP TVNILVSSANLSVGARLDDQSVMMAWPQGGVVP GLITEADKPDPAVKDLQGAVVRLPI FEQEPFIRPEKIIDSSRLSSLLPAGKRAVATEI SVATGAGGFILPNDRVDVIMVRKG AEADKLITETVLSNVRVLAIDQQIQEKDDGSKSV VGTATLELTPDQTKVLAVAQQMA DRLLSLALRSVADAQEQDTSAADYLLSGDNGSAII QVIKSGAIVTDASAAPKAE" /gene="cpaB" /locus-tag="RL0213" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0213 by SignalP 2.0 HMM
misc-feature	246348..246677	
gene	246950..247765	
CDS	246950..247765	
sig-peptide	246950..247049	



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(Signal peptide probability 1.000)
with cleavage site probability
0.335 between residues 34 and 35"
misc-feature      246968..247036      /gene="cpaB"
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                                          /inference="protein
motif:TMHMM:2.0"
                                          /note="1 probable transmembrane
helix predicted at aa 7-29"
misc-feature      247232..247627      /gene="cpaB"
                                          /locus-tag="RL0213"
                                          /inference="protein
motif:Pfam:PF06981.1"
                                          /note="Pfam match to entry
PF06981.1 CpaB"
gene              247771..249276      /gene="rcpA"
CDS               247771..249276      /locus-tag="RL0214"
                                          /gene="rcpA"
                                          /locus-tag="RL0214"
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sequence:INSDC:AE017154"
                                          /inference="similar to
sequence:INSDC:SME591782"
                                          /note="similarity:fasta;
with=UniProt:Q8KQJ0
(EMBL:AE017154); Haemophilus
ducreyi.; rcpA; RcpA (Rough colony
protein A).; length=Rough colony
protein A; id 26.269; 453 aa
overlap; query 62-499; subject
31-455 similarity:fasta;
with=UniProt:Q92T41
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE PILUS
ASSEMBLY TRANSMEMBRANE PROTEIN.;
length=511; id 60.433; 508 aa
overlap; query 19-501; subject
11-511"
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protein"
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                                          /db-xref="GOA:Q1MMU9"
                                          /db-xref="UniProtKB/TrEMBL:Q1MMU9"
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AIGVSGMVPASFATLFAAGEARAD
SDSLVRISQTGSNAHRRRLKLGKNAVVVDLPEDA
HDILVSDPTMAADAVTRTSRIIYLF
GKKVGGQTNIFVFGAGGQEIIVNLDIEIERDVSGLE
VNLRRFIRDSNINVEIVSDNIVLT
GTVRTPQDATQAADLAQVFLKGGEATTRTETASG
TGGDSSVALFAEGRQSSQVQVNLQ
IEGEDQVTLKVTTIAEVRREVLQGLGFDNLVSNSS
GMTVAQLGSPSADSATATVGGGLA
ALFKSSIGKYDISTYLNALAEQAKVVKTLAEPTLT
AISGOAATFNSGGQQLYSTTSDG
NVTVPFNYGINLAFKPVVLSSGRISLQIKTNVS
EPVAGSGNATYQRRSAETSVELPS
GGSIAGLAGLIRDVNSQTMGTGPGVSKIPLLTGLF

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sig-peptide 247771..247879

RQKGFERQETELVIIATPYLVLPV  
ARNQLNRPPDDNFSPENDGATFFLNRVNVKVGRR  
APVADAQFHGSIGFIYK

/gene="rcpA"  
/locus-tag="RL0214"  
/inference="protein  
motif:SignalP-HMM:2.0"  
/note="Signal peptide predicted  
for RL0214 by SignalP 2.0 HMM  
(Signal peptide probability 0.995)  
with cleavage site probability  
0.396 between residues 37 and 38"

misc-feature 247807..247875

/gene="rcpA"  
/locus-tag="RL0214"  
/inference="protein  
motif:TMHMM:2.0"  
/note="1 probable transmembrane  
helix predicted at aa 13-35"

misc-feature 248164..248301

/gene="rcpA"  
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/inference="protein  
motif:Pfam:PF04972.3"  
/note="Pfam match to entry  
PF04972.3 BON"

misc-feature 248446..249114

/gene="rcpA"  
/locus-tag="RL0214"  
/inference="protein  
motif:Pfam:PF00263.9"  
/note="Pfam match to entry  
PF00263.9 Secretin-C"

gene 249273..250025

CDS 249273..250025

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/locus-tag="RL0215"  
/inference="similar to  
sequence:INSDC:AE005958"  
/inference="similar to  
sequence:INSDC:AE007962"  
/note="similarity:fasta;  
with=UniProt:Q9L716  
(EMBL:AE005958); Caulobacter  
crescentus.; cpaD; Pilus assembly  
protein CpaD.; length=225; id  
36.842; 133 aa overlap; query  
120-249; subject 91-218  
similarity:fasta;  
with=UniProt:Q8UIS2  
(EMBL:AE007962); Agrobacterium  
tumefaciens (strain C58/ATCC  
33970).; ctpE; Components of type  
IV pilus (AGR-C-378p).;  
length=AGR-C- ( 250; id 55.349;  
215 aa overlap; query 28-241;  
subject 34-246"  
/codon-start=1  
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protein"  
/protein-id="CAK05704.1"  
/db-xref="GI:115254630"  
/db-xref="UniProtKB/TrEMBL:Q1MMU8"  
/translation="MSGARAAAMAENRDQAMAHM

gene 250040..251317

CDS 250040..251317

NATTPRLGISKALFATVAMSVAIL  
SGCAGPHDQLTTGGIPDDYRARHPIIVTEAEQTV  
DIPVASTDRRLTIAQRDLIRGFAA  
NYISRASGPVYVLSPOGSPNSAAAYQLRNQVRAE  
LTSRGIASSKIVNTSYAAVGPGBA  
APIRLSFTGTTAVTTCCGQWPKDISNDLTNQNY  
NFGCASQNNLAAQIANPEDLVAFR  
GMTPIDAQRRNNAIQEYRTTTTTIEDAGDSGF"  
/gene="cpaE"  
/locus-tag="RL0216"  
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/locus-tag="RL0216"  
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sequence:INSDC:AF229646"  
/inference="similar to  
sequence:INSDC:SME591782"  
/note="similarity:fasta;  
with=UniProt:Q9L715  
(EMBL:AF229646); Caulobacter  
crescentus.; CpaE.; length=517; id  
46.193; 394 aa overlap; query  
32-425; subject 124-517  
similarity:fasta;  
with=UniProt:Q92T40  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE RESPONSE  
REGULATOR PROTEIN.; length=428; id  
72.406; 424 aa overlap; query  
1-424; subject 1-424"  
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protein"  
/protein-id="CAK05705.1"  
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/db-xref="GOA:Q1MMU7"  
/db-xref="UniProtKB/TrEMBL:Q1MMU7"  
/translation="MSAIEYEIRNPSELRNAEEA  
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ALQHVMECANDRRVAKVSMRITSGGVAAAANMF  
SGAPTNNLIILETKAANAALLGEL  
APLAAVCDPTTKVVIIGYYNDIGLYRELIRNGIS  
EYMVQPVAMPDILTAMASIFVDFD  
AEP LGRSIAFIGSKGGTASTIAHNCAFGISNLF  
STETILADLDLPYGTANIDFDQDP  
AQGIAEAVFAPDRLEDEVFLDRLLTKCSEHLSLLA  
APSLLDRAVDYDFDQAFQFVLDVLQ  
RSAPVTVLDVPHAWSEWTRSVLSSVDEVVIAAVP  
DLANLRNAKNMLDALRKMRPNDRP  
PHILLNQVGMPKRPEISPSDFCEPLEIDPIAII  
FDINLFGNAANSGRMISEVDPKSP  
TAETFSQISHIVTGRVAIKKAKKGGLLGLLKRK"  
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/locus-tag="RL0217"  
/inference="similar to  
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/inference="similar to  
sequence:INSDC:C97385"  
/note="similarity:fasta;

gene 251351..252826

CDS 251351..252826

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with=UniProt:Q9L714
(EMBL:AF229646); Caulobacter
crescentus.; CpaF.; length=501; id
67.928; 502 aa overlap; query
1-486; subject 1-501
similarity:fasta;
with=UniProt:Q8UIS4 (EMBL:C97385);
Agrobacterium tumefaciens (strain
C58/ATCC 33970).; ctpG; Component
of type IV pilus.; length=491; id
84.615; 494 aa overlap; query
1-489; subject 1-491"
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/transl-table=11
/product="putative component of
pilus"
/protein-id="CAK05706.1"
/db-xref="GI:115254632"
/db-xref="GOA:Q1MMU6"
/db-xref="UniProtKB/TrEMBL:Q1MMU6"
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PPAPAAAPAAASSPSILVEPSRESA
RQQVTPPQMOTPORKRPARTDEYYDTKAQVFSAL
IDTIDLSQLSKLDGESAREEIRDI
VNDIITIKNFAMSISEQEELLEDICNDVLGYGPL
EPLLARDDIADIMVNGAGQTFIEV
GGKTIESEIRFRDNAQLLSICQRIVSQVGRRVDE
SSPICDARLPDGSRVNVIAPPLSI
DGPALTIRKFKKDKLTLDQLVRFGAITPEGATVL
QIIGRVRCNVVISGGTSGSGKTLTL
NCLTNYIDRDERVITCEDTAEQLQOPHVVRLET
RPPNIEGEGEITMRDLVKNCLMR
PERIIVGEVVRGPEVFDLLQAMNTGHGDSMGTIHA
NTPRECLSRIESMIAMGGFTLPK
TVREIISSSVDVVIAARLRDGSRRITQITEVIG
MEGDVITITQDLMRYEIEGEDANGR
LVGRHMTSGVGKPHFWDRARYFNEEKRLAALDA
MEAKTKE"
/misc-feature 251714..252586
/gene="cpaF"
/locus-tag="RL0217"
/inference="protein
motif:Pfam:PF00437.9"
/note="Pfam match to entry
PF00437.9 GSP11-E"
/gene 252832..253839
/locus-tag="RL0218"
/CDS 252832..253839
/locus-tag="RL0218"
/inference="similar to
sequence:INSDC:AJ584609"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:Q6MRH4
(EMBL:AJ584609); Bdellovibrio
bacteriovorus.; TadB; TadB protein
(Flp pilus assembling protein).;
length=Flp pilus assembling ( 291;
id 24.806; 258 aa overlap; query
87-335; subject 35-291
similarity:fasta;
with=UniProt:Q92T38
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium

```

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meliloti).; HYPOTHETICAL
TRANSMEMBRANE PROTEIN.;
length=336; id 68.452; 336 aa
overlap; query 1-335; subject
1-336"
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/transl-table=11
/product="putative pilus assembly
protein"
/protein-id="CAK05707.1"
/db-xref="GI:115254633"
/db-xref="GOA:Q1MMU5"
/db-xref="UniProtKB/TrEMBL:Q1MMU5"
/translation="MFGFDPIVLAIIVVLAASAA
AVAYALLFSKIEADKKSASRINRV
KSAESDRVKVKAARDRVQELSRRKRSVQDNLDL
EKQHEKTKKTVSMKSRLVQAGLT
ITAAKFYLISAVFASVLLIALVVGASLMVMIGI
AVVAGLGLPRWVVGFLIKRRQTKF
LNEFPNALDVITRSIKSGLPLNDAILRIATEGTE
PVKSEFLRVIEAQVGLSIPDACA
RMTIHMPLQEVNFFAIVIAIQSQAGGNLSEAIN
LSKVLRRRRKMKAKVSALSMEAKA
SAVIIGALPFIVATLVYMTSPNYMMILFTDPRGH
FIMGVSAIIMSIGIFVMRNNVNF I"
/locus-tag="RL0218"
/inference="protein
motif:SignalP-HMM:2.0"
/note="Signal peptide predicted
for RL0218 by SignalP 2.0 HMM
(Signal peptide probability 0.999)
with cleavage site probability
0.707 between residues 23 and 24"
/locus-tag="RL0218"

sig-peptide      252832..252898

misc-feature      order(252847..252915,
253153..253212,
253222..253290,
253657..253716,
253759..253827)

/inference="protein
motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted at aa 6-28,
108-127, 131-153, 276-295 and
310-332"

misc-feature      253324..253713

/locus-tag="RL0218"
/inference="protein
motif:Pfam:PF00482.9"
/note="Pfam match to entry
PF00482.9 GSPII-F"

gene              253855..254841

/locus-tag="RL0219"
/inference="similar to
sequence:INSDC:AE007962"
/inference="similar to
sequence:INSDC:AY083157"
/note="similarity:fasta;
with:UniProt:Q8KQI5
(EMBL:AY083157); Haemophilus
ducreyi.; TadC.; length=281; id
24.038; 312 aa overlap; query

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		16-324; subject 4-276 similarity:fasta; with=UniProt:Q8UIS6 (EMBL:AE007962); Agrobacterium tumefaciens (strain C58/ATCC 33970).; ctpI; Components of type IV pilus (AGR-C-371p).; length=AGR-C- ( 328; id 74.390; 328 aa overlap; query 1-328; subject 1-328" /codon-start=1 /transl-table=11 /product="putative component of pilus protein" /protein-id="CAK05708.1" /db-xref="GI:115254634" /db-xref="GOA:Q1MMU4" /db-xref="UniProtKB/TREMBL:Q1MMU4" /translation="MSQDLAATLTNPSMLIALLV AIAVFATFYTIAVPPFFERGDNLKR MKAVSTEREQIRARERARMNTETGAGKASLRQSN NRSVRQIVERFNLKALVDENTIN KLRAAGFRSENALNTFLVARFLPFLFLAALAFW VFGGLNLAEKGTPIRLFAVIGVGY LGFYAPNIYISNRMGKRQHSIKRAWFDALDMLI CVESGISIEAAMRRVSEELGEQSP ALAEEMVLTTAELSFDPDRVALENLATRTQIEL VRSVTQALIQADRYGTPVAQALRV LAQEGRDERMNEAEKKAALPPKLTVPMLFFLP VLIADVILGPAGIQVADKF" /gene="tadC" /locus-tag="RL0219" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0219 by SignalP 2.0 HMM (Signal peptide probability 0.883) with cleavage site probability 0.738 between residues 32 and 33" /gene="tadC"  /locus-tag="RL0219" /inference="protein motif:TMHMM:2.0" /note="4 probable transmembrane helices predicted at aa 15-37, 118-140, 150-172 and 300-322" /gene="tadC" /locus-tag="RL0219" /inference="protein motif:Pfam:PF00482.9" /note="Pfam match to entry PF00482.9 GSPII-F" /locus-tag="RL0220" /locus-tag="RL0220" /inference="similar to sequence:INSDC:AE005613" /inference="similar to sequence:INSDC:AP005079" /note="similarity:fasta;
sig-peptide	253855..253948	
misc-feature	order(253897..253965, 254206..254274, 254302..254370, 254752..254820)	
misc-feature	254410..254808	
gene	255044..255676	
CDS	255044..255676	

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with=UniProt:RHTC-ECOLI
(EMBL:AE005613); Escherichia coli
O157:H7.; rhtC; Threonine efflux
protein.; length=206; id 35.749;
207 aa overlap; query 6-205;
subject 4-205 similarity:fasta;
with=UniProt:Q87NK6
(EMBL:AP005079); Vibrio
parahaemolyticus.; Putative
threonine efflux protein.;
length=211; id 37.879; 198 aa
overlap; query 7-203; subject
8-205"
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/transl-table=11
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efflux protein"
/protein-id="CAK05709.1"
/db-xref="GI:115254635"
/db-xref="GOA:Q1MMU3"
/db-xref="UniProtKB/TrEMBL:Q1MMU3"
/translation="MSSAGIFISIMAAVAVGAMS
PGPSFVVVSRIAISRRLDGLAAA
LGMGAGGVVFAVALAGLTALLSQFEWLYVLLKV
AGGAYLVYIAVNIWRSAGQPLEVS
DAVNGNRALRLSFMALLTQLSNPKTIIVYASLF
AALLPRTVPLDLIVALPLGVFAVE
AGWYSIVAFALSARHPRRLYLAAKGWIDRAAGAV
MGGLGLRLILSLGSLAR"
/locus-tag="RL0220"
/inference="protein
motif:SignalP-HMM:2.0"
/note="Signal peptide predicted
for RL0220 by SignalP 2.0 HMM
(Signal peptide probability 0.993)
with cleavage site probability
0.697 between residues 26 and 27"

sig-peptide      255044..255119

misc-feature      order(255056..255124,
255161..255229,
255257..255316,
255374..255442,
255485..255553)

misc-feature      255086..255661

gene              complement(255786..2566
19)
CDS               complement(255786..2566
19)

/inference="protein
motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted at aa 5-27,
40-62, 72-91, 111-133 and 148-170"
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/inference="protein
motif:Pfam:PF01810.7"
/note="Pfam match to entry
PF01810.7 LysE"
/locus-tag="RL0221"

/inference="similar to
sequence:INSDC:HS384249"
/note="similarity:fasta;
with=UniProt:Q8UIS7
(EMBL:HS384249); Agrobacterium
tumefaciens (strain C58/ATCC

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gene 256764..258155  
CDS 256764..258155

33970).; Hypothetical protein  
Atu0215 (AGR-C-369p).; length=289;  
id 65.683; 271 aa overlap; query  
4-272; subject 20-289;  
hypothetical protein atu0215  
(agr-c-369p)"  
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protein"  
/protein-id="CAK05710.1"  
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/db-xref="UniProtKB/TrEMBL:Q1MMU2"  
/translation="MPASLITITITNRILQGAAAS  
LLVLALAGCSTTKDRMTTGSVPKL  
TKPVEEMDATELRSATDRLGQAYEKNPRDPVTGV  
NYANLLRMNGRDTQALAVMQQVAI  
ANPGDRNVLAAYGKAQAAAGQQALDTIGRAQT  
PDRPDWKLISAQGAILDQMGRAAD  
ARQRYRDALDIQNPESILSNLGSYVLITGLDRLT  
AETYLRSAAQSPTADSRVRQNLAL  
VVGLOGRFPEAEQIARRELSPOQADANVAYLRGM  
LSQSNWQKLAADKTPQAGDSNT N"  
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/inference="similar to  
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/inference="similar to  
sequence:INSDC:SME591782"  
/note="Codons 120 to the  
C-terminus are similar to codons  
80 to the C-terminus of Salmonella  
typhimurium. PepB PEPB-SALTY  
(EMBL:AE008815) ( Peptidase B (EC  
3.4.11.23) (Aminopeptidase B).),  
and to Rhizobium meliloti  
(Sinorhizobium meliloti). PUTATIVE  
AMINOPEPTIDASE PROTEIN (EC  
3.4.-.-). Q92T36 (EMBL:SME591782)  
(EC ( 463) similarity:fasta;  
with=UniProt:PEPB-SALTY  
(EMBL:AE008815); Salmonella  
typhimurium.; pepB; Peptidase B  
(EC 3.4.11.23) (Aminopeptidase  
B).; length=EC 3.4.11.23; id  
40.625; 320 aa overlap; query  
122-430; subject 78-396  
similarity:fasta;  
with=UniProt:Q92T36  
(EMBL:SME591782); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; PUTATIVE  
AMINOPEPTIDASE PROTEIN (EC  
3.4.-.-).; length=EC ( 463; id  
83.624; 458 aa overlap; query  
1-458; subject 1-458"  
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/protein-id="CAK05711.1"  
/db-xref="GI:115254637"



		/db-xref="GOA:Q1MMU1" /db-xref="UniProtKB/TrEMBL:Q1MMU1" /translation="MAPYQFIERPTPFNTKGGST LPIFAVTPAHJETGTIDPIALDWA RRAGYKAESGSLLLIPTAEGHLGGALYGLGNPS EQPYITGRALARALPAGDWHIETAP LTANRLALGFLGSYRFDRYKSEKSPAATLMIPR DADAADIKRQLAGVFLARDLINTP TNDMGPNQLEAVFRGLAAHYKAEMSVISGDDLLT QNFPLVHTVGRASADAPRLLELRW GKKGHRKVTILVKGVCFTDGLLDIKPAASMLLMK KDMGGAANVMGLALMIMDAKLKVD LRVIVPVVENAISSNAFRPGDIYRSRKGTLTVQID NTDAEGRILADALAYADEEEPEL LIDMATLTGAARVALGPDLPFPFTDDANLAHDLT EASLETDDPIWRRLPLYSGYEKDIR TKFADLTNAPAGGMAGAITAALFLKRFVSKAKSW AHFDIYGWAQSERPHSPGGGEAQA IRALFHHIRESLR" /locus-tag="RL0222" /inference="protein motif:Pfam:PF00883.9" /note="Pfam match to entry PF00883.9 Peptidase-M17" /locus-tag="RL0223" /locus-tag="RL0223" /inference="similar to sequence:INSDC:SME591782" /note="similarity:fasta; with=UniProt:Q92T35 (EMBL:SME591782); Rhizobium meliloti (Sinorhizobium meliloti).; PUTATIVE TRANSCRIPTION REGULATOR PROTEIN. PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.; length=114; id 79.825; 114 aa overlap; query 1-114; subject 1-114" /codon-start=1 /transl-table=11 /product="putative MarR family transcriptional regulator" /protein-id="CAK05712.1" /db-xref="GI:115254638" /db-xref="GOA:Q1MMU0" /db-xref="UniProtKB/TrEMBL:Q1MMU0" /translation="MPIELTASQALGLWHGVALD QVRHDDRDLTLRQMAILLHIYLPV PPHTVRGLAATLEVTKPVITRALDTMGEMGLVDR VRDDADRRNVIIKRTVGGALYLEN LGDLIRDQARRLPI" /locus-tag="RL0223" /inference="protein motif:Pfam:PF01047.8" /note="Pfam match to entry PF01047.8 MarR" /locus-tag="RL0224" /locus-tag="RL0224" /inference="similar to sequence:INSDC:BSEPEPII" /inference="similar to sequence:INSDC:SME591782"
misc-feature	257211..258131	
gene	258334..258684	
CDS	258334..258684	
misc-feature	258418..258606	
gene	258696..259553	
CDS	258696..259553	

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/note="Similar, but extended at
the N-terminus to Bacillus
sphaericus. Dipeptidyl-peptidase
VI (EC 3.4.22.-) (DPP VI)
(Gamma-D-glutamyl-L- diamino acid
endopeptidase II)
(Gamma-D-glutamyl-MESO-diaminopime
late peptidase II) (Endopeptidase
II). DPP6-BACSH (EMBL:BSEPEPII)
(EC 3.4 ( 2/1), and similar to
entire protein of Rhizobium
meliloti (Sinorhizobium meliloti).
Hypothetical protein SMC02827.
Q92KU2 (EMBL:SME591782) (284)
similarity:fasta;
with=UniProt:DPP6-BACSH
(EMBL:BSEPEPII); Bacillus
sphaericus.; Dipeptidyl-peptidase
VI (EC 3.4.22.-) (DPP VI)
(Gamma-D-glutamyl-L- diamino acid
endopeptidase II)
(Gamma-D-glutamyl-MESO-diaminopime
late peptidase II) (Endopeptidase
II).; length=EC 3.4 ( 2/1; id
26.667; 270 aa overlap; query
37-274; subject 4-271
similarity:fasta;
with=UniProt:Q92KU2
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMC02827.; length=284; id 64.539;
282 aa overlap; query 3-283;
subject 4-284"
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dipeptidyl-peptidase"
/protein-id="CAK05713.1"
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/db-xref="UniProtKB/TrEMBL:Q1MMT9"
/translation="MTMLDCRLHAYRSDLAEAGL
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ASDGYVGIVKADALLEGRPAATHI
VTVQRTFLYPEPELRKPHQAILSMGSRIVAGET
EARGNRYVVLEDGTAIFAKHVQFI
GALDGADYVEIVARFLETPYLWGGRSGLGIDCSG
LVQLAMLMTGRAAPRDTDMQAAGL
GQPIDRSELRRGDLVFWKGHVAVFEDPETILHAN
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PTGYRRPIS"
/locus-tag="RL0224"
/inference="protein
motif:Pfam:PF00877.8"
/note="Pfam match to entry
PF00877.8 NLP-C-P60"
misc-feature 259224..259499 /locus-tag="RL0225"
gene complement(259554..2609 /locus-tag="RL0225"
45)
CDS complement(259554..2609 /locus-tag="RL0225"
45)
/inference="similar to

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/inference="similar to
sequence:INSDC:RSAMDANTH"
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(EMBL:RSAMDANTH); Rhodococcus sp.;
amdA; Enantiomerase-selective
amidase.; length=462; id 28.755;
466 aa overlap; query 5-459;
subject 5-458 similarity:fasta;
with=UniProt:Q8U/K8
(EMBL:AE008241); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; gatA; Glutamyl-tRNA
amidotransferase subunit A
(AGR-L-854p).; length=465; id
73.160; 462 aa overlap; query
1-461; subject 1-462"
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LYDPESARAQAKASTERWAKAETLGFLDGIPVTL
KELIATKGQPVPSGTRAVELKPAD
ADAPAAARLREDGAVIFAKTTCPDYGMLSGLSS
FHPLSRNPWDITQNPFGSSAGASA
AAAAGYGPLHIGTDIGGSVRLPAGWTGIFGFKPS
HGRIPADPYVVGRCVGPMPARTVED
AAF5MATLSRPDWRDGTSLPNDFNWMDLDIDL
GMKIGLMLDAGCGLAVDDEIRTAV
ETAAKQFEAAGATILSVQPVLTFRMLDGLDNFWR
SRLWGDIDLDEERRDSILPYIRD
WAMGGADISGVDVAVRGFNQTIEMRKSCGRLFTEV
DALLSPTNPPIISYPAEWASPTNDP
ALPFEHIGFTVPWNMSEQPAASINCGFSRSGMPI
GLQIVGPRFDDMRVLRLSKAFEDW
MGGVRSWPPPIG"
misc-feature complement(259623..2608 /locus-tag="RL0225"
76)
/inference="protein
motif:Pfam:PF01425.8"
/note="Pfam match to entry
PF01425.8 Amidase"
gene complement(260982..2618 /locus-tag="RL0226"
45)
CDS complement(260982..2618 /locus-tag="RL0226"
45)
/inference="similar to
sequence:INSDC:AE008241"
/note="similarity:fasta;
with=UniProt:Q8U/K9
(EMBL:AE008241); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; ABC transporter, membrane
spanning protein (AGR-L-856p).;
length=273; id 68.773; 269 aa
overlap; query 18-286; subject

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5-273"
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transporter"
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SIAGISAAAIRGPFEALLMRICDVIFALPPILSA
MVLGAFGLGPGRFATAITAVFMIP
VFARVTLATSLQAWSRDYVTAARAIGNRTLITSL
RHLVPLNIIISQIIVHGAIQLGLAIL
TEAGLSFGLGLGMAPPAPTWGRMLADAQTYLALAP
WLAILPGLAIALTVFGFNMLGDGL
RDLLDPREASR"
misc-feature      complement(260988..2616
08)               /locus-tag="RL0226"
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motif:Pfam:PF00528.10"
                  /note="Pfam match to entry
PF00528.10 BPD-transp-1"
misc-feature      complement(join(261039.
.261107,261165..261233,
261342..261410,
261423..261491,
261510..261578,
261714..261782)) /locus-tag="RL0226"
                  /inference="protein
motif:TMHMM:2.0"
                  /note="6 probable transmembrane
helices predicted at aa 22-44,
90-112, 119-141, 146-168,205-227
and 247-269"
gene              complement(261849..2627 /locus-tag="RL0227"
96)
CDS               complement(261849..2627 /locus-tag="RL0227"
96)
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sequence:INSDC:AE008241"
                  /note="similarity:fasta;
with=UniProt:Q8U7L0
(EMBL:AE008241); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; ABC transporter, membrane
spanning protein (AGR-L-857p).;
length=316; id 71.111; 315 aa
overlap; query 1-315; subject
1-315"
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                  /transl-table=11
                  /product="putative transmembrane
component of ABC transporter"
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                  /db-xref="GI:115254642"
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/translation="MIPLLARRFVGLIVTLVVVS
LLIFAVMDLLPDPASIMLGTSAT
PETLAALRHSLGLDQPLLLRYGQWLAVLSGDLG
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LMAIVLSVAIALPLGVLAASRRGGIFDVIATLFS
QISIAVPFQWVALLIILFSTMLG
LMPAGGFPGWSAGLTPALQALVMPAVALAMPQAG
VLTRVARSAVLDTMHEDFARTAVA
KGLSRSAVLWRHIVFNALIFILTMIGLQFTFLVA
GAVLVENVFNLPGLGRLLALQALSQ
RDIIVMQDVVLFAGGLVIVMNFIVDLSYMAIDPR
MRKAA"

misc-feature      complement(261858..2625
14)               /locus-tag="RL0227"

/inference="protein
motif: Pfam:PF00528.10"
/notes="Pfam match to entry
PF00528.10 BPD-transp-1"

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.261944,262026..262094,
262200..262268,
262311..262379,
262440..262508,
262704..262772))

/inference="protein
motif: TMHMM:2.0"
/notes="6 probable transmembrane
helices predicted at aa 9-31,
97-119, 140-162, 177-199,235-257
and 285-307"

gene              complement(262908..2644
37)               /locus-tag="RL0228"

CDS               complement(262908..2644
37)               /locus-tag="RL0228"

/inference="similar to
sequence: INSDC:HS184254"
/notes="Similar, but truncated at
the N-terminus, to Agrobacterium
tumefaciens (strain C58/ATCC
33970). ABC transporter, substrate
binding protein (AGR-L-861p).
Q8U7L1 (EMBL:HS184254) (540)
similarity: fasta;
with=UniProt:Q8U7L1
(EMBL:HS184254); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; ABC transporter,
substrate binding protein
(AGR-L-861p).; length=540; id
74.168; 511 aa overlap; query
1-509; subject 30-540"
/codon-start=1
/transl-table=11
/product="putative solute-binding
component of ABC transporter"
/protein-id="CAK05717.1"
/db-xref="GI:115254643"
/db-xref="GOA:Q1MMT5"
/db-xref="UniProtKB/TrEMBL:Q1MMT5"
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 PFKFASWAKGDKVELARNADYWNK  
 DAAAKLDKVTFRFIADPQAAALKSGDLDAFPE  
 FAAPELMSSFDGDARLVTRIGNTE  
 LKVAVGMNTAKKPFDDKRVQALMMAIDRKTVID  
 GAWSSGLGTFIGSHYTPNDPGYQDM  
 TGVLPYDVEKAKALLAEAGYPNGFTFTIKSPQMA  
 YAPRSAQVVMQAMFAEIGVTMNIIEP  
 TEFPAKWVQDIMKDRNFDMTIVAHAEPLDIDIYA  
 RDPYYFNYKNPAPFNALMKKVVQETA  
 DPAAQSAIYGEAQKILAEDVPALYLFVMPKLGWV  
 DKKLKLWENEPISNVLSGVSWD E"

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sig-peptide	complement(264326..264437)	/locus-tag="RL0228"
		/inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0228 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.965 between residues 36 and 37"
gene	complement(264588..265508)	/locus-tag="RL0229"
CDS	complement(264588..265508)	/locus-tag="RL0229"
		/inference="similar to sequence:INSDC:AE009372" /note="Similar to Agrobacterium tumefaciens (strain C58/ATCC 33970). Transcriptional regulator, LysR family. Q8U7L2 (EMBL:AE009372) (332) similarity:fasta; with=UniProt:Q8U7L2 (EMBL:AE009372); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Transcriptional regulator, LysR family.; length=332; id 75.168; 298 aa overlap; query 1-298; subject 33-330" /codon-start=1 /transl-table=11 /product="putative LysR family transcriptional regulator" /protein-id="CAK05718.1" /db-xref="GI:115254644" /db-xref="GOA:Q1MMT4" /db-xref="UniProtKB/TrEMBL:Q1MMT4" /translation="MQIRALMYFDELVRTNSMRQ AAENLNVAPTAISRQIENLEYHFG APLVERSARGVKLTAAGELLAARAGRTLRELDHV QQLIEDLKLQGRVSIYANGATV

		ANLLAPALAEFSLKYPKLRFTVTIITSARQIDAV NSAEADIAVTLFAPPMSTGKTVRLR SEIGYDLIATPQHPPAAAHAEIPLRLADYALALP DQSFGRQAFDALFEKEGLSLDPV FVTSSLEMLKELVLSGAAVTLPLALTVRREIEAG QLLAIPLAGKTGIRTHVDLCVAPD RLSFAATKLLDFIERFMRERTNRRKETKD"
misc-feature	complement(264624..265253)	/locus-tag="RL0229"  /inference="protein motif:Pfam:PF03466.5" /note="Pfam match to entry PF03466.5 LysR-substrate"
misc-feature	complement(265323..265502)	/locus-tag="RL0229"  /inference="protein motif:Pfam:PF00126.10" /note="Pfam match to entry PF00126.10 HTH-1"
gene	complement(265565..266560)	/locus-tag="RL0230"
CDS	complement(265565..266560)	/locus-tag="RL0230"  /inference="similar to sequence:INSDC:AE017302" /inference="similar to sequence:INSDC:HS666251" /note="similarity:fasta; with=UniProt:Q72KS9 (EMBL:AE017302); Thermus thermophilus (strain HB27/ATCC BAA-163/DSM 7039).; Endo-type 6-aminohexanoate oligomer hydrolase.; length=330; id 42.724; 323 aa overlap; query 11-328; subject 12-324 similarity:fasta; with=UniProt:Q8UCD3 (EMBL:HS666251); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu2565.; length=334; id 72.755; 323 aa overlap; query 6-325; subject 6-328; putative peptidase" /codon-start=1 /transl-table=11 /product="endo-type 6-aminohexanoate oligomer hydrolase" /protein-id="CAK05719.1" /db-xref="GI:115254645" /db-xref="GOA:Q1MMT3" /db-xref="UniProtKB/TrEMBL:Q1MMT3" /translation="MPDLLNLITDIEGVSVGHAT DLVLGSGVTIVVFDEPVVASGTVL GGAPGGRDITGLLDPSMTVNAVDAFVLSGGSFGL DAAGGVQAGLRELGRGFAVGPVRI PIVPQAILMDLLNGGDKDWGLHSPYRDMGYTALQ AAAKGTFFALGTTGAGTGATTATVK GGLGSASAVSSAGHRVAAIVAVNALGSATIGDGP HFWAAPFEKDAEFGGLGMPDVADH RMRLKGMNTPATTIGAVVTDQQLTKAEAHRLSLA GHDGFARALLPAHLPLDGDVTFAA

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ATALPVEGAQKAWDRDYASS"
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48)
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motif:Pfam:PF03576.3"
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PF03576.3 Peptidase-S58"
gene complement(266793..2670 /locus-tag="RL0231"
68)
CDS complement(266793..2670 /locus-tag="RL0231"
68)
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sequence:INSDC:HS665250"
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with=UniProt:Q8UCE1
(EMBL:HS665250); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu2557 (AGR-C-4631p).; length=72;
id 71.429; 63 aa overlap; query
23-85; subject 6-68"
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/transl-table=11
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protein"
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/db-xref="UniProtKB/TrEMBL:Q1MMT2"
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DLMTRRHPKPLHA"
gene complement(267509..2704 /locus-tag="RL0232"
30)
CDS complement(267509..2704 /locus-tag="RL0232"
30)
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sequence:INSDC:PCDGD"
/inference="similar to
sequence:INSDC:SME591791"
/notes="C-terminus from codon 545
is similar to Burkholderia cepacia
(Pseudomonas cepacia). dgdA
DGDA-BURCE (EMBL:PCDGD) (
2,2-dialkylglycine decarboxylase
(EC 4.1.1.64) (DGD).), and entire
protein is similar to Rhizobium
meliloti (Sinorhizobium meliloti).
PUTATIVE AMINOTRANSFERASE PROTEIN
(EC 2.6.1.-). Q92MC9
(EMBL:SME591791) (( 975)
similarity:fasta;
with=UniProt:DGDA-BURCE
(EMBL:PCDGD); Burkholderia cepacia
(Pseudomonas cepacia).; dgdA;
2,2-dialkylglycine decarboxylase
(EC 4.1.1.64) (DGD).; length=432;
id 34.339; 431 aa overlap; query
549-970; subject 6-429
similarity:fasta;
with=UniProt:Q92MC9

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(EMBL:SME591791); Rhizobium  
 meliloti (Sinorhizobium  
 meliloti).; PUTATIVE  
 AMINOTRANSFERASE PROTEIN (EC  
 2.6.1.-).; length=( 975; id  
 64.928; 978 aa overlap; query  
 1-973; subject 1-975"  
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 VLTVRGQGYQVRLLEYLEGQGLTELTYLAPASVA  
 ALGALCARLAQALADFNHPLDRS  
 LQWDLRRAGPVAQQLLSAITSAAARDRIAKTMVM  
 AVRRIOQLAPALRLQAVHHVDVTGD  
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 GHPRFAAAIGAQWLRNLNTNSRFHY  
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 LRLAQAHSGARNMLCLLEAYHGS  
 AASDAVSTSIADNPQAPTTTRPDWVHTIVSPNTYR  
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 AAGEGLAGFIAESVYGNAGGIPLEPGYLKELYAQ  
 VRARGGLCIADEVQVGYARLGHYF  
 WGFQQQGVVPDIITVAKMGNGHPLGAVITTREI  
 AQSLEKEGTFSSSTGGSPVSCVAG  
 MTVLDIMAEKQLQENARTVGDHLKARLAALIDRH  
 PIAGAVHGMGLYLGLFVRDRTTTL  
 EPATEETAICDRLLELGVIMQPTGDHQNVLKIK  
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 28)

/locus-tag="RL0233"

CDS complement(270544..2714 /gene="purU"  
 28)

/locus-tag="RL0233"  
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sequence:INSDC:C36871"
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sequence:INSDC:HS655252"
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(EMBL:C36871); Escherichia coli.;
purU; Formyltetrahydrofolate
deformylase (EC 3.5.1.10)
(Formyl-FH(4) hydrolase).;
length=280; id 37.993; 279 aa
overlap; query 5-281; subject
8-280 similarity:fasta;
with=UniProt:Q8UCL9
(EMBL:HS655252); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; purU;
Formyltetrahydrofolate deformylase
(AGR-C-4474p).; length=294; id
83.673; 294 aa overlap; query
1-294; subject 1-294"
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deformylase"
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/db-xref="UniProtKB/TrEMBL:Q1MMT0"
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LYRWKIGALPIDIVGVVSNHFDYQKVVVNHDI
PHHIKVTKENKLQAEQIMDIVEQT
GTELIVLARYMQVLSAMCQKMSGKIIINHHSFL
PSFKGANPYKQAYGRGVKLIGATA
HYVTADLDEGP IIEQDTARITHAQSPDDYVSI
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misc-feature complement(270640..2711
73) /gene="purU"
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motif:Pfam:PF00551.8"
/note="Pfam match to entry
PF00551.8 Formyl-trans-N"
misc-feature complement(271186..2714
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motif:Pfam:PF01842.8"
/note="Pfam match to entry
PF01842.8 ACT"
gene complement(271645..2726
64) /gene="exoZ"
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CDS complement(271645..2726
64) /gene="exoZ"
/locus-tag="RL0234"
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/note="Similar, but extended at
the N-terminus, to Rhizobium
meliloti (Sinorhizobium meliloti).
exoZ EXOZ-RHIME (EMBL:B95975) (
Exopolysaccharide production
protein exoZ.), and to length=335
AAQ87046 ( id 36.812)
similarity:fasta;
with=UniProt:EXOZ-RHIME
(EMBL:B95975); Rhizobium meliloti
(Sinorhizobium meliloti).; exoZ;
Exopolysaccharide production
protein exoZ.; length=317; id
36.364; 297 aa overlap; query
37-328; subject 13-301
similarity:fasta;
with=UniProt:AAQ87046; length=335;
id 36.812; 345 aa overlap; query
5-339; subject 7-333; putative
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protein"
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production protein exoZ"
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PLYWLATLFSATVALVAPSLKST
VFDLPHLAASLFFLPWANPADPSTITPVVVPGW
LNYEMFFYFIFALLPLQEARRIP
AMFAVFAVILIAICRLLPETTIVTRFYGEPIMLEFL
AGVVLGWLYGQKVLPLNRRWAAAL
AMGFAFLFINEALMPESRFYAWGIPAIFIVYGA
ISIDFSKLPVIGWLNLYLGDSCYSYI
YITHAFTLAFLRVAADRLPIGILQQPVLFVILSL
VLSSIGGAIHEITSRPRRRKVAVA SRPPA"
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61) /gene="exoZ"
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/note="Pfam match to entry
PF01757.9 Acyl-transf-3"
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.271773,271816..271884,
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272056..272124,
272137..272190,
272209..272277,
272368..272436,
272494..272562,
272590..272646)) /gene="exoZ"
/locus-tag="RL0234"
/inference="protein
motif:TMHMM:2.0"

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/feature="10 probable transmembrane
helices predicted at aa 7-25,
35-57, 77-99, 130-152,159-176,
181-203, 208-227, 237-254, 261-283
and 298-320"

gene      complement(272824..2740 /locus-tag="RL0235"
14)
CDS       complement(272824..2740 /locus-tag="RL0235"
14)

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(EMBL:XC22511); Xanthomonas
campestris.; gumE; GumE.;
length=432; id 28.571; 399 aa
overlap; query 1-384; subject
17-402 similarity:fasta;
with=UniProt:Q8PJF0
(EMBL:AE011898); Xanthomonas
axonopodis (pv. citri).; gumE;
GumE protein.; length=433; id
27.990; 393 aa overlap; query
6-384; subject 23-402"
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exopolysaccharide biosynthesis
protein"
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DYFANTRGRLPLSYNTTGLFQNAL
GFPERFSFGIIDHRSSSIFLEQVSLANFCGVIAV
YLISMWEKLSRNDRLLMIGTAVLI
LVTNDTRTMLIFCFACIVGYVFVFPKIPKFNAL
MPLIVAAGFLVYVLKPNATGDNFT
GRINLTMMKIMELDPLAVLGLSVDRVAEFADSGY
VYLIYAATIFGVIALWLFLVCLFPA
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GLLWVVGVMRFHDSPIRQDRPA DVLS"

misc-feature complement(join(272893.
.272961,273019..273087,
273217..273273,
273292..273387,
273415..273483,
273616..273684,
273775..273843,
273877..273936,
273946..274014))

/inference="protein
motif:TMHMM:2.0"
/feature="9 probable transmembrane
helices predicted at aa 35-57,

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61-80, 92-114, 145-167, 212-234,  
244-275, 282-300, 344-366 and  
386-408"

gene complement(274119..2752 /locus-tag="RL0236"  
01)

CDS complement(274119..2752 /locus-tag="RL0236"  
01)

/inference="similar to  
sequence:INSDC:AF233448"  
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with=UniProt:Q9F0G8  
(EMBL:AF233448); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; endS; Endoglucanase  
precursor.; length=364; id 49.008;  
353 aa overlap; query 10-359;  
subject 15-364"  
/codon-start=1  
/transl-table=11  
/product="putative carboxymethyl  
cellulase"  
/protein-id="CAK05725.1"  
/db-xref="GI:115254651"  
/db-xref="GOA:Q1MMS7"  
/db-xref="UniProtKB/TrEMBL:Q1MMS7"  
/translation="MLRFAAIARMPMKTTTRHLTA  
LLLAALIPSPALAAEAPCYRGVN  
LSGGEYGERGGIYGTINYTYPSEDTIGYFAEKGMT  
IIRLPFRWERLQPALGGRLLDEDEL  
KRIKDTIGLIRKHGMVLLDPHNFYGYDKTVQGT  
APATDAAFGDFWARLAVEFANQDG  
VLFGLMNEPHDIKATDWLDAANAARSIRAVGAR  
NLILVPGTAWSGAGSWEKDVIGGA  
NGTVMLGVDPDLDFYAYEVHQYLDADSSGTHPTC  
EGAGAAVAINGVTAWLKQNHKRG  
FLGEFGASADKDCMSGLTEIYATMSDSDVWLWG  
SYWAAAGDWWPANEPFNVPKRGPE  
RPQMRLLAEVAKAGAGTCSAVKPAKG"  
/locus-tag="RL0236"

misc-feature complement(274233..2750  
78)

/inference="protein  
motif:Pfam:PF00150.7"  
/note="Pfam match to entry  
PF00150.7 Cellulase"

sig-peptide complement(275096..2752  
01)

/inference="protein  
motif:SignalP-HMM:2.0"  
/note="Signal peptide predicted  
for RL0236 by SignalP 2.0 HMM  
(Signal peptide probability 1.000)  
with cleavage site probability  
1.000 between residues 34 and 35"  
/locus-tag="RL0237"  
/locus-tag="RL0237"

gene 275304..276911

CDS 275304..276911

/inference="similar to  
sequence:INSDC:AE009744"  
/note="similarity:fasta;  
with=UniProt:Q8YAW9  
(EMBL:AE009744); Brucella  
melitensis.; SUCCINOGLYCAN  
BIOSYNTHESIS TRANSPORT PROTEIN

		EXOP.; length=572; id 30.784; 536 aa overlap; query 5-507; subject 26-560" /codon-start=1 /transl-table=11 /product="putative exopolysaccharide related transporter" /protein-id="CAK05726.1" /db-xref="GI:115254652" /db-xref="GOA:Q1MMS6" /db-xref="UniProtKB/TrEMBL:Q1MMS6" /translation="MNQYDRNRVSRLPDWRSEFEP SQTAPGVRVRSPVIRPDDFVRPS PEPAPPPFVPPASIAETROYEPPAPPPKPPVVD APPNAEPAAAAPLLDLRSSIAAIW SRRLIVFGLALLGALAGGAVAPLIAQKFTAVSSL YFDPFRQIGLADAGAQSSGSPSEMI SALIDSQVQILTSGNVLRRAEAMKLDQDPEFTG GRTDGAALIGTLQKALVITREAST YVVS LAATTNDPEKSARLANQVVSFTTEENSAS NGIYENTSS TLDGRLDDLRQKVLE AEQAVETFRADNDMAATEGNLISDQRLLSLNTLL VTAQEKTIQAKARADAVANLRVED IVAGNQAEGGVTSPLVSLRQQYATQAAAVGSLES QMGTRHPRLQAARSSLQSI SVEIR GELQRLATSARGEYEQA KAAEDSIAKELAVQKAL HASSDDKQVELNELQRKATAARDI YETVLKRSSQTSEEQNLNQS NIRVISPAEPPVKA DGP GKILLVAGIIGGFLAGFVVG AGFAILAGLFGHPVIRSYFFKSSAAAA" /locus-tag="RL0237" /inference="protein motif:Pfam:PF02706.5" /note="Pfam match to entry PF02706.5 Wzz" /locus-tag="RL0237"  /inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted at aa 106-128 and 497-519" /locus-tag="RL0238" /locus-tag="RL0238" /inference="similar to sequence:INSDC:AE008995" /note="similarity:fasta; with=UniProt:Q8UIT0 (EMBL:AE008995); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0212.; length=128; id 34.722; 72 aa overlap; query 41-108; subject 48-119" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05727.1" /db-xref="GI:115254653" /db-xref="UniProtKB/TrEMBL:Q1MMS5"
misc-feature	275571..276032	
misc-feature	order(275619..275687, 276792..276860)	
gene	277070..277402	
CDS	277070..277402	

		/translation="MRLMLLLISLAAPVGLAPA SAFAVDWTKSVDSGVQPLYPYKGL PGVKAQPDKKEEESYNCRTEVQIRRRYDEIFRS GGMPTLMYVCERDGFVTTGGKVPL RGHYQPVVR" /locus-tag="RL0238" /inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0238 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.996 between residues 24 and 25" /locus-tag="RL0239"
sig-peptide	277070..277139	
gene	complement(277814..278572)	/inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:P72897 (EMBL:SSD901); Synechocystis sp. (strain PCC 6803).; Slr1619 protein.; length=249; id 45.267; 243 aa overlap; query 10-246; subject 7-244" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05728.1" /db-xref="GI:115254654" /db-xref="UniProtKB/TrEMBL:Q1MMS4" /translation="MTTKDDRLFEFAHKREMSLA LKGDSEASFQQSLNTLIGLDKFDYS YLWSWMCVPIIQLPVDILATQEWETKPDVIE TGIARGGSLIFMASILAAMGNDAA KVVGVDDIDIRAHNRESIETHPMSSRIKMIQGGSV DDDVIVAVKAEIPPSARVMVVLDS DHSYEHVLAECRAYGLVTEGCVLVVADTFIGHL TEEQAFTRSKVWLRGNEPLKAVT DYLAETDRFEVDPVLNGKLVLSPPGGYCVCRKA "
CDS	complement(277814..278572)	/locus-tag="RL0239"
misc-feature	complement(277823..278572)	/inference="protein motif:Pfam:PF04989.2" /note="Pfam match to entry PF04989.2 CmcI"
gene	complement(278605..279753)	/locus-tag="RL0240"
CDS	complement(278605..279753)	/inference="similar to sequence:INSDC:AF047478" /inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:O68392 (EMBL:AF047478); Brucella melitensis.; perA; Perosamine synthetase.; length=367; id 35.484; 341 aa overlap; query

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19-359; subject 17-352
similarity:fasta;
with=UniProt:P72893 (EMBL:SSD901);
Synechocystis sp. (strain PCC
6803).; rfbE; Perosamine
synthetase.; length=378; id
73.829; 363 aa overlap; query
3-365; subject 4-366"
/codon-start=1
/transl-table=11
/product="putative perosamine
synthetase"
/protein-id="CAK05729.1"
/db-xref="GI:115254655"
/db-xref="UniProtKB/TrEMBL:Q1MMS3"
/translation="MTNRIFYTKPSITQLETDYA
TDAATGWGAHCYDIYNRFERDFK
TYLGSQFAIATSSCTGAMHMGAAALGVGEGDEVI
LADINWVATVSPIVHLGAKPVFVD
VLPDSWCIDPSEVERHITPKTKAIIATHLYGNLC
DMDALLEIGQRTGIPVIEDAAEAV
GSVWNGRRAGSMGTFTGTSFHGKTKLTITGEGGMF
VTINDALSERVLTLSNHGRARGQT
KQFWPDEIGFKYKMSNIQAAIGCAQLERIEELVA
RKREILAAYMVRSLSALPGISMNFE
YSGTINGAMMPTAVFHPSTGTTREIMQQAFEAAAN
IDARVFFFYPLSSLSMFEDRPENVN
AWSIPGRAINLPSYHDMSEADIDRVAATLLDVAG
GRIYHNRTALRQSV"
misc-feature complement(278662..2797
26) /locus-tag="RL0240"

/inference="protein
motif:Pfam:PF01041.7"
/note="Pfam match to entry
PF01041.7 DegT-DnrJ-EryC1"
gene 280053..280805 /locus-tag="RL0241"
CDS 280053..280805 /locus-tag="RL0241"

/inference="similar to
sequence:INSDC:SSD901"
/note="similarity:fasta;
with=UniProt:P72897 (EMBL:SSD901);
Synechocystis sp. (strain PCC
6803).; Slr1619 protein.;
length=249; id 43.145; 248 aa
overlap; query 7-246; subject
8-246"
/codon-start=1
/transl-table=11
/product="onserved hypothetical
protein"
/protein-id="CAK05730.1"
/db-xref="GI:115254656"
/db-xref="UniProtKB/TrEMBL:Q1MMS2"
/translation="MTTKDDRQFEFANKREMSLA
LGRDIDVFRQTLDTLVLSDKYDYS
YLSWWMGMP IIQMPADVMATQEV I WATKPDVIVE
TGVARGGSIMIFQAAMLQLIGKGKV
VGVDIDIRAHNRQAIESHPMAHRVELIEGPSTSA
EIMAKVKASIEPGASVMVILSDSH
SKAHVLDELARNYAPLVTGDQYLVVADTILGRYEP
SQVPTKRKSKVLLPGDEPLVALNDY
LQETDRFELDTIINGKLVLSPPGGYLRCVRS"

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misc-feature	280101..280799	/locus-tag="RL0241" /inference="protein motif:Pfam:PF04989.2" /note="Pfam match to entry PF04989.2 CmcI"
gene	280888..281466	/gene="wbbJ"
CDS	280888..281466	/locus-tag="pRL0241A" /gene="wbbJ" /locus-tag="pRL0241A" /EC-number="2.3.1.-" /inference="similar to sequence:INSDC:AE004113" /inference="similar to sequence:INSDC:HS968215" /note="similarity:fasta; with=UniProt:WBBJ-ECOLI (EMBL:HS968215); Escherichia coli.; wbbJ; Putative lipopolysaccharide biosynthesis O-acetyl transferase wbbJ (EC 2.3.1.-).; length=196; id 25.455; 165 aa overlap; query 27-185; subject 40-195 similarity:fasta; with=UniProt:Q06962 (EMBL:AE004113); Vibrio cholerae.; rfbO; RfbO protein (Acetyltransferase RfbO, CysE/LacA/LpxA/NodL family).; length=188; id 45.109; 184 aa overlap; query 4-187; subject 3-186" /codon-start=1 /transl-table=11 /product="putative lipopolysaccharide biosynthesis O-acetyl transferase" /protein-id="CAK05731.1" /db-xref="GI:115254657" /db-xref="GOA:Q1MMS1" /db-xref="UniProtKB/TrEMBL:Q1MMS1" /translation="MHLGSTFYDETLRSLPFRH LGANVVIKRTAGLFFVENISIMDD ARIDDFTIIVASREHVEIGCNVHIASQCYISGSD GFVMEDFSGLAPGVKIYTSDDYT GEKMTNPTLPRHLIGGPAGKVVLRRKHVIIGNSNV VLPKVTIIEGSSVGSLSLVNKSILP AWGVYAGIPVRLRDRSQNILILEKELGASRA"
gene	complement(281701..2829 39)	/locus-tag="RL0242"
CDS	complement(281701..2829 39)	/locus-tag="RL0242"  /inference="similar to sequence:INSDC:AE008792" /inference="similar to sequence:INSDC:SSD901" /note="similarity:fasta; with=UniProt:RFBV-SALTY (EMBL:AE008792); Salmonella typhimurium.; rfbV; O antigen biosynthesis abequosyltransferase rfbV (EC 2.4.1.-).; length=333; id 32.386; 176 aa overlap; query

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6-159; subject 3-170
similarity:fasta;
with=UniProt:P72899 (EMBL:SSD901);
Synechocystis sp. (strain PCC
6803).; Slr1063 protein.;
length=689; id 30.180; 222 aa
overlap; query 6-225; subject
9-220"
/codon-start=1
/transl-table=11
/product="putative O antigen
biosynthesis protein"
/protein-id="CAK05732.1"
/db-xref="GI:115254658"
/db-xref="UniProtKB/TrEMBL:Q1MMS0"
/translation="MSGIKLSICIPTYNREAYLR
NALTICENDYTFPFPEIVICDNA
STDGTQQVVVEEFIARGQPIRYKRETNAGAAANV
TSALRLGKGEYLIYLADDDMLIAD
AVADTIRYLDNNQEVTCAHAPWFFFYDEVAKIDIE
KFYNVEEDRKFPFGSGFDVFPYIC
EGHIFPEIAIYRSSALRSAWIPREFCFYPPFFLA
HFLDQGAVSFLQRPFYRSIVNSAI
ARDRPEQGTNDVMTSWDRYRGGLYFLYMGVKRG
AMTLTPETHLKYEMCKVFTLNRM
AVAFRFAERKNFIKAYELYTRIMWGGMLNHPEI
RNFRRRLPLMWAIQTLVSEVNSAI
GIDTLLGGFSEITALEGLMRELGLNEKVMTVK
LSDSPLESTAVFVSVNSDREYFVA
LGYPNLNVFHEHDLRSRHIIM"
misc-feature complement(282400..2829
21) /locus-tag="RL0242"
/inference="protein
motif:Pfam:PF00535.10"
/notes="Pfam match to entry
PF00535.10 Glycos-transf-2"
gene complement(282936..2834
39) /locus-tag="RL0243"
CDS complement(282936..2834
39) /locus-tag="RL0243"
/inference="similar to
sequence:INSDC:AP003591"
/inference="similar to
sequence:INSDC:RME591985"
/notes="similarity:fasta;
with=UniProt:P96449
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; ExpA8 (Putative
dTDP-4-dehydrorhamnose
3,5-epimerase protein) (EC
5.1.3.13).; length=187; id 44.898;
147 aa overlap; query 1-145;
subject 13-159 similarity:fasta;
with=UniProt:Q8YT94
(EMBL:AP003591); Anabaena sp.
(strain PCC 7120).; rfbC;
DTDP-4-dehydrorhamnose
3,5-epimerase.; length=189; id
47.134; 157 aa overlap; query
1-157; subject 14-170"
/codon-start=1

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/transl-table=11
/product="putative
dTDP-4-dehydrorhamnose
3,5-epimerase protein"
/protein-id="CAK05733.1"
/db-xref="GI:115254659"
/db-xref="GOA:Q1MMR9"
/db-xref="UniProtKB/TrEMBL:Q1MMR9"
/translation="MEVDARSDDRGMFARTFDAQ
TFAAQGLVPVYPQCNVSNHKGRT
LRGMHYQAEPRPEIKLVRATRGRVFDVALDLRPD
SPSYLKWASVELDAIRHNAFYIPA
GCAHGFLTLEDDCELYYQMSETYVPELARGVRWD
DPAFSIAWPFTPSIINERDAALDS YGQETSL"

misc-feature complement(282948..2834 /locus-tag="RL0243"
27)

/inference="protein
motif:Pfam:PF00908.7"
/note="Pfam match to entry
PF00908.7 dTDP-sugar-isom"

gene complement(283475..2847 /locus-tag="RL0244"
10)

CDS complement(283475..2847 /locus-tag="RL0244"
10)

/inference="similar to
sequence:INSDC:AF170880"
/inference="similar to
sequence:INSDC:RME591985"
/note="similarity:fasta;
with=UniProt:Q9L9E7
(EMBL:AF170880); Streptomyces
sphaeroides.; NovU.; length=420;
id 37.778; 405 aa overlap; query
6-410; subject 11-414
similarity:fasta;
with=UniProt:Q92U91
(EMBL:RME591985); Rhizobium
meliloti (Sinorhizobium
meliloti).; Putative NDP-hexose
3-C-methyltransferase protein.;
length=410; id 55.231; 411 aa
overlap; query 3-410; subject
2-410"
/codon-start=1
/transl-table=11
/product="putative
methyltransferase"
/protein-id="CAK05734.1"
/db-xref="GI:115254660"
/db-xref="GOA:Q1MMR8"
/db-xref="UniProtKB/TrEMBL:Q1MMR8"
/translation="MTAHNCRFCNAPLKHFRVVDL
GSTPLANAYLTEEQKLPEPSYPL
RAFVCTECWLQADAFVPPEDIFSHYAYFSSYSYD
GWVEHARQFTIMARERFGLDATSQ
VIEVASNDGYLLKHFEAGVPVLGIEPAENVAEV
ARQIGVPTEARFFGKETAADLVSR
GLAADIVIGNNVLAVHPDINDFVGGLSAVLKPDP
VVSVEFPHLLRLMENIQDFTVYHE
HFYYLSLLAVEKVFAAHLKVFDEELPTHGSSL
RVLACRATSMVHAIGHGLAKVRAD
EAAAGFDKVVETYEAFQSRVAPIKDGLLAFLTEAK

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gene	complement (284707..285780)	RSGKKVAAYGAAAGNTLLNFCGV GTDLLEYVVDNRNPHKQGHFLPGSKLPYAPEKMD ETQPDYVLILFPWNINKNEVVAANSR VGAWGGRFAVAVPELTVLG" /locus-tag="RL0245"
CDS	complement (284707..285780)	/EC-number="4.2.1.45" /inference="similar to sequence:INSDC:AE008792" /inference="similar to sequence:INSDC:RME591985" /note="similarity:fasta; with=UniProt:RFBG-SALTY (EMBL:AE008792); Salmonella typhimurium.; rfbG; OrderedLocusNames=STM2091; CDP-glucose 4,6-dehydratase (EC 4.2.1.45). CDP-glucose 4,6-dehydratase (EC 4.2.1.45).; length=359; id 45.714; 350 aa overlap; query 8-352; subject 5-353 similarity:fasta; with=UniProt:Q92U92 (EMBL:RME591985); Rhizobium meliloti (Sinorhizobium meliloti).; Putative CDP-glucose 4,6-dehydratase protein (EC 4.2.1.45).; length=356; id 50.720; 347 aa overlap; query 8-352; subject 8-352" /codon-start=1 /transl-table=11 /product="putative CDP-glucose 4,6-dehydratase" /protein-id="CAK05735.1" /db-xref="GI:115254661" /db-xref="GOA:Q1MMR7" /db-xref="UniProtKB/TrEMBL:Q1MMR7" /translation="MEAMGLTDFWNGRRVFLTGH TGFKGSWLSLWLEKLGAEVTAVSL EPETNPFLYGRLPANWGQGHIIADIREAAFTKQH FIDFEPEIVIHMAAQALVRRSYEN PTETFATNVMGATANVLDAVRETPSVKTAALVVTSD KVYANNNGSGVPFVETDMLGKGDY SNSKACTELVVRYSYRDSFFKGRDIKLATVRAGNV IGGDGWSKDRLIPDFIRAFESSQP ILLRYPEAIRPQHVLEPLGGYLAFAEALTLAG QELPEALNFGPDQPSFATVSELA ALGLAHGVNDVWKPALGKHLPEAPALTLSALAL SAIGWRPRLGLKQTIIDWTAAWYKA NREGADMRAFSLGQIAAYEETIS"
gene	complement (285762..286535)	/gene="ddhA"
CDS	complement (285762..286535)	/locus-tag="RL0246" /gene="ddhA" /EC-number="2.7.7.33" /inference="similar to sequence:INSDC:AE016923"

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/inference="similar to
sequence:INSDC:YE46859"
/note="similarity:fasta;
with=UniProt:Q56860
(EMBL:YE46859); Yersinia
enterocolitica (type 0:8).; DdhA.;
length=261; id 58.984; 256 aa
overlap; query 1-256; subject
5-260 similarity:fasta;
with=UniProt:Q/NR91
(EMBL:AE016923); Chromobacterium
violaceum.; ddhA;
Glucose-1-phosphate
cytidyltransferase (EC
2.7.7.33).; length=256; id 63.672;
256 aa overlap; query 1-256;
subject 1-256"
/codon-start=1
/transl-table=11
/product="putative
glucose-1-phosphate
cytidyltransferase"
/protein-id="CAK05736.1"
/db-xref="GI:115254662"
/db-xref="GOA:Q1MMR6"
/db-xref="UniProtKB/TrEMBL:Q1MMR6"
/translation="MKVVILAGGLGSR LAEETSI
RKPFLVEIGMPILWHIMSIYAHH
GLNDFIICAGYKGYLKEIFYVNLVLHNDITVDL
ASNSINYHGGTRPNWRVTVDITGM
YSMTGGR LGRIRDHLTPGEFFCMTYGDGVGDIDI
AAEVAFHRSHGLKATMCAVTPPGR
YGATNIEGQFITSFVEKPRGDDGQRINGGFVLPD
SVVDLIPSDDTIWEAGPLEWLAAN
NQLAAFKHDGFWQPM DTLRERNQLEELWSSGKAP
WKLWA"
misc-feature complement(285819..2865 /gene="ddhA"
32)
/locus-tag="RL0246"
/inference="protein
motif:Pfam:PF00483.9"
/note="Pfam match to entry
PF00483.9 NTP-transferase"
gene complement(286621..2870 /locus-tag="RL0247"
04)
CDS complement(286621..2870 /locus-tag="RL0247"
04)
/note="no significant database
hits"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="CAK05737.1"
/db-xref="GI:115254663"
/db-xref="UniProtKB/TrEMBL:Q1MMR5"
/translation="MVAGLKS L DVF SRRQPTKGG
EFRDP EAGEFRDSEVGFFLRPTRR
AFARRQSAGYLTIFYQDRPRLVGS IAPAWRPLVK
LEGRAFQGTGCLERQAVPLL NARP
AKRAAVGSHTPASLAQERNRIPGQG"
gene complement(287084..2873 /locus-tag="RL0248"
74)

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CDS complement(287084..2873 /locus-tag="RL0248"  
74)  
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hits"  
/codon-start=1  
/transl-table=11  
/product="hypothetical protein"  
/protein-id="CAK05738.1"  
/db-xref="GI:115254664"  
/db-xref="UniProtKB/TrEMBL:Q1MMR4"  
/translation="MIRYATSAASNPPPPKAREV  
SAAEPPVEMSRTPKPVIEVASAGAA  
LAAAYPLLPSSGESDELGSDTLPKTTKPPRRAATKR  
KPKVAEADDAPLQLSLEA"

gene complement(287614..2877 /gene="tRNA-Leu"  
00)

tRNA complement(287614..2877 /gene="tRNA-Leu"  
00)  
/product="tRNA-Leu"  
/note="anticodon CAG"

gene 287869..288288 /locus-tag="RL0249"  
CDS 287869..288288 /locus-tag="RL0249"  
/inference="similar to  
sequence:INSDC:SME591783"  
/note="similarity:fasta;  
with=UniProt:Q92SV2  
(EMBL:SME591783); Rhizobium  
meliloti (Sinorhizobium  
meliloti).; Hypothetical protein  
SMc00338.; length=175; id 39.640;  
111 aa overlap; query 31-139;  
subject 71-175"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
exported protein"  
/protein-id="CAK05739.1"  
/db-xref="GI:115254665"  
/db-xref="UniProtKB/TrEMBL:Q1MMR3"  
/translation="MLAPRTL LLAGLLAILTPAI  
AGADSLKLGKPGVGPLNTGSTLCD  
FRGCFGFPGQQWHRPAYVQPNYRPRGAGPTYR  
GAAGPPQLTYDPPPAQRVQPKARD  
MNRHAAWCSNEYRSYNPRTDRFLTYEGIYKTCRS  
PYR"

sig-peptide 287869..287935 /locus-tag="RL0249"  
/inference="protein  
motif:SignalP-HMM:2.0"  
/note="Signal peptide predicted  
for RL0249 by SignalP 2.0 HMM  
(Signal peptide probability 1.000)  
with cleavage site probability  
0.698 between residues 23 and 24"

gene complement(288300..2886 /locus-tag="RL0250"  
62)

CDS complement(288300..2886 /locus-tag="RL0250"  
62)  
/inference="similar to  
sequence:INSDC:SME591783"  
/note="similarity:fasta;  
with=UniProt:Q92SU7  
(EMBL:SME591783); Rhizobium

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meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc00345.; length=93; id 82.796;
93 aa overlap; query 24-116;
subject 1-93"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAK05740.1"
/db-xref="GI:115254666"
/db-xref="GOA:Q1MMR2"
/db-xref="UniProtKB/TrEMBL:Q1MMR2"
/translation="MLCEGDCAHAPQALNLSKRR
DIAMTEKARVTILYCTQCNWLLRA
SWMAQELLHTFSDSLGEVALIPATGGNFEIRVNG
DLIWERKRDDGGFPGPRELKQQRVD
IVEPGRDLGHVDRASLES"
/locus-tag="RL0250"

misc-feature      complement (288309..2886
17)

gene              288797..289573
CDS               288797..289573

/inference="protein
motif:Pfam:PF05169.2"
/note="Pfam match to entry
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29.464; 224 aa overlap; query
30-239; subject 28-236
similarity:fasta;
with=UniProt:Q7D1W7
(EMBL:AE007963); Agrobacterium
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33970).; AGR-C-389p.; length=254;
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DPLLSPLGGEFTIFEWHADTFSLP
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misc-feature	289807..289860	<p>/gene="nodL"</p> <p>/locus-tag="RL0252"</p> <p>/inference="protein"</p> <p>motif:Pfam:PF00132.9"</p> <p>/note="Pfam match to entry PF00132.9 Hexapep"</p>
misc-feature	289867..289920	<p>/gene="nodL"</p> <p>/locus-tag="RL0252"</p> <p>/inference="protein"</p> <p>motif:Pfam:PF00132.9"</p> <p>/note="Pfam match to entry PF00132.9 Hexapep"</p>
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 CDS complement(292892..2935 /locus-tag="RL0255"  
 93)  
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 tenA; Transcriptional activator  
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 aa overlap; query 34-231; subject  
 22-218 similarity:fasta;  
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 (EMBL:AE006856); Sulfolobus  
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 Transcriptional activator  
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 YAVALLSSILPCFWIYWHVGEAIKN  
 RPVIEGNAPQAWINTYGDQFAAGAREVIALTDM  
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CDS	293730..294308	/locus-tag="RL0256" /inference="protein motif:Pfam:PF01381.9" /note="Pfam match to entry PF01381.9 HTH-3" /locus-tag="RL0257" /locus-tag="RL0257" /inference="similar to sequence:INSDC:AE007964" /inference="similar to sequence:INSDC:PSTTRG" /note="similarity:fasta; with=UniProt:TTR-PSESZ (EMBL:PSTTRG); Pseudomonas syringae (pv. tabaci).; ttr; Acetyltransferase (EC 2.3.1.-) (Tabtoxin resistance protein).; length=EC 2.3.1.-; id 39.412; 170 aa overlap; query 4-171; subject 6-173 similarity:fasta; with=UniProt:Q8UIP7 (EMBL:AE007964); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Acetyltransferase (AGR-C-420p).; length=172; id 70.175; 171 aa overlap; query 1-171; subject 1-171" /codon-start=1 /transl-table=11 /product="putative acetyltransferase"
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gene	294333..294851	
CDS	294333..294851	

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(EMBL:OCA82447); Oligotropha
carboxidovorans (Pseudomonas
carboxydovorans); Hydrolase of
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26.425; 193 aa overlap; query
2-180; subject 4-186
similarity:fasta;
with=UniProt:Q92NB5
(EMBL:SME591790); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc01745.; length=211; id 50.521;
192 aa overlap; query 1-192;
subject 4-195"
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GITLLLATNQEHRRARYLMEQIGLSAHFDDIIYS
AALGHSKSPDFFRLLATERAGVLP
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		/db-xref="GI:115254676" /db-xref="GOA:Q1MMQ2" /db-xref="UniProtKB/TrEMBL:Q1MMQ2" /translation="MTDETVPSDIPTSRMLSWAR NSTVYRLERRMMTEKQLFDIAIRK AKEKFAGISAAQLKAVADFVKKFAYDNKVLDDHA YAEVSTRSAVRGGKSKRAIAQKLA AKGVSSDKVEAALEEADLYAAAIFARKRAFPGPF RRVELDEKRRKAKELSAFARNGFSF DIGRKVDFDMSFEDAEEIIVAGRSAAPQHQRS" /locus-tag="RL0260" /inference="protein motif:Pfam:PF02631.5" /note="Pfam match to entry PF02631.5 RecX" /locus-tag="RL0261" /locus-tag="RL0261" /inference="similar to sequence:INSDC:C90740" /inference="similar to sequence:INSDC:SCO939119" /note="similarity:fasta; with=UniProt:YBIF-ECOLI (EMBL:C90740); Escherichia coli O157:H7.; ybiF; Hypothetical transport protein ybiF; length=295; id 36.630; 273 aa overlap; query 32-302; subject 14-285 similarity:fasta; with=UniProt:Q9K3X0 (EMBL:SCO939119); Streptomyces coelicolor.; Putative integral membrane protein.; length=295; id 40.441; 272 aa overlap; query 27-296; subject 11-280" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05751.1" /db-xref="GI:115254677" /db-xref="GOA:Q1MMQ1" /db-xref="UniProtKB/TrEMBL:Q1MMQ1" /translation="MDIKNIETGTDGAALIAQPG ISPTSGGLAAGVAMCLMSMSISQF GAALSSSAIATYGAGATWLRALAFAAIILAAVVR PSVLRYSGAQWQATLLLTGTTTAAAM TLCFFAAIQRLPLGLAIAIDFLGPLSVAVFGYGL TWRLTWPLIAAAGILFLAHGEGW VGNSSGVLFALGSVGVAVYIILTKVGAAPFKGL EGLSMSLIVAGLVATPFGLAETGG AFTAQGLVEVLGLAILVPLIPYALEMVALRRMPS ASFGILMSLEPALGALAGFLILAQ PMTALQMLGTALVVAASAGATAAIAKT" /locus-tag="RL0261"
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298129..298197)
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motif:TMHMM:2.0"
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helices predicted at aa 20-42,
55-77, 87-109, 116-138,161-183,
196-214, 224-246, 253-275 and
279-301"
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/note="Pfam match to entry
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CDS complement(298251..298718) /locus-tag="RL0262"
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sequence:INSDC:SME591791"
/note="similarity:fasta;
with=UniProt:Q92MN5
(EMBL:SME591791); Rhizobium
meliloti (Sinorhizobium
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153 aa overlap; query 1-153;
subject 1-153"
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meliloti (Sinorhizobium
meliloti).; HYPOTHETICAL
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length=327; id 78.834; 326 aa
overlap; query 1-326; subject
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misc-feature	order (299693..299761, 299798..299866)	/inference="protein motif:TMHMM:2.0" /note="2 probable transmembrane helices predicted at aa 268-290 and 303-325" /locus-tag="RL0264"
gene	complement(300040..300639)	
CDS	complement(300040..300639)	/locus-tag="RL0264" /inference="similar to sequence:INSDC:C97389" /note="similarity:fasta; with=UniProt:Q8UIP1 (EMBL:C97389); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0252 (AGR-C-433p).; length=204; id 58.376; 197 aa overlap; query 4-199; subject 8-204" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05754.1" /db-xref="GI:115254680" /db-xref="UniProtKB/TrEMBL:Q1MMP8" /translation="MRIKGFVAMMAMFAMATAA IPAPSRNASMVTGNATSQPIGHYD FCQIHRSECGADRAGPVMNPGKWSLVRVSNAT ANRITPTMTDKEIYGKDEVWAYPT TAGDCEDFALLKRRMLIQRGFPAADLLMTVVVRKP DGEQHAVLTLRTAEGDFVLNLLAA DVKPFWFGTPYSFVKRQSSYNAGRWWTIENGRDVL VGLR" /locus-tag="RL0264"
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sig-peptide	complement(300579..300639)	/inference="protein motif:SignalP-HMM:2.0" /note="Signal peptide predicted for RL0264 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.560 between residues 19 and 20" /locus-tag="RL0265"
gene	complement(300805..301629)	
CDS	complement(300805..301629)	/locus-tag="RL0265"  /inference="similar to sequence:INSDC:AE008997" /note="similarity:fasta; with=UniProt:Q8UIP0 (EMBL:AE008997); Agrobacterium tumefaciens (strain C58/ATCC 33970).; Hypothetical protein Atu0253.; length=272; id 70.000; 260 aa overlap; query 5-263; subject 11-270" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05755.1" /db-xref="GI:115254681" /db-xref="UniProtKB/TrEMBL:Q1MMP7" /translation="MSDQLSNAQPQFLTVGEGEA AREIATLVRPAQTGNGAPALVWLS GYRSDMSGTKAVELDGLAELGLACIRLDYSGHG LSGGSFRDGTISRWLEELAVIRH VAPDRVILVGSSMGWGIALRLAQELARQGGPKLA GMVLIAPAPDFTSELIEPNLKAKE RKSLAERGYFEERSQYSPEPNIYTRALIEDGRKN RVLDGIIETGCPVHILQGMKDAV PHAHAMKLVEHLPAADVVLTFVRDGDHRLSRPGD IALLSAVKGIIRSSTNRQMPT"
gene	301757..302344	/gene="infC" /locus-tag="RL0266"
CDS	301757..302344	/gene="infC" /locus-tag="RL0266" /inference="similar to sequence:INSDC:AE005395" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:IF3-ECOLI (EMBL:AE005395); Escherichia coli O157:H7.; infC; Translation initiation factor IF-3.; length=180; id 58.537; 164 aa overlap; query 33-195; subject 14-177 similarity:fasta; with=UniProt:IF3-RHIME (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium

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meliloti).; infC; Translation
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length=177; id 85.393; 178 aa
overlap; query 18-195; subject
1-177"
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ARKKQKIVEVKEIKMRPNIDTHDYEVKMKAMGRF
FDEGDKVKVTLKFRGREMAHQELG
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K"
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/notes="Pfam match to entry
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/notes="Pfam match to entry
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gene 302656..302859 /gene="rpmI"
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CDS 302656..302859 /gene="rpmI"
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with=UniProt:RL35-THETH
(EMBL:TTH224858); Thermus
thermophilus.; rpmI; 50S ribosomal
protein L35.; length=65; id
52.381; 63 aa overlap; query 2-64;
subject 1-62 similarity:fasta;
with=UniProt:RL35-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; rpmI; 50S ribosomal
protein L35.; length=67; id
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subject 1-67"
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protein L35"
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misc-feature	302665..302841	
gene	302898..303302	
CDS	302898..303302	
misc-feature	302901..303224	
gene	303453..304535	
CDS	303453..304535	

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with=UniProt:SYFA-ECOLI
(EMBL:B64930); Escherichia coli.;
pheS; Phenylalanyl-tRNA synthetase
alpha chain (EC 6.1.1.20)
(Phenylalanine--tRNA ligase alpha
chain) (PheRS).; length=327; id
51.453; 344 aa overlap; query
1-344; subject 1-326
similarity:fasta;
with=UniProt:SYFA-RHIME
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; pheS;
Phenylalanyl-tRNA synthetase alpha
chain (EC 6.1.1.20)
(Phenylalanine--tRNA ligase alpha
chain) (PheRS).; length=360; id
87.778; 360 aa overlap; query
1-360; subject 1-360"
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chain"
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/db-xref="GOA:Q1MMP3"
/db-xref="UniProtKB/TREMBL:Q1MMP3"
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TDYYNFTALNFPPEGHPAREMHDTF
FFNPDENGERKVLRTHTSPVQVRTMEAQTPPIRI
IIPGKTYRQDS DATHSPMFHQVEG
LVVDKKANVANLRWVLEEFCKTTFEVDVSVTRMR
PSFFPFTEPSFEVDIQCDSRGPV
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/inference="protein
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/note="Pfam match to entry
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/inference="protein
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/note="Pfam match to entry
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gene 304552..306975
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CDS 304552..306975
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/locus-tag="RL0270"
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sequence:INSDC:I41284"

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with=UniProt:SYFB-ECOLI
(EMBL:I41284); Escherichia coli.;
pheT; Phenylalanyl-tRNA synthetase
beta chain (EC 6.1.1.20)
(Phenylalanine-- tRNA ligase beta
chain) (PheRS).; length=795; id
36.965; 817 aa overlap; query
1-806; subject 1-794
similarity:fasta;
with=UniProt:SYFB-AGRT5
(EMBL:B97390); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; pheT; Phenylalanyl-tRNA
synthetase beta chain (EC
6.1.1.20) (Phenylalanine-- tRNA
ligase beta chain) (PheRS).;
length=807; id 84.015; 807 aa
overlap; query 1-807; subject
1-807"
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chain"
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NLTPNRPDCTS IHGIARDLAASGLGTLKMRPAPS
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LAVRRAAEGETVLALDQREYKLSNNVVISDENG
IESIGGIMGGEHSGCDENTVDVLI
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NGKILTTQLIRTLAKRALAARGM
LEAVTWSFIPEDQAKLFGGGSPALKLANPIAAEM
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misc-feature	305002..305439	
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gene	complement(307030..307389)	
CDS	complement(307030..307389)	/locus-tag="RL0271"  /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92SS8 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC00367.; length=119; id 62.712; 118 aa overlap; query 1-118; subject 1-118" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05761.1" /db-xref="GI:115254687" /db-xref="UniProtKB/TrEMBL:Q1MMP1" /translation="MSDRQAVEQTVHLYVEGMAF ANEAALKKAFHPKSSIIGHYENAV EWLTRDEFIAAILQEFPAPPGTQPYMDIQSV DVE GDAASVKVTDDFAGMRFTDYLSLL KIDGRWTIIVSKLFLHHR" /locus-tag="RL0272"
gene	complement(307497..308492)	
CDS	complement(307497..308492)	/locus-tag="RL0272"  /inference="similar to sequence:INSDC:AP003005" /note="similarity:fasta; with=UniProt:Q98CQ3 (EMBL:AP003005); Rhizobium loti (Mesorhizobium loti).; Oxidoreductase, aldo/keto reductase family.; length=332; id 71.818; 330 aa overlap; query 1-330; subject 2-331" /codon-start=1 /transl-table=11

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SATIRRAHAVHPIAALQSEYSLWTRDPEEEVLAT
CRELGIGFVYPYSPLRGFGFTGAIR
KAEDLDADDERRQVPRFOAENFDANAALVATLER
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77)

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motif:Pfam:PF00248.9"
/notes="Pfam match to entry
PF00248.9 Aldo-ket-red"

misc-feature      complement(308409..3084
77)

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helix predicted at aa 26-48"
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sequence:INSDC:SME591783"
/notes="similarity:fasta;
with=UniProt:Q92SS5
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE TRANSCRIPTION
REGULATOR PROTEIN.; length=296; id
72.542; 295 aa overlap; query
1-295; subject 1-295"
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transcriptional regulator"
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VKEGFDAGIRLEESLEADMIARV
SPDLTTVIAASPEYFEHHKPKPEHPRDLVHRCIK
RRFTNGSIYRWEFEKDGQELVVS
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sig-peptide      308617..308689
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gene	complement(309571..310068)	
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misc-feature	complement(309580..310053)	/locus-tag="RL0274"
		/inference="protein motif:Pfam:PF05974.1" /note="Pfam match to entry PF05974.1 DUF892"
gene	310215..310832	/locus-tag="RL0275"
CDS	310215..310832	/locus-tag="RL0275" /inference="similar to sequence:INSDC:SME591783" /note="similarity:fasta; with=UniProt:Q92SS2 (EMBL:SME591783); Rhizobium meliloti (Sinorhizobium meliloti).; Hypothetical protein SMC00373.; length=224; id 77.833; 203 aa overlap; query 1-203; subject 1-203"

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IWDNRDFDGCMAAVCIAVPWMVDHYRVESDWQR
LAWWIHDHLPYASLCFFPKLWAFN
IQWHERPKRVIQSYVSPRGILTKPGMANWESDHS
EWYTGFPLLKS"

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65)

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(EMBL:AE007965); Agrobacterium
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33970).; Acetyltransferase
(AGR-C-449p).; length=147; id
57.143; 147 aa overlap; query
1-147; subject 1-147"
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acetyltransferase"
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SDGHIRYRISF"

misc-feature complement(310855..3111 /locus-tag="RL0276"
09)

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PF00583.9 Acetyltransf-1"

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90)

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with=UniProt:Q8UIN0
(EMBL:AE007965); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Oxidoreductase
(AGR-C-452p).; length=AGR-C-452p;
id 68.038; 316 aa overlap; query

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KALIVTKVSGDMGQKTLKETYILKAVEDSLRRL
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AYAKLKQGGKIRAIKGSNYDAKLLQASFDAAEKA
GLPRYDVLQPEYNLYERSSFEGPL
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gene              312406..313392
CDS               312406..313392

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sequence:INSDC:SP10405"
/note="similarity:fasta;
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(EMBL:SP10405); Streptomyces
purpurascens.; rdmF; RdmF.;
length=346; id 28.354; 328 aa
overlap; query 2-324; subject
10-329 similarity:fasta;
with=UniProt:Q92SS0
(EMBL:SME591783); Rhizobium
meliloti (Sinorhizobium
meliloti).; PUTATIVE
OXIDOREDUCTASE PROTEIN.;
length=328; id 80.488; 328 aa
overlap; query 1-328; subject
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(strain PCC 7120). A110042
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with=UniProt:O05377
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transglycosylase, dTDP-4-rhamnose
reductase, complete cds.;
length=234; id 25.688; 218 aa
overlap; query 9-220; subject
1-213 similarity:fasta;
with=UniProt:Q8Z0P8
(EMBL:AP003581); Anabaena sp.
(strain PCC 7120).; A110042
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296 aa overlap; query 11-306;
subject 11-306"
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LVRTLTERADMVVGTRRGVHSDAGRQGHALGNR
LFNLLYRMIFGPDFDTIDIFSGYRAF
SRRFVKSFPVAVSGGFEIETEMSVHASRLKLPVSE
LELDYGRRPEGSHSKLSTFRDGAK
ILWMFAMLMKETRPFAPFFSAISATFMLASLGfMA
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314112..314180))

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misc-feature complement(314373..3148 /locus-tag="RL0280"
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length=456; id 34.990; 483 aa
overlap; query 14-495; subject
8-438 similarity:fasta;
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(EMBL:AE007966); Agrobacterium
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33970).; xseA; Probable
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IRGFNALEPSTGIPRPDVLIVARG
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LOCUS (LOC): AP008934 GenBank (R)  
 GenBank ACC. NO. (GBN): AP008934  
 GenBank VERSION (VER): AP008934.1 GI:72493824  
 CAS REGISTRY NO. (RN): 864028-20-6  
 SEQUENCE LENGTH (SQL): 2516575  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 26 Dec 2007  
 DEFINITION (DEF): Staphylococcus saprophyticus subsp. saprophyticus ATCC  
 15305 DNA, complete genome.  
 SOURCE: Staphylococcus saprophyticus subsp. saprophyticus ATCC  
 15305  
 ORGANISM (ORGN): Staphylococcus saprophyticus subsp. saprophyticus ATCC  
 15305  
 Bacteria; Firmicutes; Bacillales; Staphylococcus  
 PROJECT (PJID): GenomeProject:15596  
 COMMENT:

This work was done in collaboration with Makoto Kuroda, Miyuki  
 Kumano, Kazuya Morikawa, Masato Higashide, Atsushi Maruyama, Yumiko  
 Inoue, Kimio Matoba, Toshiko Ohta (University of Tsukuba), Hideki  
 Hirakawa, Satoru Kuhara (Kyushu University), and supported by the  
 Research for the Future Program of the Japan Society for the  
 Promotion of Science.

REFERENCE: 1  
 AUTHOR (AU): Kuroda,M.; Yamashita,A.; Hirakawa,H.; Kumano,M.;  
 Morikawa,K.; Higashide,M.; Maruyama,A.; Inoue,Y.;  
 Matoba,K.; Toh,H.; Kuhara,S.; Hattori,M.; Ohta,T.  
 TITLE (TI): Whole genome sequence of Staphylococcus saprophyticus  
 reveals the pathogenesis of uncomplicated urinary tract  
 infection  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 102 (37), 13272-13277  
 (2005)  
 OTHER SOURCE (OS): CA 143:280290  
 REFERENCE: 2 (bases 1 to 2516575)  
 AUTHOR (AU): Hattori,M.; Yamashita,A.; Toh,H.; Oshima,K.; Shiba,T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (11-MAR-2005) Contact:Masahira Hattori  
 Graduate School of Frontier Sciences, University of  
 Tokyo; 5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8561,  
 Japan

## FEATURES (FEAT):

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gene 5173..7098  
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CDS	complement(9889..10701)	/locus-tag="SSP0007" /locus-tag="SSP0007" /note="similar to gi 15922997 ref NP-370531.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 83 in 270 aa, BLASTP E(): e-131" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17152.1" /db-xref="GI:72493831" /translation="METLSQVSIPIKRDETHKGD YGRILLIGGNANLGGAIMLAARAC VYSGSLITVATHPTNHAALHSRCPEAMVIDIND TKMLTKMIENTDCILIGPGLGCDP KGNNAITFLLQNIQPHQKILVDGDAITIFSCLKP DIPTCKVIFTPHQKEWERLSGIFI EEQTYERNREAADRIGATIVLKMHGTEIYFRGKD YKLPIGTPAMATGGMGDTLSGMIT SFVQGQFNDTEEAVTSATYTHSYIGEQLAEKMYVY PPSRLISEIPHAMKALEN" /locus-tag="SSP0008" /locus-tag="SSP0008" /note="similar to gi 15922998 ref NP-370532.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 79 in 498 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="histidine ammonia-lyase" /protein-id="BAE17153.1" /db-xref="GI:72493832" /translation="MTLQLNGEMLTINDIKTFLN KEDTVEVTQEALERVVKKSRQTVEH IENKETIYGITTFGFLGSDVRIDKDEYNQLQVN LIRSHACGVGKPFSEEVALLVMVL RLNTLLKGHSGTTVALVEQLVYYINNRRIVPVIQ QGSLGASGDLAPLSHLALALIGEG NVFFKGEEVDSRYVLNQLNRRNPIQLQAKEGLALI NGTQAMTAQGVINYIEAEALGYQA EWIAALTHQALNGITDAYNEKVHKARNFQEQIDV AARMLDWLDGSELTITQGDIRVQD AYTLRCIPQIHGASFQVFNVKEKLEFEMNAAND NPLIFDEGDETLVISGGNFHGGPI AFALDFLKLGVSELANVSERRLERLVNPQLNNGL PAFLSPQPLQSGAMIMQYAAASL VSENKTLAHPASVDSIPSSANQEDHVSMGTIASR HGYHIIENARRVLAETIIALQAV EYKDIDKLSPKTYEKYQELRHIVPSITEDRQFHK DIEAVSQYLQDLAYM" /locus-tag="SSP0009" /locus-tag="SSP0009" /note="similar to gi 49484921 ref YP-042142.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 82 in 428 aa, BLASTP E(): 0.0"
gene	11098..12597	
CDS	11098..12597	
gene	12929..14212	
CDS	12929..14212	

gene 14528..15229  
CDS 14528..15229

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MVPQLVNADSMYGTGQLPKFEEDL
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RLHQFDKVMVRIEKPEDSQALEDMTHHAEAIL
EELGLPYRRVILCTGDIGFGSSKT
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K"
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12228], percent identity 75 in 228
aa, BLASTP E(): 2e-98"
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amino acid permease"
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RIGLATLVTDTEFGVAVTPHLKGEKINDRWLHGL
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PDVLGLDFAITAMFIFLAVSQFESIRRSKVKIYL
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LASTITAAALGVVMER"
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gene 15226..15555  
CDS 15226..15555

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12228], percent identity 61 in 109
aa, BLASTP E(): 3e-34"
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/transl-table=11
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protein"
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gene 15827..16795  
CDS 15827..16795

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12228], percent identity 80 in 322
aa, BLASTP E(): e-154"
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homoserine-o-acetyltransferase"
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gi|27466930|ref|NP-763567.1|
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12228], percent identity 68 in 303
aa, BLASTP E(): e-118"
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protein"
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ATPIFKPLYAWQMSRSLLYIIV
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/locus-tag="SSP0014"
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/note="similar to
gi|27466931|ref|NP-763568.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 82 in 655
aa, BLASTP E(): 0.0"
/codon-start=1
/transl-table=11
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protein"
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gene      17076..17987
CDS       17076..17987

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gene      18002..19969
CDS       18002..19969

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CDS	19966..20412	AIKNLPIMGIILDENENIEWMNR MSERLNRNVISDPVNEVYPNLIKLEKTQEIEN ENEYHYRVRYSEKEHVLFFDITK EVYTNELYESSKPIIATFLDNYDEITQNMNDTQ KSEINSMVTRVISRWATEHNIYFK RYSDDQFVAYLNQNILNEIATNFSILSOLREKS VGYRAQLTLISIGVGEGSENILDLG ELSQSGLDLALGRGGDQVAIKHINGNVRFYGGKT DPMKTRTRVARVISHALKDILME GDKVIMGHKRPDLDAIGAIGVSRFAMNNLDA YIVLNESDIDPTLRRVMDAVNEKP ELKDRFITSDEAWDIMTSKTTLVVVDTHKPEMVI DENILNKANRKVVVDHHRGSEFI SSPLLVMPEYASSTAELVTELLEYQPTQRLTR LESTVMFAGIIVDTRNFTLRTGSR TFDAASYLRAHGADTILTQHFLKDDLDTYINRTE LIQTVKLQDNGVAIAHGSDEKIYH PVTVAQAADLSDGVEASYVIARREDNVVGMS ARSLGAVNVQLTMEALGGGGHLTN AATQLKDVTVDEAIEKLQQAITEQMSRSENS" /locus-tag="SSP0015" /locus-tag="SSP0015" /note="similar to gi 27466932 ref NP-763569.1  [Staphylococcus epidermidis ATCC 12228], percent identity 88 in 148 aa, BLASTP E(): 7e-70" /codon-start=1 /transl-table=11 /product="50S ribosomal protein L9" /protein-id="BAE17160.1" /db-xref="GI:72493839" /translation="MKVIFTQDVKGKGGKGEVKD VPVGYANNFLLKKNMAVEATPGNL RQLEQKNKAAEAERQOEIEDAKKLKEQLSEIEVE VSAKTGEGGKLFQSVSTKQITQAL QQQHDIKIDKRKMDLPNGIHALGYTNVPVKLDKE VEGTIRVHTVEQ" /locus-tag="SSP0016" /locus-tag="SSP0016" /note="similar to gi 27466933 ref NP-763570.1  [Staphylococcus epidermidis ATCC 12228], percent identity 93 in 464 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="replicative DNA helicase" /protein-id="BAE17161.1" /db-xref="GI:72493840" /translation="MDGMDGMYEQNQMPHSNEAE QSVLGAIIDPELINTTQEVLLPE SFYRGAAQHIFRAMMNLNEDNKDIDVVTIMDQLS QEGRLNEAGGPQYLAELSSNVPTT RNIQYYTEIVFKHATKRKLIQTADSIANDGYNDE LELDTILNDAERRILELSSTRES GFKDIDVLGDVYENAEALLDQNSGGQTPGIPTGYR DLDDMTAGFNRRNDLIIAARPSVG KTAFALNIAQKVATHEDHFSVGFISLEMGAQLA
gene	20443..21852	
CDS	20443..21852	



gene 22148..23431  
CDS 22148..23431

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WNRFTIAGKLSRTKIFIDDTGIRITDIRSKCR
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RFSQDNRQQEVSSEISRTLKAIAARELECPVIALSQL
SRGVEQRQDKRPMMSDIRESGSIE
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DDNGEIEIIIAKQRNGPTGTVKLH
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/note="similar to
gi|57285312|gb|AAW37406.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 89
in 427 aa, BLASTP E(): 0.0"
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synthase"
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SVVLHRSSRASGITDLSINSIDL
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gene complement(23521..24732 ) /locus-tag="SSP0018"  
CDS complement(23521..24732 ) /locus-tag="SSP0018"

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/note="similar to
gi|42781882|ref|NP-979129.1|
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percent identity 41 in 398 aa,
BLASTP E(): 1e-85"
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glycosyltransferase"
/protein-id="BAE17163.1"
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AALNNAQALSETEMNDVEDTFNH
LQQHIQTTYGVEVNSRYETMNNPGDFNIAIYLEK
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AALKDLDVSVIVSIGEANNAADF"

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tRNA	25017..25091	/product="tRNA-Glu" /note="SSPtRNA01"
tRNA	25098..25170	/product="tRNA-Asp" /note="SSPtRNA02"
gene	25365..25823	/locus-tag="SSP0019"
CDS	25365..25823	/locus-tag="SSP0019" /note="similar to gi 20089628 ref NP-615703.1  [Methanosarcina acetivorans C2A], percent identity 29 in 105 aa, BLASTP E(): 2e-05" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17164.1" /db-xref="GI:72493843" /translation="MTNHKHIETDLINLISDRH HDLRQKQVEYMTAQQLPQVHFGSSSE WYLIIMIKYDQPTFAELTHKINLIRQAIHKAVKQ LEQKQVVQIESVPNNKKEKRVILT EFGIMCYEKYIKNKQHIIEHQVIGASEVAHLE QLLQADWQLENDKPDE" /locus-tag="SSP0020" /locus-tag="SSP0020" /note="similar to gi 16077336 ref NP-388149.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 45 in 456 aa, BLASTP E(): e-117" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17165.1" /db-xref="GI:72493844" /translation="MATQVNVKSPKMFALVLMIG GFMGLFSETALNMALTDIMADFKV SAATVQWLTTGYLLVMACLVPASSYLIKWFSTKT LIVSGILLSLLGVVIGALAPNFGI LLLGRLIQALGTGILLPIMVTVLMILIFPIEKRA VMGIMGLVITAGPALGPTLSGVII SASSWHYIFWISAVLYLVVLGLAFTNTENVGEIS KPKIDILSICLSTIGFAGLIFALS SMAEAAFTNVIVWLPVLVIGILALIIFVVVRQFKID SPMLNLNVFKYPMFVGAAMVFIT ILCILSTGILLPLYLKGAFLFSSVIAGLTLLPGN AVNLVLSPPVVGSLFDRFGARYFGI IGYLLMFIAMTFALIISASTPVWAILITFMVLF FGITMVMPAQTNALNQLPHDLA DGSATITTLIQVGSAGTAITAITLYTTAMKSFGA ANPNVSQEIIILSHGVQFTFFFIT LTVIGFILSLFVKQKQSV" /locus-tag="SSP0021" /locus-tag="SSP0021" /note="similar to gi 27466936 ref NP-763573.1
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CDS	26277..27683	
gene	28100..28801	
CDS	28100..28801	

gene 28814..30646  
CDS 28814..30646

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12228], percent identity 96 in 233
aa, BLASTP E(): e-128"
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/locus-tag="SSP0022"
/locus-tag="SSP0022"
/note="similar to
gi|57285314|gb|AAW37408.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 87
in 608 aa, BLASTP E(): 0.0"
/codon-start=1
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/product="two-component sensor
histidine kinase"
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ATSKQSTRSLINQKANDNSIQKALSLSGEINSHVT
LKDYGNGKQQRVWVYNLPVKTSNDG
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TSMNSYIEALESQAWKDELAPQFLSVTREETER
MIRLVNDLLQLSKMDNESEQITKE
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/note="similar to
gi|49482273|ref|YP-039497.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity
57 in 447 aa, BLASTP E(): e-154"
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gene 30636..31976  
CDS 30636..31976

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		QMHSNHNLIIPDLTDEFLILDFSYDMPLATYLGQ
		ALNIDAKVPNNFKFDRLLIDNNKD
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		HKMKQPYSEIITNKDTIDRATHIF
		APKAPEAMKSYHTIYNRISVDTMNSILFNDSVVV
		RSTKSGTATYNNNTGVANYNDETE
		KYRYTNLSEDENRSTNMQDSIPSTYDIYNNHGGF
		TDDYRLFNIDNKGELTYQMFLNG
		RPTFNDEYLNNIKVSWGDKGVFSYARALLKANVT
		IDSGGNETKLPGAETVRSELANNP
		EINFEDVTNMTIGYRMEEKPKDSIEIQRNSEFK
		PQWYVQYNGEWAYEDGRLE"
gene	31977..32759	/locus-tag="SSP0024"
CDS	31977..32759	/locus-tag="SSP0024"
		/note="similar to
		gi 27466939 ref NP-763576.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 58 in 263
		aa, BLASTP E(): 1e-83"
		/codon-start=1
		/transl-table=11
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		VGNDQYTTALKSYVKDNVYKGDYEMSNIDNDKVT
		FEQTYHDYPIMNNNKARLEFNINN
		DGKATSYKQTAMKSIAFSEGANNKKQVNSAKSA
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		gi 27466940 ref NP-763577.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 91 in 263
		aa, BLASTP E(): e-138"
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		/transl-table=11
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		ANEKTWTAIEKKDSKIPMDQKQFIF
		NPYETKSLAGFDIESFNVSHDAIDPQFYIFHNHY
		KKFTILTDTGYVSDRMKGMIIQGS
		AFVFESNHVDMLRMCGYPWTKQRILSDMGHVS

gene	33192..33983
CDS	33192..33983

gene	34583..35062	NEDAGRAMTDVITGSTKRIYLSHL
CDS	34583..35062	SQDNNMKDLARMSVGQVLNENDIDTEKEVLLCDT DKANATPIYTL" /locus-tag="SSP0026" /locus-tag="SSP0026" /note="similar to gi 27466941 ref NP_763578.1  [Staphylococcus epidermidis ATCC 12228], percent identity 86 in 159 aa, BLASTP E(): 3e-75" /codon-start=1 /transl-table=11 /product="hypothetical protein orfX" /protein-id="BAE17171.1" /db-xref="GI:72493850" /translation="MKITILTVGKLKEKYWKQAI AEYEKRLSAYSKIEIIEVPDEKAP ENMSDKEVEQVKEKEGORLLAKVQQOSTVITILEI KGNMLTSEGLAKEIESRMRGQSD FTFIIGGSNGLHKDVLDRSDYALSFSKMTFPHQM MRVILIEQVYRAFKIMRGEAYHK" /locus-tag="SSP0027" /locus-tag="SSP0027" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17172.1" /db-xref="GI:72493851" /translation="MDSGYHLPHNAVVEEFEM LSLLDVSKEYYYIEDLKALFFEEM VKNGLFEKFHGRMYERIKNSINMKIIFYKVYNGK ATYDDIKKLYYTDSEKKPSKNFNQ NWNIEIRDYLEFMAFLGVLPITYYKGNRENDKKH YISDTLIKYNKGTLLLSDIILGMK FRNASKDYSNFEMYDITLRFVVAIKILQLAKEL GVLEVDGAVLCGLVKLQNNESLKD MSNIDFSNRNNNNWTKKQIKEFGRGLTFMKQWLN IVLEIPLVNRNRIKFDITNFDINN YDFYHESIFIGETYNHLEITPQIANIIICPEKN DEEVLISLKDAKLINENKQNAHIN FDTDLPSRELVEADRLFKSKSKIEFELDEVQIQ EFSMSNENFDIGFQIAKSSDGTAY ENFIYQQLNLTENSQVRLGSQFTGQRLSDTVI DCVVYHHQMSRIKIIIECKAGKA IKSFDERKEINNVTNLKLANINDYDGVVYIITD SNQIPTQTHGGYRSNNNSYSFEEK LLTLQFDIQMSTGKPTIVTAFSYEMFMKFLSDIK EINGIITSQSTKHFWVWSKKFVNK AYISVQA" /locus-tag="SSP0028" /locus-tag="SSP0028" /note="similar to gi 57015737 gb EAL52527.1  [Campylobacter upsaliensis RM3195], percent identity 31 in 267 aa, BLASTP E(): 1e-30" /codon-start=1 /transl-table=11 /product="putative DNA modification methylase" /protein-id="BAE17173.1" /db-xref="GI:72493852"
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CDS	35198..36919	
gene	36942..37721	
CDS	36942..37721	

		<pre> /translation="MAKLNLDLGKEWVKSTKSWF TLQSRQRYKTIKHGKFPEELAEK FILEFSKKNEVVDPPFMGVGSTAVASEENNREFK GIELESSFISMANSRLNENNNIIE GDSRYAKYKIDIEADFIITSPPYWMLGKSRGNS NSQHKDRIQKNLDLVYSDSSNDLG NIDDYSTFMKNLQKVFKNCNKVLKSRKYMVIVVQ NFRDSNGEYVTFWDSVKYVEREG FTFVGEQIWCQDNKKLGIWGFSTFISNNHHYC LVFRKNE" /locus-tag="SSP0029" /locus-tag="SSP0029" /note="similar to gi 13542247 ref NP-111935.1  [Thermoplasma volcanium GSS1], percent identity 27 in 379 aa, BLASTP E(): 6e-27" /codon-start=1 /transl-table=11 /product="putative modification methylase" /protein-id="BAE17174.1" /db-xref="GI:72493853" /translation="MSNIYSYHAKFHESIPNEYI NKYSQEFETILDFFCGSGTTLKES LKLGRNAIGIDVSPIALLSKSVNTNFYDKNKLKR VYDYILKQFNSNISINVIKFPDYE RWYTEENHLQLSKLKNIIDNIEENSUREFFLLCF LSISNKVSNRRKTWNIIGYLDNVL PDLDSKFVADSFKQKVSKEIENIDFEELYKLG RSIHIEKKDINTAKLDCKVDMVMT SPYPFPAVDRIYHRLSMYWLQENIEQLTRQEIG ARNKRKKNLGLSLFNEIEKSFN IMRVVRTDGYWAMTIADTTTRNKVKIPFIDWTINL FYEHWILVEDRIRELQQQTMAQK RIPEEHILVFKKI" /locus-tag="SSP0030" </pre>
gene	37714..38757	
CDS	37714..38757	
		<pre> /locus-tag="SSP0030" /note="similar to gi 22652813 gb AA03831.1  [Enterococcus faecalis], percent identity 29 in 167 aa, BLASTP E(): 2e-15" /codon-start=1 /transl-table=11 /product="putative replication protein RepA" /protein-id="BAE17175.1" /db-xref="GI:72493854" /translation="MNRTLQILKRQKSLNFSVY SEFESQLSMFNDDKTMIDFEGKK LSITLNPDFVYLLNFDENSICFSMSDFTNLKSI YSKHLRYLFTYQDESTYTFISIEA FREFLDINSKYPHMKIDKPVLRMIKEELNQFYQ YFEYKKVLEMPQRVTEIKFNFIVK KNSCTNYISH" </pre>
gene	complement(38843..39355)	
	)	
CDS	complement(38843..39355)	
	)	
		<pre> /locus-tag="SSP0031" </pre>
gene	complement(39676..40182)	
	)	
CDS	complement(39676..40182)	
	)	

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/ note="similar to
gi|22094438|gb|AAM91898.1|
[Staphylococcus aureus], percent
identity 84 in 167 aa, BLASTP E():
3e-76"
/ codon-start=1
/ transl-table=11
/ product="hypothetical protein"
/ protein-id="BAE17176.1"
/ db-xref="GI:72493855"
/ translation="MENITNTLVTTAIFDEKRTH
RYLLTKTWDSEKQTLTIITMYPHY
DGILNIDLTTQLIMNKVSEMDAFGSIYFVNLYSN
ITTPINLKHLEENAYDNHTNIQIM
KAVKESDEVILAWGAYAKKPVVEARVNEVLEMLK
PHKKKIKKLINPATNEIMHPLNPK ARQKWILN"
gene      complement(40196..40507 /locus-tag="SSP0032"
)
CDS       complement(40196..40507 /locus-tag="SSP0032"
)

/ note="similar to
gi|14021046|dbj|BAB47670.1|
[Staphylococcus aureus], percent
identity 74 in 103 aa, BLASTP E():
4e-41"
/ codon-start=1
/ transl-table=11
/ product="hypothetical protein"
/ protein-id="BAE17177.1"
/ db-xref="GI:72493856"
/ translation="MNRYITRGIANNLPNLIQHQ
LWQLVSEREQEQTKDNTLVDYFHI
FQFNTHRNQOLYIKHKQERPAYVKTKKANINQPIN
INKVYIIREDDVDLSYYIMLLPNE Y"
gene      complement(40500..40601 /locus-tag="SSP0033"
)
CDS       complement(40500..40601 /locus-tag="SSP0033"
)

/ codon-start=1
/ transl-table=11
/ product="hypothetical protein"
/ protein-id="BAE17178.1"
/ db-xref="GI:72493857"
/ translation="MHKYIKITQLVITILSEIII
WMKESERKEVSYE"
gene      complement(40603..40941 /locus-tag="SSP0034"
)
CDS       complement(40603..40941 /locus-tag="SSP0034"
)

/ note="similar to
gi|16579848|gb|AAL26663.1|
[Staphylococcus aureus], percent
identity 94 in 112 aa, BLASTP E():
9e-57"
/ codon-start=1
/ transl-table=11
/ product="hypothetical protein"
/ protein-id="BAE17179.1"
/ db-xref="GI:72493858"
/ translation="MTLEQQLKHYITNLFNLPKD
EVWHCESIEEIADDILPNQYVRIG
PLSNKILQNTYYSDDLHESNIYPFILIYQQLI

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AIGYIDENHDMDFLYLHNTIMPLL
DQRYLLTGGQ"
gene      complement(41416..43044 /locus-tag="SSP0035"
)
CDS       complement(41416..43044 /locus-tag="SSP0035"
)

/note="similar to
gi|14020973|dbj|BAB47597.1|
[Staphylococcus aureus], percent
identity 86 in 542 aa, BLASTP E():
0.0"
/codon-start=1
/transl-table=11
/product="cassette chromosome
recombinase B"
/protein-id="BAE17180.1"
/db-xref="GI:72493859"
/translation="MQQLKQKRVGIYVRVSTEMQ
SAEGYSIDGQINQIKEYCNFHHFE
VKDIYADRGISGKSMNRPALQRLHDANKGHIDC
VMVYKTNRLARNTSDLLKIVEDLH
KQNVFFFSLSERMEVNTSSGKMLQILASFSEFE
RNTILENIYTGQHORALEGYQGN
LPLGYNNIPDNKDLMINQHEANIVKYIFESYAK
GHGYRKIANALNHKGYVTKKGNPF
SISAVTYILSNPFYIGKIQFAKYKDWNDRKRKGL
NDKEVIAEGKHAPIIGKDLWDKVQ
ARKKQVSEKPPQVHGKGTNLTGLISCPQCSASMS
ASTTVNTLKDGTKKRIRYVSCSNF
RNKGSKVCSSANSVRADVIEKYVMDQILEIVKSK
VIKQVVERVNQEHQIDMAALNNDHI
AYKQOQYDEVQIKLDNLIKTLEDNPDLTSLVKNT
IHQYEKQLNDITTQINQLKQOQNO
EKPSYDTKQIAALLQOIFQNVESMDKVQLKALYL
TVIDRIDIRKDGNNHKKQFYVILKL
NNEIIRKQLFNDTPLDEVLLSTSSFLPQTLFLQI
"

gene      complement(43065..44414 /locus-tag="SSP0036"
)
CDS       complement(43065..44414 /locus-tag="SSP0036"
)

/note="similar to
gi|49484945|ref|YP-042166.1|
[Staphylococcus aureus subsp.
aureus MSSA476], percent identity
92 in 448 aa, BLASTP E(): 0.0"
/codon-start=1
/transl-table=11
/product="cassette chromosome
recombinase A"
/protein-id="BAE17181.1"
/db-xref="GI:72493860"
/translation="MKQAMGYLRQSTTKQQSLAA
QKQTIKVLAEKHNIQHITFYSDKQ
SGRTDKRNGYQQITELIQGQCQDVLCCYRLNRLH
RNLKNALKMLMKLCQTYHVHILSVR
DGYFDMNKAQFDRKLKLNIFISLAELESDNIGEQQV
NGLREKAKQGKGLITTHAPFGYHYH
NGTFTIDTVKSPTVKAVFNYYLQGYGYKKIAQYL
EADNKFINRKPYQVRNIIILNPNYC
GRVINQYQYENMFPAIVSTTIYEEAQVTRTQKQ
VKRKPSENQLKQIKICPYCHSTLT

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NMTVRKPDHSLRYYVCPQNMNNARFVCEFGKGINA
QELETSVLATCQDFFQNOQLYSKI
NHTIQRLKKQKDIEAKNTLTQEQLIEKLAQGKI
DAESFRKQTQSSRQHSKPILSINA
YQIQKAFQNI IQORFTLNMLYPYIDEIHINKNKT
LTGIYFKNEPLNIVNQTQTSTIA"
gene      complement(44592..44849 /locus-tag="SSP0037"
)
CDS       complement(44592..44849 /locus-tag="SSP0037"
)
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="BAE17182.1"
          /db-xref="GI:72493861"
          /translation="MKTNVNLLNYTIDSVEVDDH
QKSIIVNYIDRYYHIQQYVLNETE
QKLLKFYHLYPEFMNEKEITEHFIPSTRLERITM
QHVINSI"
gene      complement(44914..46704 /locus-tag="SSP0038"
)
CDS       complement(44914..46704 /locus-tag="SSP0038"
)
          /note="similar to
gi|14020968|dbj|BAB47592.1|
[Staphylococcus aureus], percent
identity 74 in 522 aa, BLASTP E():
0.0"
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="BAE17183.1"
          /db-xref="GI:72493862"
          /translation="MSNNIFKQYPYWLSTGWYE
LIRAKNKNDKDIIRLSPPIIEN
KFLDPTTGVEKLTITDGKNIERIETSDILTQKL
PRLVMFGFSINEKYIKSLGNALQL
MRQSLPISTLYTGVGVLSLDEGTVISLDEPYLSK
DIKQSQADEIICETKYDLQPKGTF
EGWQWQMYLDEVKGNLLELAVIFGVSSLVTAFLK
TKHEVEYFGTIFSGMNSSTGKST
AAALAVSIAGNPSKGDQTLFRGNWNGTRNAIEGYL
SNNFGVPIALDELSAATFKDTNGL
LYSLAEGQGRRLANREGNVKNPHHFGSSVISTAE
HTIFKDASANDGLRARCIEISDVF
TTSADNADAIKKGTSKNYGHVMPLVAEYLLNRES
EVIKWFHKEHDWFKAQLNNETNNV
GIRMFKRYATITTSARILERVATPIDLVAVREY
LVSYHVDVSERSLAAKAIDSVVQ
FVARNRSKFAESKKLSIMTENYGLIELKDDHIQV
KMLKDVFHKHMLEENQYQDVKNVID
SLRAEGYIQMDSRIAIRNVKDTQGKTKTILFY
HLVLPSEFAPVLGLSSDSEPYTPP
QFDNNTTNKGLLNKFVKDGREWEKGDLEL"
gene      complement(46830..48257 /locus-tag="SSP0039"
)
CDS       complement(46830..48257 /locus-tag="SSP0039"
)
          /note="similar to
gi|17025996|dbj|BAB72124.1|
[Staphylococcus aureus], percent
identity 87 in 476 aa, BLASTP E():

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0.0"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17184.1"
/db-xref="GI:72493863"
/translation="MNFENYKYFTGKDLMKECNL
SEKMFKNMMDKLERVYKLDITRYK
SNPSATNSGYSFNLFELELFKILLNNIEDFPVPT
SAKKFDDIDLREELKKNNQFIS
YITNISDSIDNKKNDALKAQIYASENYSFTLEWL
SAQSKCNDALSSFFNYTNSLDLDDK
SSKLYRKLAHRIDELLFETLMDNMFTDNDNFNK
QLYKAHQYNKENNPENFIYQVE
PDDSKYSNVNHEVARYISNEPTIDEYSERTDNKL
LDFFIIDILNKLYLPSLNKRINH
IVTDDIQNDESKIREKLKKEIVKYPFNVNGYFL
SIENDLFSNYQRIINTINQYKNST
FDLQNFESRLDNIINSSKPLISNDKFLNIYKEYF
LSLSKFSNLFYTNRQSYIDDMGMS
NQVESFLNDLYRIHLLLDKYSFNEDIEPLSKTNI
TELTNAFHLFEEIKSTQIKDEIVS
KQVNDLSSWSIAKTLSETLDNLKFE"
gene      48684..49877
CDS       48684..49877
/locus-tag="SSP0040"
/locus-tag="SSP0040"
/notes="similar to
gi|23128205|ref|ZP-00110058.1|
[Nostoc punctiforme PCC 73102],
percent identity 31 in 394 aa,
BLASTP E(): 3e-50"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17185.1"
/db-xref="GI:72493864"
/translation="MDNDEKLLVEFLKDVLDILNE
IEANVDNFNVFELGTINTEIRHS
NMLAWLFNPNVEVHGLDLFKKFFIEIYLNKSSVE
MDDSFVLKMLLKDFDDVIVRREWN
HIDILLISEVNVKIFAIENKIWSKESKGQLNRYQ
HVLESEFFDYEKNYIFLTPEAEDS
SDIDTWISMSYIDVITCLENIVSMKKEINPKVT
SFINQYIDILRRYIVKDLENLEKLC
TEIYFKHRALEDLIFEYKPDIHSDISNKLQSIVK
ETESLILDSSKSLVRFTSQKLDE
KMGRNNYESKWTSSNRYLLFEVRNNNNRKSLHLV
IGPSDEETRKNLHEKALAHNPVFK
KVKKKLSPVYNNIYTKELYSSNKQFEYEDIITEV
EKNFEQFLTHELHKIEIILLNEEI SYNTK"
/locus-tag="SSP0041"
/locus-tag="SSP0041"
/notes="similar to
gi|16802510|ref|NP-463995.1|
[Listeria monocytogenes EGD-e],
percent identity 22 in 599 aa,
BLASTP E(): 6e-22"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17186.1"
/db-xref="GI:72493865"
/translation="MEMNSYMIENFATDAVKNYC

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LHTSKIYSIANEDKEPGYDGLHK  
 IYDSISQTKDDYLGNIPIVQIKGKKAKKKHPSLEK  
 QNKVNKRDLLEYLKDGGCYFVVL  
 INENGESQVYGRQLLPMYLLKYLLKSKSKSVTIEM  
 YEITSYKDFYDNCIQYLKQSKKQA  
 NPIEFSINKKRNQKMTITSPENIVTDKNGFPLND  
 FYSFIHINDSDIKVTVPDEILRPE  
 RFSKLQKGSIIYSEKVIYEGNIRFDVTSITYTSII  
 IDESFYLTKYNESKKAKYSLLPK  
 NIDRYLEVNLVKLSLNGGEFIFEDVQVILDKFK  
 LDKSIDRLTSILTQFKQVTVETDN  
 LIKSTIINDDNIEKQLGEMVGIKIIKNKEFNA  
 YNMKKDKFYKILFGNNNFILWKYN  
 NVIYNVFSDFLKRVELVDNETMLAIYSFNTSF  
 MINTINFDFQLEKYLKTEDFSNI  
 SIQKWNYYINNFCLELIKSYDITKELGFLNIAEFI  
 LSNIDIKDIDSTFITKINLAQVKI  
 RKDERLESDLKKLLVELKSKLKSINDDASLHLS  
 IIFGSKTEAMIYFENLSEELGVF  
 KNYPIYYLYQKLL"

gene 51947..53422  
 CDS 51947..53422

/locus-tag="SSP0042"  
 /locus-tag="SSP0042"  
 /note="similar to  
 gi|14021054|dbj|BAB47678.1|  
 [Staphylococcus aureus], percent  
 identity 90 in 491 aa, BLASTP E():  
 0.0"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical protein"  
 /protein-id="BAE17187.1"  
 /db-xref="GI:72493866"  
 /translation="MLSDNIIKELYSKEDIRIEL  
 ELTPHMFNKRMETIAKLFKIDMKN  
 FHNKYGQDKNNQYTFNGVAKELIKVLLKSDVYYP  
 VDINSKDFKQNGQPKKEMIENTISA  
 SSYMYYTYQLMKAINIEIQYKRLIADIHMKDVYQN  
 TKAWLGIGESINKKEQELYQYMKP  
 LPLHKRIELQNEVLKSIDETIFQFMAKEHRNTQI  
 KENNELEEYTNAIKEGKYPKKDYE  
 LNHLLYKKNEIPLDSLKDWDYDETEYIELDWL  
 IADMLKRSQRASNFIESLEKKNK  
 LRKNIHKDSIKSISRLIDHVELKNNRKNWDAEFY  
 KNQQFWNSSSLRRNSQKFGILYYK  
 KNRLHTMNSNIKKIKIIEANLESANKQPSYLD  
 FFLQAKFDLERLESELMKYSINPK  
 YYNKINSYVRYAIEDVHNNAIKIDRYISNDKVK  
 VNYSNAQMVRNEITEQGSYFVQ  
 ALNMVSKVEESGYFDNFMVGPFFVEDFKKAIKNR  
 RFGSKTD"

gene 53649..54749  
 CDS 53649..54749

/locus-tag="SSP0043"  
 /locus-tag="SSP0043"  
 /note="similar to  
 gi|14021052|dbj|BAB47676.1|  
 [Staphylococcus aureus], percent  
 identity 87 in 366 aa, BLASTP E():  
 0.0"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical protein"  
 /protein-id="BAE17188.1"  
 /db-xref="GI:72493867"

gene 55110..56750  
CDS 55110..56750

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/translation="METRDKLMSLTQSNKTQQWL
MDKSSNQDYVQQLQQQFSQQLDQQ
YNALLADEKAKLDQYVEVHHNLEVLKKEIESEPI
MLNIDKLPIKSTMLEKAKNDEHS
DRIEKLFDRLQALNGTNRLYTQLSLIGTRTHRI
TTKNFNLQGLPKAVQRTILPSKYK
KVYTVDFKSFEPSPVVAYMTQDSKLIDFLNQKDGL
YDALLSELELQDEQRVLVKRAFIG
SFLPGGNFDSPKFKLKQYVSEVQWLDVAVSQFTKV
IELKKQIEEHKTIPMPYIGIEHDS
AFQGSISIMAFYVQTVASYIFKHILLEVYKAQCTQ
KSFGIILPIHDAIMIECDDEETAQ
SVAQLMKSANKLFNGEFAHVTVEALGGVSN"
/locus-tag="SSP0044"
/locus-tag="SSP0044"
/note="similar to
gi|49257044|dbj|BAD24833.1|
[Staphylococcus aureus], percent
identity 81 in 547 aa, BLASTP E():
0.0"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17189.1"
/db-xref="GI:72493868"
/translation="MNHILETLIKLLKVGMEAID
RKGLIAILTSSIGNDEDDSEQAV
MVYNELIDKLQLNIPKDVDRPNIYSYFGIQKPK
NDTILVEMMISIFHKIRFDSSELFV
FKDKGWQKVNDELQGLISKMIQVLLVDYKPSLS
ILKNVVVGLQNSIDVEELVENKQY
IGCGHNMFNLDAFEVVGNSIKIFPATRLNLELVK
SDVITEKTPPHFNRYMLEFANFDS
DLQYFLFOHIAVLLTANTKYRRALLLYGGAKNGK
SVFINLVRSFFYSIEDIVSKALNEL
QGRFDKESLVGKKLMASDEIGESRIQEKIVNDLK
KLVSVEPVHVDRKGTQVETLLD
KLAFTGNARLNFFSAHAKALERRIAVIPCEYYVE
KADPDLEKLQDEKKEIFLYLMYV
YKQIVKNDIEYLQNDRVTEISHDWLNFGYEFVSS
KSASIANQKACINLLRLKLEIKPG
SRIKVSSELNKNVINEIKVSSQVIKQLIQANFDTQ
TKLYNGDYDWIDLGWKEADKKEIH
DISKKDNIISLDKKNENITDDETLDEENLDFDWD
FDDE"
/locus-tag="SSP0045"
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/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17190.1"
/db-xref="GI:72493869"
/translation="MNNEQIEAFVEVLVPIIEER
INKGK"
/locus-tag="SSP0046"
/locus-tag="SSP0046"
/note="similar to
gi|49257045|dbj|BAD24834.1|
[Staphylococcus aureus], percent
identity 95 in 537 aa, BLASTP E():
0.0"
/codon-start=1

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gene 56743..56820  
CDS 56743..56820

gene 56975..58657  
CDS 56975..58657

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/transl-table=11
/product="cassette chromosome
recombinase C"
/protein-id="BAE17191.1"
/db-xref="GI:72493870"
/translation="MSGKIALYSRVSTSEQSEHG
YSVKEQEQVLKEVVKNFPGYDYE
TYIDSGISGKNIEGRPAMKRLLDQVDNKKIEMVL
SWKLNRIISRMRDVFNIIEHFEKH
GVGYKSIENIDTSNASGEVLVTMFLGISIERS
TLISNVKMSMNAKARSGEAITGRL
QGYRLSLNPLTQKNDLVIDEENANIVREIFDLYL
NHNKGLKAITTVLNQKGRTINQK
PFSVYGVKYILNNPVYKGYVRFNNHQNNAVQRRS
GKSDKNDVILVKGKHEAIISEEVF
DQVHEKLASKSFKPGRPIGGDFYLRSLIKCPECG
NMVCRRTYYKTKKSKERTIKRIY
ICSLFNRRSGSSACHSNAINAEVVERVINVHLNRI
LSQPDIIKQIASNVIELKQKHSN
QTEIKYIDISLEKQAKLKTQQRLELFLDDQM
DSEMLKAKQSQMNGQLKMLDKQIK
EAQQATESQDEVNPFDKLSRLTMMISRFSVYLR
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YGTQKYSIDKITTATLS"
/locus-tag="SSP0047"
/locus-tag="SSP0047"
/notes="similar to
gi|16579848|gb|AAL26663.1|
[Staphylococcus aureus], percent
identity 93 in 112 aa, BLASTP E():
6e-58"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17192.1"
/db-xref="GI:72493871"
/translation="MTLELQKHYYITNLFNLPRD
EKWECESEIEVADDILPDQYVRLG
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AIGFIDENHDMDFLYLHNTVMPLL
DQRYLLTGGQ"
/locus-tag="SSP0048"
/locus-tag="SSP0048"
/notes="similar to
gi|14021046|dbj|BAB47670.1|
[Staphylococcus aureus], percent
identity 95 in 103 aa, BLASTP E():
2e-51"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17193.1"
/db-xref="GI:72493872"
/translation="MNRYITRGIDNNLPILQQQ
LWKLVQAQRENEQSKELEAIDYFHI
QFNMHNDQLCICKKQERPEYIKTHKANYSKAIN
IKKVYIIRDDVDLSYYVMLLPEE Y"
/locus-tag="SSP0049"
/locus-tag="SSP0049"
/notes="similar to
gi|22094438|gb|AAM91898.1|

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gene	58756..59094
CDS	58756..59094
gene	59190..59501
CDS	59190..59501
gene	59517..60023
CDS	59517..60023

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[Staphylococcus aureus], percent
identity 75 in 168 aa, BLASTP E()):
5e-71"
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/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17194.1"
/db-xref="GI:72493873"
/translation="MQNIQCILETEAIFSDDNQH
RYLLKKTWDKDKKIISVITCYPNF
EGTKKLDLTTQLILNKVSEMKDFGSINFVNLYSN
MITTNIKHMANSHDKHTDIHMK
VVKESDEVILAWGAYAKKPIVEMRVNEILEMLKP
HKKKVKQLINPETNEIMHPLNPKA RQKWILKS"
/locus-tag="SSP0050"
/locus-tag="SSP0050"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17195.1"
/db-xref="GI:72493874"
/translation="METKQINIVSLQMIKIDTSL
YLKRRITSPHQIVKYNSRVFLIMH R"
/locus-tag="SSP0051"
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/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17196.1"
/db-xref="GI:72493875"
/translation="MIVGNHYHNEVDEYTSKLV
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ALPDEEDIPELEKEKQKLIERYG"
/locus-tag="SSP0052"
/locus-tag="SSP0052"
)
)
/note="similar to
gi|7658152|gb|AAF66082.1|
[Lactococcus lactis subsp.
cremoris], percent identity 35 in
438 aa, BLASTP E(): 2e-60"
/codon-start=1
/transl-table=11
/product="putative restriction
endonuclease S subunit"
/protein-id="BAE17197.1"
/db-xref="GI:72493876"
/translation="MTNEVKNVPKLRFRFEDEM
KKKRLKDIVEPLKGNKSGENKLPV
LTISAKKGWLNQKFRFSQVIAGNSLSKYNELKKG
DLSYNGKSKVALYGIVYKLGFDN
ALVPNVYKSFPRKPNVSDFELEKYFHTKILDRQL
RRVITSTARMDGLLNSIDYDFYNM
SLNIPVNNQKKIGDFFSKLDQQIELEEKKLAKL
EEQKKGVMQKIFSQELRFKDENGN
DYPEWEEINLGSLYKKGKAGGTPKSTESKYNGK
VPFLSISDITKQGFNLNTEKKIT
QEGLDNSTAWLPVNSINYAMASVGYLSINKIE
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CDS       complement(61908..63464 /locus-tag="SSP0053"
           )
           /note="similar to
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           in 518 aa, BLASTP E(): 0.0"
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           EIENQRFDIEHLVQAIRKQVETSTLQNSSEEDFIG
           LFSMDLSSTRLGNTVKERTALIS
           KVMVNLGDLPPVHSDMEIDMLGDYAEFLIGRFAA
           NAGKAGEFYTPQQVSKILAIQIVT
           LGKDKLRNVYDPTCGSGSLLLRVGKETTIVYRYNG
           QERNNTTYNLARMNMLLHDVRFEN
           FDIQNDDTLNPAFEGEKFDVAVVANPPYSAKWSA
           DSKFNDDERFSNYGKLAPKSKADF
           AFIQHMVHYLDDEGTMAVVLPHGVLFRGAAEGVI
           RKYLIEEKNYLDAVIGLPANIFYG
           TSIPTCVLVFKKCREADQDVLFDASNEFEKGKN
           QNHLTDEQVEKIIATYKNREAVDK
           YSYAANLKEIDENDYNLNIPRYVDTFEEEEPVDL
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           LKELGVYKHD"
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CDS       complement(63578..66370 /locus-tag="SSP0054"
           )
           /note="similar to
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           aureus MRSA252], percent identity
           75 in 928 aa, BLASTP E(): 0.0"
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           /transl-table=11
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           restriction-modification system
           restriction subunit"
           /protein-id="BAE17199.1"
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           CQNKFOITNQVSDVDDTYKARYDVTILINGPLPVQ
           IELKRRGIDINEAFNQVMRYRKQN
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 KDAIHGDNVLGFSVDYINTIKAQN  
 IDTETDELVEGINTDEVWLSQDQRELIARHITEN  
 HDKYTRNRQYSAIFTVQSIPALVK  
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 KLFSTQEDTDRVLMRDYDEYKAEF  
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 LVSKLVRLKAFDEFDTKANIGM  
 NEQEFEDYKSKYFAIYDEVKPKRGEVEKVSILND  
 IDFEIILRNDRIINVSYIMDLVRQ  
 IDLKDKAEQQRNRDQIRRMNLNADDFTLRLKRD  
 LREFIDDVPELSEEDNIDEAYIL  
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gene 66627..67700  
 CDS 66627..67700

/locus-tag="SSP0055"  
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 gi|28829800|gb|AA052302.1|  
 [Dictyostelium discoideum],  
 percent identity 25 in 344 aa,  
 BLASTP E(): 8e-23"  
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 /db-xref="GI:72493879"  
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 SQNSRTITIDEAKSIAFNSEIDILN  
 FTQNKDELIYNKDKSNNDIEFETPFGGINESVK  
 HHAIIDKNTGKIIKTGGAITSPDG  
 PIKAENGYIDKDIYNSTDDFYNTYVYKGMPEFE  
 TATSDVPEQKYKELSNIVGNYWQK  
 EQGYDNESNQSTSNNNQSQNEKNNQTSNDSKQS  
 TKDKAKVDQNRNIETNNDESQK  
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gene 67735..68484  
 CDS 67735..68484

/locus-tag="SSP0056"  
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 gi|55820776|ref|YP-139218.1|  
 [Streptococcus thermophilus LMG  
 18311], percent identity 51 in 251  
 aa, BLASTP E(): 1e-62"  
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 /db-xref="GI:72493880"  
 /translation="MVSVTQRISQIKQPRGYLN



gene 68526..69032  
CDS 68526..69032

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QTIGLVVDYLTRMVINQDKEKSFASILTGA  
ELQTAESLLKNDNDLSIIKAC  
QLVNYDMVYRAGSMPEKFKIPDQDTINN  
RSLFFNQIGEVKMDGFTFEGGYT  
SIIDTGDGDFLTEDTLWDFKVSQLPQKN  
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YD"  
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/note="similar to  
gi|17227189|ref|NP-478355.1|  
[Staphylococcus aureus], percent  
identity 56 in 157 aa, BLASTP E():  
1e-39"  
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IASVEP  
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gi|17227189|ref|NP-478355.1|  
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identity 52 in 149 aa, BLASTP E():  
5e-37"  
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hypothetical protein"  
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INNNM  
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/note="similar to  
gi|57285193|gb|AAW37287.1|  
[Staphylococcus aureus subsp.  
aureus COL], percent identity 76  
in 284 aa, BLASTP E(): e-122"  
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/transl-table=11  
/product="UTP-glucose-1-phosphate  
uridylyltransferase"  
/protein-id="BAE17204.1"  
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VAAGIEDIIIVTGKHRAIEDHFDNQKELE  
MILE

gene 69029..69502  
CDS 69029..69502

gene 69784..70647  
CDS 69784..70647

gene	71017..71685	EKGKSDLLQSVKYSSNLNMFYVR
CDS	71017..71685	QKEQKGLGHAIWTARQFIGNEPFAVLLGDDIVQA DTPAIKQLMNQYETTGSIIIGVQQ VNEIETHRYGIVDPEESYNELFSVNKFVEKFEIG TAPSNLAIMGRYVLKPDIFDYLER QEIGRGGEIQLTDAIEHLNSEDVCVAYNFEGERY DVGEKIGFVKTTIQFALKDDYMKK EITEFIKSINK" /locus-tag="SSP0060" /locus-tag="SSP0060" /note="similar to gi 506697 gb AAA64640.1  [Staphylococcus aureus], percent identity 62 in 221 aa, BLASTP E(): 2e-72" /codon-start=1 /transl-table=11 /product="capsular polysaccharide biosynthesis protein" /protein-id="BAE17205.1" /db-xref="GI:72493884" /translation="MEETIDLNKLFAILKKNMKY LIILPIVFLVLSMMMTFLFITPKY SSSTQVLVNQKETDSOMMAQVQSDQLQLVNTYSE IKSPRILDKVSKNLKGYSSEI AGMLTVSNQAESQILNIAVENESREAAGKVANEI ANVFSKDVNKMIMNVNVSILSKAD YVSGKSDSPKPLINAVVGVLGLIVALIIIFLKEI LDKRKIKTEEDVEELLDLPVLGVQI RFDY" /locus-tag="SSP0061" /locus-tag="SSP0061" /note="similar to gi 506698 gb AAA64641.1  [Staphylococcus aureus], percent identity 65 in 229 aa, BLASTP E(): 2e-80" /codon-start=1 /transl-table=11 /product="capsular polysaccharide synthesis protein" /protein-id="BAE17206.1" /db-xref="GI:72493885" /translation="MAKKIDTEITTLITHKKPKA VVSEKFRGIRSNILFSTADAEIQT LLIASDKPSSGKSTVSANIAVTYAQAGFKTLID GDMRKPTQHYIFNKNINIKGLSNVI INKSTFEDAVYSTEVNLNLDVLTSGPIPPNPSELI GSSNMMDLFEELKQRYDFILIDTP PVNTVTDQQLFGELTKNAVYIIDVETNNKESVKK GKNLLEKSGTKILGAVLNKAQLDK SSSSYYYGEEES" /locus-tag="SSP0062" /locus-tag="SSP0062" /note="similar to gi 49484857 ref YP-042081.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 54 in 251 aa, BLASTP E(): 1e-76" /codon-start=1 /transl-table=11 /product="capsular polysaccharide biosynthesis protein"
gene	72393..73157	
CDS	72393..73157	

gene	73181..75016	/protein-id="BAE17207.1"
CDS	73181..75016	/db-xref="GI:72493886"
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		/locus-tag="SSP0063"
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		/note="similar to gi 506700 gb AA64643.1  [Staphylococcus aureus], percent identity 73 in 599 aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="capsular polysaccharide biosynthesis protein"
		/protein-id="BAE17208.1"
		/db-xref="GI:72493887"
		/translation="MKYISIKQRFMMLLFIDSII VTFSVFLGYIILEPFFKGYINVL ILSSLILLISHHVFAQIFDLYHRAWAYASVSELI LIVKSVTSSIVATGIIIVIFTQA PFLRLYFITMMHLLLIGGSRLSWRIYRKTFISK EGKKKPTLIVGGGRGSLLIQMM NTPYMGMEPVLVDDDSNKQKMSIASGVKVQGC KDIPELVKKFNKIKIIAIPTLSQ QRLREINKLCEGTNVEVFKMPNIENVMGSEIEVN KLKKEVEDELLGRDPVELDMASIS KELTHKITLVTGAGSGIGSEICRQVCKFTPDRIM LLGHGENSIYHIHQELIGLYKEEI EVIPIIADVQDKERMKKVMQAYKPYVVYHAAAHK HVPLMEYNPQEAIKNNVLGTRNTA EAAKLAEVSKFVMVSTDKAVNPPNVMGASKRVAE MVIQSMNNETSKTDFVAVRFGNVL GSRGSVIPLEKKQIEAGGPVTVTHPGMTRYFMTI PEASRLVLQAGALATGGEIFVLDM GKPVKIVDLAKNLIRLSGYKEEDIGIEFSGIRSG EKLFEELLNKDEIHFEQVYEKIYR GKVQKIEKEELYNKIDDFLINESVRDEIIFVNN NKTGEEKCKMD"
gene	75001..75765	/locus-tag="SSP0064"
CDS	75001..75765	/locus-tag="SSP0064"
		/note="similar to gi 56964929 ref YP-176660.1  [Bacillus clausii KSM-K16], percent identity 38 in 248 aa, BLASTP E(): 2e-45"
		/codon-start=1
		/transl-table=11
		/product="putative glycosyltransferase"
		/protein-id="BAE17209.1"
		/db-xref="GI:72493888"
		/translation="MQNGLVSVIMPLYNNEDYIE KSILSVINQTYENWEILINDKSV

gene 75762..76850  
CDS 75762..76850

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EKQINFMKNNDYNFTCTYYGKMDSSENSVLPTVIK  
PKYSLNYNQILKNNIGNSTAIINV  
KKLGKFTVPLIKRNDYALWLKVIKAKKVHTLE  
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IL"  
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/note="similar to  
gi|28211867|ref|NP-782811.1|  
[Clostridium tetani E88], percent  
identity 28 in 273 aa, BLASTP E():  
9e-22"  
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transferase"  
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KINENNESEVFYPRKNGYTYNNNQ  
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NEFSIIHAHTLYTDGYQAYILNKK  
YNIPYIVTVRSDIDINIFYKYRKDLYFIARNIKN  
SKGIVFLSKSYLTRTEKLFNINLK  
SKSNIITNGIDDFISNIYNKPKYNDNTKTILT  
VGYISKRKNQKICKAINKLNKRGY  
SIKYVIGKSLDKILRKILKYSFVEYKEFMDKN  
TLIKEYRKADIFAMASLHETFGILT  
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gi|57285349|gb|AAW37443.1|  
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aureus COL], percent identity 29  
in 404 aa, BLASTP E(): 5e-47"  
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synthesis protein"  
/protein-id="BAE17211.1"  
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NILSINIGAINLILFCIFTFLANNRNYFMVNYRL  
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FLNYLDRFLIIPILGAASMGYFAASAISKIIM  
ILTPINNVLSSHITNLDNMNKRRL  
LILLYLITLLFIPLFYIINFSNFLVDILYINL  
ADEAKKLIPITIGILFNIVTNLL  
NNFLLKKYPITYQTIQFVYGVTVYLMAILLSTN  
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VLVFKQNKQKN"

gene 76840..78051  
CDS 76840..78051

gene	78051..79217	/locus-tag="SSP0067"
CDS	78051..79217	/locus-tag="SSP0067"
		/note="similar to gi 2499141 sp Q48453 YC07-KLEPN [Klebsiella pneumoniae], percent identity 23 in 354 aa, BLASTP E(): 3e-09" /codon-start=1 /transl-table=11 /product="putative glycosyl transferase" /protein-id="BAE17212.1" /db-xref="GI:72493891" /translation="MKKVLVFSKTRGFFNHLFNT KFNGWMISLNNSEYKFTMKKKIL SLVGRSTILDIIGYIHTIKTVTNKADIYATYNRF LEANVPYIIYLENPTALFHYKLR YSTKMGRNLTKLINDKNLKAIVCMSEACREGFI KLYGPIIERDDLIIEQIYPLITEE KLQIDTRHNDNKKFSLLFIAQGGKGFISKGGIEV NTFIQLEKKIKNIELNIITSSNDI PPKILLKINSENINLIEFGISYDELKKYIESN VLIHLTRQDSFGLTILEAMKYGT VITTKLYSIPELIKENKGYLTPEPSYWFFNQENL PNPAVWNRRNTIFS KKS SDEK FLYDKIIYLYENREDYNQLKDTAYRNSKEKPFSE EFIINKWENLLNKIEMRKEK" /locus-tag="SSP0068" /locus-tag="SSP0068" /note="similar to gi 45533027 ref ZP-00184022.1  [Exiguobacterium sp. 255-15], percent identity 62 in 330 aa, BLASTP E(): e-116" /codon-start=1 /transl-table=11 /product="putative UDP-glucose 6-dehydrogenase" /protein-id="BAE17213.1" /db-xref="GI:72493892" /translation="MNYNSLNRFSNNLESSLED AEYIIATPTDYDENNNYFDTSTV EEVIEKCIKMNDNATIIIKSTVPVEYTKKIKEKY NKKNIIFSPEFLREGNLYDNLYP TRIIVGEKSDKGKEIAELFRKGALNNNAKILLTN STEA EAIKLF SNTYLAMRVSFNE LDMYAEINDLNSKDIIEGVSLDSRIGEHYNNPSF GYGGYCLPKDTKQLKANYKNIPNN IISAVVDSNNTRKKFITNQIMSKNPKTVGIYRLT MKTNSDNFRYSSIQDIMHNLNEKT ELIIEPTYKEDTFENIKVEHDLKKFKNTSDIIL SNRYEKDLEDVLNKVYTRDIFKRDR" /locus-tag="SSP0069" /locus-tag="SSP0069" /note="similar to gi 42784434 ref NP-981681.1  [Bacillus cereus ATCC 10987], percent identity 22 in 384 aa, BLASTP E(): 2e-17" /codon-start=1
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CDS	79372..80376	
gene	complement(80430..81650	/locus-tag="SSP0069"
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CDS	complement(80430..81650	/locus-tag="SSP0069"
	)	

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polymerase"
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ISITLYDTIKDGYLYKQSLVSIIFIFFIVYIFI
SYFYSPSADSLTKSLHFSLTSGWA
FIGSFLIIKSNNSFNKVFKGIIILALISSIFGLK
EYFNNTIHTQLNVFGSDYDLALGRL
LGISILILLANILLIKQSITNKIFTSMTTLFLL
ILIVSGGRAPLFLLIITILIFLLF
QVNLNNKTLKYNKLLPSFIVFLITVVLIFFKSNL
AIFETFKTRLFLTTSQGGGASAS
GRIDRFKIAFDMFKDSPYKGGIDFSKYYGMAN
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FSNIYRHNSINKN"
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/locus-tag="SSP0070"
/note="similar to
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[Staphylococcus aureus], percent
identity 74 in 185 aa, BLASTP E():
7e-78"
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/transl-table=11
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QTFILDMFIIYKTIIRNTITSEGVKH"
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/locus-tag="SSP0071"
/note="partial similar to
gi|49485038|ref|YP-042259.1|
[Staphylococcus aureus subsp.
aureus MSSA476], percent identity
52 in 109 aa, BLASTP E(): 2e-24"
/codon-start=1
/transl-table=11
/product="truncated capsular
polysaccharide synthesis protein"
/protein-id="BAE17216.1"
/db-xref="GI:72493895"
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FKVALLRSSMIYGESAPGNFSKLI
KLSKHFTSISSN"
/locus-tag="SSP0072"
/locus-tag="SSP0072"
/note="partial"
/codon-start=1

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gene	81821..82378
CDS	81821..82378
gene	82573..82917
CDS	82573..82917
gene	83048..83251
CDS	83048..83251

gene 84032..85018  
CDS 84032..85018

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NYNDDFITETEAYIKTLKHKHSRF"  
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/note="similar to  
gi|16129122|ref|NP-415677.1|  
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identity 50 in 74 aa, BLASTP E():  
2e-13"

/codon-start=1  
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/product="putative restriction  
endonuclease"  
/protein-id="BAE17218.1"  
/db-xref="GI:72493897"  
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QGGMRRSHLTNTLVLSNHNKNDVY  
RDHTVIDDEGNETLHYTMGQKGDQDIEHGQNKI  
LNHSEDLSIKVYLFESFISGEHIF  
RGEVRLYDKPYITEQNDRMVVFPPLTFNNSEYYI  
PGNISDEKYREQANLKNLSDNDI  
YERAIKVKQVGRKEAVTKVYARNIHVAHVKNRS  
NGYCDLCNKPAPFFKDRNGRAYLEC  
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SDVKFLKDRLNYYQSKNL"

gene 85137..88361  
CDS 85137..88361

/locus-tag="SSP0074"  
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/note="similar to  
gi|49482343|ref|YP-039567.1|  
[Staphylococcus aureus subsp.  
aureus MRSA252], percent identity  
58 in 1069 aa, BLASTP E(): 0.0"  
/codon-start=1  
/transl-table=11  
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protein"  
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EIRNNKSANIEQIFNDSKRRKFQQR  
FNEIIADEPINKDKLRLDATYRDFFAVLISETN  
GIFKHYFVIEYVKNSESPPDNFNS  
FFIGDIERARKDPNQTILKAYIEGINGEKRIEVD  
NKEIFDEFLHPANLPDGRWPSQIE  
HKLYLMQQLAVNQITSSKEHISTVNGPPGTGKTT  
LLKIDIFAHLVVERAKAFALDEPR  
DAFENFKIHETDTSPIKVLKEEFSKFKMVVASSN  
NGAVENISKDLPKMEEVARDHEGK  
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gene	92039..92248	NFYLKKEDEKPLYLSNDKYYVYKKNKYKKRMHII LQKIIKKDENIFLKLYSKNSELKY LEIKNRKDPNTYTVLEIKKHLFKTGEYTVQFKAN ELSKGKLALTVLDDKDLNGAAIKSG MQDFDYETVNGNLGYIKK"
CDS	92039..92248	/locus-tag="SSP0077" /locus-tag="SSP0077" /note="similar to gi 15894750 ref NP_348099.1  [Clostridium acetobutylicum ATCC 824], percent identity 34 in 66 aa, BLASTP E(): 6e-05" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17222.1" /db-xref="GI:72493901" /translation="MNQKGLKLKHLQKRKTIEY IPTINTLSEQDIYDVIFVTMKYSD FYNVVPTLAENKSNQIIFVGNMCH" /locus-tag="SSP0078" /locus-tag="SSP0078" /note="similar to gi 25010861 ref NP_735256.1  [Streptococcus agalactiae NEM316], percent identity 42 in 243 aa, BLASTP E(): 2e-42" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17223.1" /db-xref="GI:72493902" /translation="MQKRNDIFVKLLLEKASIQNG MRVLVGCATGEVTOIVANKVGDDQ GEVIGVDMNQDMLHMAEENNQFENVKYIKGDIYN LPKDIGKFDAIVGRRVLMYLPGAY EALNVLKGHLKPNIGFCFQESDAINGGVGADNLP MHQKAIQLVVKTVSEGGDIHIGQ KLYILFQKVGVPVEFISEAVIQTSDNDNLKWLII DIMATRMKERQVVKSSFSIEQFLN DLTNESEKHHSFAIRDMAFGICGKI" /locus-tag="SSP0079" /locus-tag="SSP0079" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17224.1" /db-xref="GI:72493903" /translation="MKDCLSLAGLNYRLQKLSNI FIKPMNWHLKFLLVVMRIMTNYLI ITALYRFICLAYLILCLAIRSRNKMMLHLSINES SPPKSSVKLIHYFMSMLMWPILGT INFMPLTLTTYKGGEVHEVALDLSVLGIGMAIIG VLFSEKFISSKWMHLLFILSIVITI SWYVLEDILLFKVLMLLFLGLTFGGARIIFRKMII VTTYASHTVKHIYSLGNALGLPIL ALCIYLSILNLNFWLPSFILLIVLLFLLKIGHH ERISSHEKSPN"
gene	92485..93216	
CDS	92485..93216	
gene	complement(93543..94334)	
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gene	complement(94318..95466)	

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        laumondii TT01], percent identity
        30 in 349 aa, BLASTP E(): 2e-45"
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        LAIRTCQTLGITRGVAHVEIKIKG
        DQLYVIEAARPGGDAIMDLVENAYDMNPYQLHI
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gene      complement(95886..97382 /locus-tag="SSP0081"
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CDS      complement(95886..97382 /locus-tag="SSP0081"
)
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        12228], percent identity 84 in 493
        aa, BLASTP E(): 0.0"
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        TISNPFEFIRLPHISFVRGKNNVQFLKDRYEAM
        KEFFPMFNDIEYTEDIEEMRWIPL
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        GERTLLFGPFASIGPKFLKQGSNL
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        TKEGTMNHRLRTYPEARDEDWQLY
        NAGKRQVQIKDTPENGKGFIQFGTEVVNSDHTV
        IALLGESPGASTSVSVALEVLKN
        FPPEYKSEWTPKIKKMIPSYGQSLIEDPDLMRRT
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gene      98147..99811 /locus-tag="SSP0082"
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aureus MSSA476], percent identity
91 in 554 aa, BLASTP E(): 0.0"
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ESLSEVMTNAMRTATSGKNGASF
SIPQDVISAPVESQAIALCQKPSLGVPSQNVNE
VIEAIKNAKFPVLLAGMRSSSSDE
TNAIRKLVEKTNLPVVETFGAGVISRELESHFF
GRVGLFRNQVGDDELLRKSDDLVTI
GYDPIEYEASNWNKELDTKIINIDEIQAEITNHM
QPAKELVGNIAGTIELISDKVDEP
FISQKHLDELETLRAHILESTGKIPKTHEDGVLHP
VEVIKSMQKVLSDTTVTVDVGS
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AALVRPNTQVVSAGDGGFLFSAQ
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12228], percent identity 82 in 234
aa, BLASTP E(): e-112"
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MLSENLFSAVKISGTGFKKMHVRMPGQEPYPTRL
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12228], percent identity 70 in 533
aa, BLASTP E(): 0.0"
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gene	99870..100574
CDS	99870..100574

  

gene	100592..102196
CDS	100592..102196

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permease 2"
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TIIIAKNMSFKTAGHLLGLTVKEL
WISVLTICFILAVSKITTYGGLSNAMQGQISKTG
AAFPLLSPLLGWIGVFMGTGSVVNN
NSLFAPIQASVAEQIKTGSKLLVAANVAGGVTA
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gene      complement(102564..1031 /locus-tag="SSP0085"
96)
CDS       complement(102564..1031 /locus-tag="SSP0085"
96)

/notes="partial similar to
gi|15896604|ref|NP-349953.1|
[Clostridium acetobutylicum ATCC
824], percent identity 31 in 207
aa, BLASTP E(): 3e-22"
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transcriptional regulator"
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/notes="similar to
gi|57285035|gb|AAW37129.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 57
in 125 aa, BLASTP E(): 6e-37"
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superfamily"
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CDS	104039..104836	CTTSTGSIAGYITPETKKGEGISFLV"
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		gi 27468756 ref NP-765393.1
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		aa, BLASTP E(): 2e-67"
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		ASSYFFVVYAIVSIFSRPVCGRMLDAKNENIVY
		TSIIFQAICFLVIAFSHASAMLLI
		GGALLGLGYGNITSTSQSVSVVVPKEIARATS
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		HAPREILNPFSSRI"
gene	105104..106153	/locus-tag="SSP0088"
CDS	105104..106153	/locus-tag="SSP0088"
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		gi 15923298 ref NP-370832.1
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		aureus Mu50], percent identity 73
		in 349 aa, BLASTP E(): e-146"
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		LFGVTDDSFVPMIDGKKFNADNEVVVDLTKLKE
		KGFKLGDTLSSLQSDEKLKIVGFS
		ESAKYNASPVLSNNKTIENINPSLTEDKTNNAV
		VKDKDQSKDLNHNLEAIGIESFV
		KNLPGYTAQNLTNFMISFLFIISATVIGIFLYV
		ITLQKTNLFGVLKAQGFSSNGYLAK
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		SILTIRKVDPLKAIG"
gene	106172..106834	/locus-tag="SSP0089"
CDS	106172..106834	/locus-tag="SSP0089"
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		gi 31616138 gb AAP55232.1
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		identity 72 in 218 aa, BLASTP E():
		7e-87"
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gene	107587..108891	
CDS	107587..108891	
gene	complement (109057..109785)	
CDS	complement (109057..109785)	

		gi 15925187 ref NP-372721.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 71 in 240 aa, BLASTP E(): 1e-97" /codon-start=1 /transl-table=11 /product="putative regulatory protein SIR2 family" /protein-id="BAE17237.1" /db-xref="GI:72493916" /translation="MNQNIIEHLKKIIKDANQITF FTGAGVSVASGVDPDFRSMGGLFDE ISKEGYAPEYLLSAEYQLNDPEGFIDFYHKRLLL ADKQPNVVHEWIAQLEHHQRLSLGV ITQNI DGLHTDAGSANVDLHGLTLNRFYCIQCEH KYDKATVMAKPLRHCECTCGSPIRP DIVLYGEMLDQQTISNAIQKIQEADTLVVLGSSL VVQFAAGLISYFEGQHLIIINKDA TPYDRDADVVIHDDMVVVNAIRD" /locus-tag="SSP0093" /locus-tag="SSP0093" /note="similar to gi 49484408 ref YP-041632.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 68 in 287 aa, BLASTP E(): e-114" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17238.1" /db-xref="GI:72493917" /translation="MKKLWIWGASIIAIVIVVGI VMVAVFSQKPSKVTHSKFVNHP PTLFLHGYGGSANSEKFLVQQAENKAVTHDVITA VVSNGNVITFKGQLNKNAINPIVK VELENNKGDGYDKNAKWFKNVLVALQKEYQFKQF NFVGHSMGNLSFATYMLNYGNDAS LPRLNKQVNIAGTFNGVLNMNEQVNEISVDKEGK PSRMNPPYQQLRELKAIYQKGQIK VLNIYGDLEDCTHSDGRVSNSSSKSLKYLLSSSP ESYQESKYHGKQAQHSQLENRDV ANEIIKYLWGTG" /locus-tag="SSP0094"
gene	109992..110858	
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gene	complement(111330..1117	
	19)	
CDS	complement(111330..1117	
	19)	

gene	112362..113207	NILINIRKICVLLWKKNSRKKFLMKKA"
CDS	112362..113207	/locus-tag="SSP0095" /locus-tag="SSP0095" /note="similar to gi 24113127 ref NP-707637.1  [Shigella flexneri 2a str. 301], percent identity 39 in 246 aa, BLASTP E(): 7e-41" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17240.1" /db-xref="GI:72493919" /translation="MSTEIKGITFFDNLVDISS HACNTFNVNPTYKELFFDNNVYIM SSAQGGKFRLSNNHPLKVANYAQIEQYAIFFVGNV FHTMGAFSSINSQLFPVNTIVGRYS SIAAQVRRMAGNHMPMERFTTSMITYSKNTCAFND YLDAAGVEFDHRPSTVGGMEPIVI GNDVWIGQDVLFSKGIAGVGDGAIVAAGSVVTKN VPPYAIIVGPNPAKVIYRFEAHII ERLLKLKWWQYGFADFKGVTADDSIEVFLEKVEK LVSTNIQIQPFRPTTISVKDFLDIE KSSEE" /locus-tag="SSP0096"
gene	complement(113511..114047)	
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gene	complement(114117..115025)	
CDS	complement(114117..115025)	/locus-tag="SSP0097" /note="similar to gi 29345868 ref NP-809371.1  [Bacteroides thetaiotaomicron VPI-5482], percent identity 39 in 290 aa, BLASTP E(): 4e-49" /codon-start=1 /transl-table=11 /product="putative truncated beta-mannosidase precursor" /protein-id="BAE17242.1" /db-xref="GI:72493921" /translation="MCACKYQLYSCMGAYYPSD



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CDS      complement(114929..1160 /locus-tag="SSP0098"
29)

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gi|21436685|emb|CAD33708.1|
[Thermobifida fusca], percent
identity 32 in 339 aa, BLASTP E():
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74)
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74)

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percent identity 47 in 80 aa,
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CDS      complement(116343..1168 /locus-tag="SSP0100"
52)

/note="similar to

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gi|1723203|sp|P55178|YAG5-STALU
[Staphylococcus lugdunensis],
percent identity 52 in 131 aa,
BLASTP E(): 2e-35"
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amidohydrolase"
/protein-id="BAE17245.1"
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KISSLIETHYTNADIIVLPEMWN
GYALNQLKDKADIDLQOSLPFIQQLAQQYTHIV
AGSVANMRTNAIYNTAFVSKDKT
LLNVTDKIHLVPMLEDPFYLSPLGNQPNFNSING
IQASQIICYDLRYPEVARASIKND
ANFITSTCH"
gene      complement(116858..1175 /locus-tag="SSP0101"
14)
CDS       complement(116858..1175 /locus-tag="SSP0101"
14)

/note="similar to
gi|16081122|ref|NP-391950.1|
[Bacillus subtilis subsp. subtilis
str. 168], percent identity 49 in
220 aa, BLASTP E(): 3e-63"
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hydrolase"
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ISEALKIPIFTYKNELPYINGELP
YPNKTHTENTGVQYIVKPLETNTNLPFNYYLTPG
HAPGHVVIYFHNQDKILICGDLFIS
DAQHLHIPIKKFTYNTMTENIKSGQIIDNLCPKLI
TTSHGDDLYSDDIYSIYKFYEE"
/locus-tag="SSP0102"
/locus-tag="SSP0102"
/note="similar to
gi|15613300|ref|NP-241603.1|
[Bacillus halodurans C-125],
percent identity 43 in 88 aa,
BLASTP E(): 3e-14"
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regulator"
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/translation="MKLNMSDYGSCNLVIQRCGP
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YFYNALHREVSIGSRKILTEQLNDLIALQIVKRE
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NELAQVLKMN"
gene      complement(118073..1189 /locus-tag="SSP0103"
18)
CDS       complement(118073..1189 /locus-tag="SSP0103"
18)

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gi|2462704|emb|CAA74935.1|
[Staphylococcus xylosus], percent
identity 78 in 276 aa, BLASTP E():
e-128"
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transcription activator"
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SSIVDTHVLINKNTKDIQSIKKICNL SQT IQSN
NSHDILIMQHIIYQLVYALQDKFPK
HFSVQVDIVNEDIQYAVEYINSNYQKDITIVDVA
KSVNISRSHLFKLFKRNLCSPKE
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identity 88 in 462 aa, BLASTP E():
0.0"
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PQTAMYVYISILYISWGMYTMMDIPYWSWLPNL
THNPREREVSVIPRFFASLAAFT
VGTFGLYFIHQLDGVFGNGSDSVGIFIFAIICSA
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MILCEMVGLLLLPRIKWKVGRTKAFNTAVSFII L
GLLIILIIAGFIAPKSTLLIILGAG
ILRIGSGFMIGITTVSLADVIDYGEVKFGQRNES
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TAFLYHKFANLKGDFLTDIEKTLQ
FKRQREHRRERIK"
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/note="similar to
gi|2462706|emb|CAA74937.1|
[Staphylococcus xylosus], percent
identity 65 in 991 aa, BLASTP E():
0.0"
/codon-start=1
/transl-table=11
/product="beta-D-galactosidase"
/protein-id="BAE17250.1"
/db-xref="GI:72493929"

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CDS	119102..120490
gene	120502..123480
CDS	120502..123480

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PYVPRENP CGRYKRSFEINDYNEQSDYHLNFEGV
DSAFYIWIWEQFVGYSQIAHSISE
FDITPYVQKGINSIEVIVLKYS DGTTFENQDMFR
HSGIFRDVYILKRKSRVDDFKIE
TTINHESNNGKINF TLOGKHHLGNINLVLYNPKG
LEIDRAIVSKHHQFVIDNPQLWSS
ENPVLYKIIIE TENEVITQKIGREVKIQDNQFY
INGKSIKIRGVNYHDSHPQNGFVM
YERDFEKLKLMKQGNFAIRTAHYPKAPLFYEM
TDQYGFYVMSEADLETHGVVRLYG
EENTEHFNIADNPKFETSIIERIEASIKPLKNY
SSIVSWSIGNESGFGINMVKGLER
AKQLDITRPLHYEGALYRDKENYDMSNVDMISR
MYASPEEILETYLENPKLDKPFIL
CEYAHAMGNSPGDLNAYQTLIEKYDSF IGGFVWE
WCDHSIQVGIKEGKPIFRYGGDFG
EALHDGNFCVDGIVSPDRIPHEGYEFKHEHRPL
RLVNEEDYRFTLKNQDFDTNAEDS
LIVEGEAIYLDGERKVFNIPLTAFAPHISQTFDL
RDYVTLDNISSMLRLYKLEEEESY
RDKYFEVGHQDIIYQRRALPYLNEEKMEFQCKDM
EHSINISVGNKYAYSFDKKQGLK
SVLHNNIEIFNNNTETKIWRAPIDNDAYIKKEWL
YSGYNNIQT LVNTYKIIEDESNIS
LVFEINIESEAVPPVLKGS LTTWTVYQDGKVNVDY
NLEKDNNAPFLPRFGLLITLPSTY
EQINYNGNPMSSSYQDKGIATYLDMFETTIVNNG
DVHIKPOEAGSHNQTTIMNITNNE
HTLITISEDTF SNASHYSLNQLTEAKHVDELEI
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gene      complement(123703..1254
48)

CDS       complement(123703..1254
48)

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[Azotobacter vinelandii], percent
identity 42 in 370 aa, BLASTP E():
3e-67"
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hypothetical protein"
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VTTSHKFRDKNGKYNALVSFSGRS
FSILKGSDL SMVYDNGSDIEQR IKDILPGRFNAN
YEDFNDIEVDGRSDDKGPEVESIE
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gene	125625..126572	PTGKPLMLMVSFELSGTTSTFELNEIDETFDQTHP
CDS	125625..126572	DGQNDTDNAQQSNNSDEHDDTDET KGEYNTDVTQDDEEDTVAQDNDSVTSVTNIED NVIENTGKSPAINTQTTDIDNSDNL NSENIVAVHHGPTLNNNATLNISKISRNVNEA SNHTLKMSDANRLNHNQYQLATK KTNQINHQKLIINMNSPIATNTEIEHPEAKNEGNH SINKQQLPNTGQSQNHAPLWSSLI LGVALLIGRKQKSK" /locus-tag="SSP0107" /locus-tag="SSP0107" /note="similar to gi 27467395 ref NP_764032.1  [Staphylococcus epidermidis ATCC 12228], percent identity 60 in 315 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="putative glucosyl transferase" /protein-id="BAE17252.1" /db-xref="GI:72493931" /translation="MIRILIPCFEASVLEQTYA KLTEIMQRDSISNNKYELLEIDD GSKDRTLAIKALAQRDHA VKFISFRNFGKESA MYAGLCASTEAEALVILDGDLQHP PTLIPQMIAHYRDGEDQVVAKRDRGTGEHVIRKTV SQLYYAVINKIVDVLEDDGVGDFR LLSQRAIREVVNLGEYNRFSGLFAWIGFEFKVI EYENVVRADGESKWTFSLLNNGI DGLISFNNKPLRAILYFGLFVCAMSFYILFNEFI YTVSYGVSTPGYFTTIVAVLFLGG VQLTSLGVIGEYIGRIYEVKQRPYIIRQTNLS DCEVD" /locus-tag="SSP0108" /locus-tag="SSP0108" /note="similar to gi 57284748 gb AAW36842.1  [Staphylococcus aureus subsp. aureus COL], percent identity 40 in 492 aa, BLASTP E(): e-117" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17253.1" /db-xref="GI:72493932" /translation="MRALHINKIHLITGLFIFY ILMAIFTPLTHDDWDWYSQYGIQM LQEHFANLNGRYLGNLFEIVAVRFDFWRLAYAV FSMLIIWVISQFVKHKQTSIICLA AFILMVTMPNEIYKOTYGVFAGFYNYVPATLCVL FILFIVTVLIFYRNHKKPSTNIIF YCVCFGQGFIEENATLNTLIIAIALVLHIYFYK KAYPKFVVGWFISALGTIIMFLNP NYRKIFFEGSDYQQVSSDTGIVDKYKVTVTIILP DWIFFNQIVITIIIVGILLVMLYK TRQMTKTYTSRYWFI VCGLTLLPIYFFIFIKQFE LQHFHMITLNTILNMTVCFIPLCA LILAHTVISQKEVRYTLYLLIASIILVCGPLII VSPIGPRNFYTVYAIYVVILLILL AQLEVPNRKSEKWTGLAIFCAVMYLGVFYNIHA ANEARISQLKEAVHADSKQRIYSM
gene	126574..128076	
CDS	126574..128076	

gene 128404..128592  
CDS 128404..128592

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protein"

gene 128626..130131  
CDS 128626..130131

/protein-id="BAE17254.1"  
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CKLIIVLLMLMGLVKLFI"  
/locus-tag="SSP0110"  
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/note="similar to  
gi|15925638|ref|NP-373172.1|  
[Staphylococcus aureus subsp.  
aureus Mu50], percent identity 59  
in 502 aa, BLASTP E(): 0.0"  
/codon-start=1  
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/product="putative  
glycosyltransferase"  
/protein-id="BAE17255.1"  
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RSKDIGQTVLQNKGPARGVVIHAEHYNESTND  
TYILWNNHYEYVFMNAHEIDFFIT  
ATDIQNQLLAQQFEKKNYHRKPRIYITIPVGSLSLT  
VKPNRRKPYSIITASRLATEKHVD  
WLVKAVLKAKASVPEITFDIYEGGQRLLSKLI  
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gene 130124..131449  
CDS 130124..131449

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gi|49487426|ref|YP-044647.1|  
[Staphylococcus aureus subsp.  
aureus MSSA476], percent identity  
40 in 443 aa, BLASTP E(): 3e-97"  
/codon-start=1  
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protein"  
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ERVEWLNKRGHGTQYIDYNNKVGKRYAQVVLANS

QKSILKRYFNYNNEVMMVENFVTN  
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 MINSLSISSAVLNLGLSEYGNDSIF  
 WQGDITPEIMKHMENALAKEKRNFKIILPSPSAY  
 EKVIELIDEQYKNRIFQSGVYVRF  
 VKENRHSNQVLTLTNSDQIPHLEEIVQAHNPLEF  
 HVAALTEMSMKLLSLNKYDNNLY  
 PNAKRQKFISLYKSCDIYLDINKNGEILDVRAA  
 FDYNLVILGYNETSHNKDVTPENN  
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 gene complement (131950..1324 /locus-tag="SSP0112"  
 17)  
 CDS complement (131950..1324 /locus-tag="SSP0112"  
 17)  
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 gi|42519880|ref|NP-965810.1|  
 [Lactobacillus johnsonii NCC 533],  
 percent identity 39 in 148 aa,  
 BLASTP E(): 5e-27"  
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 /product="putative transcriptional  
 regulator"  
 /protein-id="BAE17257.1"  
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 VKRIRLSILSMIFILIAIVSALLF  
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 /codon-start=1  
 /transl-table=11  
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 /db-xref="GI:72493937"  
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 SGFSFVLIIGLLMFFAIGGYLCHYFENKIHK"  
 /locus-tag="SSP0114"  
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 /note="similar to  
 gi|15614707|ref|NP-243010.1|  
 [Bacillus halodurans C-125],  
 percent identity 67 in 254 aa,  
 BLASTP E(): 5e-97"  
 /codon-start=1  
 /transl-table=11  
 /product="putative oxidoreductase"  
 /protein-id="BAE17259.1"  
 /db-xref="GI:72493938"  
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 GWHSVIDIVLNGTWHCTQAVGKEWIKNGQGRRI  
 NMVATYAWRAGIGVIHSAKAGV  
 LSMTRTLAVEWGSKYGINVNAIAPGPIDNTGGSG  
 KLSLSEAKQQTLDVPLERMGPQ

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EEIAGLAKFLMSEDASYINGACMTMDGGQWLNQN
PF"
gene      complement(134063..1345 /locus-tag="SSP0115"
69)
CDS       complement(134063..1345 /locus-tag="SSP0115"
69)

/note="similar to
gi|13309880|gb|AAK18070.1|
[Staphylococcus caprae], percent
identity 57 in 159 aa, BLASTP E():
5e-48"
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/transl-table=11
/product="similar to ica operon
transcriptional regulator IcaR"
/protein-id="BAE17260.1"
/db-xref="GI:72493939"
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ENLHQFLDFIFNIDEKYIRLYLO
LSYALFQFKDEFLOHIKNIHQILDNIANYNSI
EISVNDKDEFTTMILMFLESWYLNW ASFIDMEQ"

gene      complement(134975..1352 /locus-tag="SSP0116"
11)
CDS       complement(134975..1352 /locus-tag="SSP0116"
11)

/note="partial similar to
gi|15925659|ref|NP-373193.1|
[Staphylococcus aureus subsp.
aureus Mu50], percent identity 60
in 78 aa, BLASTP E(): 6e-24"
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intercellular adhesion protein C"
/protein-id="BAE17261.1"
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YLMHPLILDALYSYISTFENATIIIFVAISLLFII
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/locus-tag="SSP0117"
/locus-tag="SSP0117"
/note="similar to
gi|27468612|ref|NP-765249.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 62 in 239
aa, BLASTP E(): 1e-72"
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/transl-table=11
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protein"
/protein-id="BAE17262.1"
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QPQQTQASTEQPAQEAAPQTEETQPPQQEATTQ
TTSSSNESTSNESSSEASEGSSV
NVNSHLQAIQAQRESGGDLKAVNPSSGAAGKYQFL

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gene	137123..137872	QSTWDSVAPSEYQGVSPTEAPEAV
CDS	137123..137872	QDAAAVKLYNTAGASQWVTA" /locus-tag="SSP0118" /locus-tag="SSP0118" /note="similar to gi 27468612 ref NP-765249.1  [Staphylococcus epidermidis ATCC 12228], percent identity 54 in 250 aa, BLASTP E(): 2e-66" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17263.1" /db-xref="GI:72493942" /translation="MKKTVIASLTAVGLGVTGIA AGNSADASEQGVDKAQLAQQAQSN PESLNAAPIQDGAYNINFNYNNTDYSFQSDGENF SWSYGESEGSSESSQATDNSS QQTAEQPPQVEQPQQTQASTEQPAQEAAPQTEA TQQPQQEATTQSASSSNES SSSEASESSSSGVNAHQQAQRESGGDIHATNP SSGASGKFOFLQSTWDSVAPAEYQ GQPAASAPESVQDAAAQKLYDTEGASQWVTA" /locus-tag="SSP0119" /locus-tag="SSP0119" /note="similar to gi 45656557 ref YP-000643.1  [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130], percent identity 40 in 191 aa, BLASTP E(): 9e-34" /codon-start=1 /transl-table=11 /product="putative dihydrofolate reductase" /protein-id="BAE17264.1" /db-xref="GI:72493943" /translation="MRKLIVLHSTLDGFVEGPK GAMDIGWVAYNEELEKFADDVLSN TDITVWGRKTYEMMYDDYWPVPSDENANEHELN HAQWIENVEKVFSKALNHVWSN SKLVKDHVEEEEINKLKQEGGDIVLGSPRFAHY LMQLNLVDEYKITISPTLIGKGLP LFQNIHDKVDLKLKIKSETFESGALGLNYQVLN" /locus-tag="SSP0120" /locus-tag="SSP0120" /note="similar to gi 15896706 ref NP-350055.1  [Clostridium acetobutylicum ATCC 824], percent identity 46 in 295 aa, BLASTP E(): 2e-73" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17265.1" /db-xref="GI:72493944" /translation="MMRNQKIVPHLWFDTKAEQA IDFYKNVFPETELIKKVTLDQTPS
gene	138190..138768	
CDS	138190..138768	
gene	complement(138876..139772)	
CDS	complement(138876..139772)	

GDAQQLIFNIFNFRFMAINAGPYFVKNPSSISFTV  
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 RIEPTLLFMNENVGRAEEAIIHFYN  
 KVFKNSEPGDKFYYPEGLEPNKTSQLAHARFKIE  
 NQWFTCMDSAYDYGQFNEGISLM  
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 /note="similar to  
 gi|15673115|ref|NP-267289.1|  
 [Lactococcus lactis subsp. lactis  
 Il1403], percent identity 31 in  
 143 aa, BLASTP E(): 4e-05"  
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 /product="putative truncated  
 transcriptional regulator"  
 /protein-id="BAE17267.1"  
 /db-xref="GI:72493946"  
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 KNPFA"  
 /locus-tag="SSP0123"  
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 /note="similar to  
 gi|50123306|ref|YP-052473.1|  
 [Erwinia carotovora subsp.  
 atroseptica SCRI1043], percent  
 identity 41 in 536 aa, BLASTP E():  
 e-112"  
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 /product="putative  
 phosphotransferase system IIABC  
 component"  
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 NYSIGQTYAKEENESGKRNIINII  
 FSYISGTFSPLLPALAGSGMLKALLEILKSLNWI  
 NDKGATFAILNATSNGVFYFLPIF  
 IGMSASKLNVNPNYIGGVIAASLLEPSTNLLKS  
 EENLTFIGLPLVVDFASTVFPLL

gene	139985..140254
CDS	139985..140254
gene	140316..140741
CDS	140316..140741
gene	140907..142493
CDS	140907..142493

gene 142496..142759  
CDS 142496..142759

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gi|46907267|ref|YP-013656.1|  
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F2365], percent identity 41 in 82  
aa, BLASTP E(): 2e-12"  
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gi|16802364|ref|NP-463849.1|  
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percent identity 61 in 469 aa,  
BLASTP E(): e-176"  
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FRYKKNVKYWIITFNEINMILHAPFNGGGIQQDL  
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IGHEINSDFQIGCMIAGTPTYPLTSNPDDVIAAM  
NKDREIYFFADVHVHRYGYPYSDMR  
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CATVNPGDIEQSKGNIMNIKNPY  
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gi|23468715|ref|ZP-00124050.1|

gene 144396..145187  
CDS 144396..145187

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[Pseudomonas syringae pv. syringae
B728a], percent identity 37 in 261
aa, BLASTP E(): 3e-52"
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DITNEHAMVVANLLGEGDSELSKLVKAPLKTNQF
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VQGTSYNYEEIQWIKENNFSKIAIHFDIDVLD
PNEFRATYFAEPHIESFFAAAGQM
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gene      complement(145234..1461
84)
CDS      complement(145234..1461 /locus-tag="SSP0127"
84)

/note="similar to
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in 314 aa, BLASTP E(): e-149"
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protein"
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gene      complement(146472..1466
93)
CDS      complement(146472..1466 /locus-tag="SSP0128"
93)

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gene      146840..147310 /locus-tag="SSP0129"
CDS      146840..147310 /locus-tag="SSP0129"

/note="similar to
gi|28900156|ref|NP-799811.1|
[Vibrio parahaemolyticus RIMD

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2210633], percent identity 65 in
156 aa, BLASTP E(): 2e-56"
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methionine sulfoxide reductase"
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AQQFIDGIEDHHLIATEVLPNTNYVRSAAENQDR
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gene      complement(147380..1475 /locus-tag="SSP0130"
11)
CDS        complement(147380..1475 /locus-tag="SSP0130"
11)

/notes="similar to
gi|1778752|gb|AAB49287.1|
[Staphylococcus lugdunensis],
percent identity 61 in 42 aa,
BLASTP E(): 8e-08"
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peptide"
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gene      147786..148286
CDS        147786..148286

/notes="similar to
gi|27467176|ref|NP-763813.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 26 in 171
aa, BLASTP E(): 1e-10"
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gene      complement(148353..1489 /locus-tag="SSP0132"
19)
CDS        complement(148353..1489 /locus-tag="SSP0132"
19)

/notes="similar to
gi|27467011|ref|NP-763648.1|
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12228], percent identity 57 in 177
aa, BLASTP E(): 4e-55"
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regulator"

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		/locus-tag="SSP0133"
		/locus-tag="SSP0133"
		/note="similar to gi 27467012 ref NP-763649.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 242 aa, BLASTP E(): e-107"
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		/transl-table=11
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		/db-xref="GI:72493957"
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gene	149784..150878	/locus-tag="SSP0134"
CDS	149784..150878	/locus-tag="SSP0134"
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		/transl-table=11
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		/db-xref="GI:72493958"
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gene	151261..158211	/locus-tag="SSP0135"
CDS	151261..158211	/locus-tag="SSP0135"
		/note="similar to gi 15991793 gb AAL13053.1

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[Streptococcus gordonii], percent
identity 57 in 1543 aa, BLASTP
E(): 0.0"
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DEKDNKKKNELESHNHRINKVE
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KPEDNATRSNLINSVNHSLKQLDN
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KDKVQANVPASKRAETNNESLSIETNTNIEKTL
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QSGRNVNHLVFANTSYEILGGGKKYNQVFMIMDG
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LNNQFRDQSPDYANLTQVRNPK
IIINSDGSATVDLGDIGTLGYIIRSKPNTLPDFS
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SSIQFVRAELAGFGGGYVWFDDKNDGVQNDN
AAAAGITVNLDPGTGIRLATITTD
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CDS complement(158256..15908)  
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/note="similar to  
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 [Staphylococcus epidermidis ATCC  
 12228], percent identity 32 in 250  
 aa, BLASTP E(): 3e-36"  
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 SKLVALFSMYIIYYVILFVVSSEILYFTYIHQYDY  
 ASGAFLSNVHETNYSTILCIVGIF  
 CITLIAICFSVMLSMKLSTGFDILSVIVLLFMFV  
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 LLTKLGLMILTLLYSVICYLVLGLKMFKKLEY"

gene complement(159013..15984)  
 /locus-tag="SSP0137"

CDS complement(159013..15984)  
 /locus-tag="SSP0137"

/note="similar to  
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 [Staphylococcus epidermidis ATCC  
 12228], percent identity 40 in 286  
 aa, BLASTP E(): 2e-53"  
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		/transl-table=11
		/product="transcriptional regulator"
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		/db-xref="GI:72493963"
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gene	162475..163101	LEEMGYVQRAYSDNKRKIKLIMLSD
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CDS	163828..164751	
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gene 165391..167241  
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[Staphylococcus aureus subsp.
aureus Mu50], percent identity 79
in 612 aa, BLASTP E(): 0.0"
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reductase"
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12228], percent identity 72 in 176
aa, BLASTP E(): 1e-73"
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gene 167238..167774  
CDS 167238..167774

gene	167856..168851	VDGPFINHLRPNLPYKGS MNQRV
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gene	complement(169138..170064)	
CDS	complement(169138..170064)	/locus-tag="SSP0147"  /note="similar to gi 49482569 ref YP-039793.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 61 in 308 aa, BLASTP E(): e-112" /codon-start=1 /transl-table=11 /product="putative dioxygenase" /protein-id="BAE17292.1" /db-xref="GI:72493971" /translation="MNIIGHHHISMYTKGAQINK NFYITQLGLRLVEKSVNQDNPTMY HLFYGD EIGITPGTLLSFFEIPNLGKNRPGTNSIH RVSLLLVPDESALTYFERRLNEQHI TTQMTYLNHHALLFKDMDGLEILLANNRHTP NAWRKNPYTDIPEAYQILMGMPVE LRLRDIQPTLHFLKNDLRYSLRENVD ETVLTLD S DGLYTD FVLVEEQGSRRARPQGQYV HHIAVNTPNDSLDYAVLDTINHNPGNHSGIIDRY FFKSLYYRHNSIMFEFATAAPGFT VDTA IKDLGKKNL PDEFMENORTEIEEKLHDL" /locus-tag="SSP0148" /locus-tag="SSP0148" /note="similar to gi 30020510 ref NP-832141.1  [Bacillus cereus ATCC 14579], percent identity 43 in 160 aa, BLASTP E(): 1e-36" /codon-start=1 /transl-table=11 /product="truncated"
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CDS	170479..170964	

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		/translation="MEKLSKLTGVSTSSLNEIEK
		GNTIPSINTVWKISNGLKLSFSSL
		MSEAESDYVQVNKEDVVPVTEDDGKYRVYPYFPF
		EKSKSEFFFYVELDPGATLDSEPH
		LSGSEESIIVDGQLEMHLENEVIDLGKGDALRF
		KSDITHSYTNHGEDMTLISMVIDY K"
gene	171194..171466	/locus-tag="SSP0149"
CDS	171194..171466	/locus-tag="SSP0149"
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		percent identity 43 in 87 aa,
		BLASTP E(): 3e-12"
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		/db-xref="GI:72493973"
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		GIMLVNIVIANIGIPESSQDITY
		KKFLDFFIESKFFSIFHIYLVLFIFLCKEQKRN
		LEINILYICAVE"
gene	171406..172209	/locus-tag="SSP0150"
CDS	171406..172209	/locus-tag="SSP0150"
		/note="similar to
		gi 396084 emb CAA80248.1
		[Bacillus acidopulluliticus],
		percent identity 42 in 269 aa,
		BLASTP E(): 2e-52"
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		TPLPYFILGLASAQFGMIFKFNRY
		KIWSVVALISGIISTIGWYLLKAYVVPNFKLLR
		QKSEVSINHYAENVHDYHLLITIF
		SPFMSIFYASCLILLNLSWARKVLSPLKYYGSM
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		THVDTLWICVCVYVFQLLISTYWLKYFKLGPLEY
		IWKMATYMKIKMIK"
gene	172633..173283	/locus-tag="SSP0151"
CDS	172633..173283	/locus-tag="SSP0151"
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		identity 50 in 201 aa, BLASTP E():
		9e-55"
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		/transl-table=11
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		/protein-id="BAE17296.1"
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gene      complement(173425..1738 /locus-tag="SSP0152"
47)
CDS       complement(173425..1738 /locus-tag="SSP0152"
47)

/notes="similar to
gi|27466966|ref|NP-763603.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 79 in 133
aa, BLASTP E(): 2e-56"
/codon-start=1
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protein"
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gene      complement(174106..1749 /locus-tag="SSP0153"
63)
CDS       complement(174106..1749 /locus-tag="SSP0153"
63)

/notes="similar to
gi|23100728|ref|NP-694195.1|
[Oceanobacillus ihayensis HTE831],
percent identity 50 in 284 aa,
BLASTP E(): 4e-72"
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DQNAHTQALHQICISNSSLNIELTT
DIDNAIWYKLLVNLAINSVTALTRSTASVLEVP
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YHLLLAQQK"
/locus-tag="SSP0154"
/locus-tag="SSP0154"
/notes="similar to
gi|57286520|gb|AAW38614.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 72
in 268 aa, BLASTP E(): e-108"
/codon-start=1

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gene	175855..176703	/transl-table=11
CDS	175855..176703	/product="3-methyl-2-oxobutanoate hydroxymethyltransferase" /protein-id="BAE17299.1" /db-xref="GI:72493978" /translation="MKTNLQQLKVNKEKISMV TAYDYPSAKQVEAADIDIILVGDS LGMTVLGYDSTVQVTVADMIHHTKAVRRGAPNTY LIVDVFFGAVGVNDQYDLEIAVKL YKETDANAIAEGAHLTYQIKNCNMGPVIVSHL GLTPQSVGIMGYKMQAGNKEAARQ LIEDAYAVQQAGAVMLVLEAVPSDLAAEISDKLD IPVIGIGAGKETDGOVLVYHDLN YAVEHRAKFKVQFGDFSVGIDALKQYNNEVKAEQ FPGEAHTYKKQIMNEVTE" /locus-tag="SSP0155" /locus-tag="SSP0155" /note="similar to gi 23100730 ref NP-694197.1  [Oceanobacillus ihyenssis HTE831], percent identity 65 in 281 aa, BLASTP E(): e-103" /codon-start=1 /transl-table=11 /product="pantoate beta-alanine ligase" /protein-id="BAE17300.1" /db-xref="GI:72493979" /translation="MTQLITTEEMRSIIANLHN QRRSVGFIPMTGALHDGHLKMSL SLNENDVTIISIFVNLQFGPNEDLDSYPRDIVG DTAKAESVGVVDYIFHPTVKEMYFE LPTIELKAGRLASVLEGAERPGFDGVVTVVKNL FNIVRPHKAYFGKKDAQQLAIVEK MVEDFNHPIEIKGVDIVREDDGLAKSSRNILYTK NERIEAVHLYKSLCLAQSLYKNGE RNSEKIIKATRDYLTHTSGTIETVAIYSYPELV EQTIKDSIFISLAVKFSKARLID NIIIEG" /locus-tag="SSP0156" /locus-tag="SSP0156" /note="similar to gi 27467184 ref NP-763821.1  [Staphylococcus epidermidis ATCC 12228], percent identity 71 in 494 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative malate:quinone oxidoreductase" /protein-id="BAE17301.1" /db-xref="GI:72493980" /translation="MSEKNSKDVILIGAVLSTT FGTLKELAPDWNKIFERLDKPA IESSNERHNAGTGHAAELNLYTVEQKDGSDIVE KAKEINEQFEISKQFWSHLVKSQ IQNPQAFIRPLPHISFVQGDKNVNFLLKRRFEALS PLSMFKGIEYTEDHEKLVVMPLM MEGRDPNETVAASKIDEGTDVNFELTRKMAKNL SEHDNAELFYRHEVQDFSRKDKG WEVKIKDLTKKVEHHITDYLFIGAGGAAPLILQ KTGIPESKHLGGFPITGEFLVCNN FEVVAKEHVKAYGKEPEGTPPMTVPHLDRRIQD
gene	176953..178440	
CDS	176953..178440	

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ENSLLFGPFAAIGPKFLKNGSNLD
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KEDRMKELRRFVPDAKDEDWDIMQ
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ALLGESPGASTSVSVALEVIEKNF
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ASNAELELNHK"
gene      complement(178592..1788 /locus-tag="SSP0157"
34)
CDS       complement(178592..1788 /locus-tag="SSP0157"
34)

/note="partial similar to
gi|57285494|gb|AAW37588.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 57
in 77 aa, BLASTP E(): 2e-19"
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KN"
gene      178948..180822 /locus-tag="SSP0158"
CDS       178948..180822 /locus-tag="SSP0158"

/note="similar to
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identity 44 in 673 aa, BLASTP E():
e-147"
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protein"
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NQSQTNNHIKTKVTVKRATTFDENIKTVNKSETP
NKNIIIGTSRAYKKLTDKDIKLRK
LLAKHDLHYHPVVTKSVMREIEDSSLEALDYSNDY
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SQENKKIKTSETSGYFLTPSETLINSIVSSNSDT
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PKLVPYIGSIELHSYDFYGVSGFD
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NALPETVGIRLVIKYNQSPNNILT
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gene	180838..181224	/locus-tag="SSP0159"
CDS	180838..181224	/locus-tag="SSP0159"
		/note="similar to gi 31616158 gb AAK38834.2  [Staphylococcus aureus], percent identity 45 in 111 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="truncated biofilm-associated surface protein" /protein-id="BAE17304.1" /db-xref="GI:72493983" /translation="MKILDENGLTISIDTLNEDG TFSMQVPKLPKPGTYTIAIESPNYT NDEVNTFKVIDIKEILKPSINPVNDQSKIEIENG VEGSTIIIKDENNVIVGQTILNNG QTTSIINLKTIKSRNYFNSNSRKKWH" /locus-tag="SSP0160" /locus-tag="SSP0160" /note="similar to gi 31616158 gb AAK38834.2  [Staphylococcus aureus], percent identity 47 in 324 aa, BLASTP E(): 2e-81" /codon-start=1 /transl-table=11 /product="truncated biofilm-associated surface protein" /protein-id="BAE17305.1" /db-xref="GI:72493984" /translation="MTRSLAPTMKDFTSNDTQIT GESEPNSTVEITFPDQGQKVTTAD DQGHYIVDIPAGSLNNGGEVSAKATDKAGNESPK TIRNIVDETAPMAPTMKDFTSNDT QITGESEPNSTVEVTFLDGQKVIVIADEQGDYIV DIPSGSLNNGGEVSAKATDKTGNE SPKTTKDVADETVPEAPKVDNVTSNDIIGKTE PHASVTIQFPNKQIITGKADEQGD FSIGILSEIKLLGNEILINITDKAGNISNKTSTV IVIDKTEPNAPIVDLTDTDITIT GQGEPNTKVIIINLPNGKRITGRVNSHGKYEIKLP KDITLNNINDKISILLEDDSIQLS ASMLSASIIYRASEKWCHGSDVPAETIYQSVTPY IISGLVSRK" /locus-tag="SSP0161" /locus-tag="SSP0161" /note="similar to gi 30021303 ref NP-832934.1  [Bacillus cereus ATCC 14579], percent identity 52 in 109 aa, BLASTP E(): 2e-25" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17306.1" /db-xref="GI:72493985" /translation="MGIIIIIIILGIFIMTG LKILSGAMKQEFKLGYPPIFNKI TGLFELIGGIAMLVGIFYIPLAIFASILLATML
gene	181259..182392	
CDS	181259..182392	
gene	182413..182760	
CDS	182413..182760	

AGAGSLVFLGKDPIKKAIPAIVLF  
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 gene complement(182981..1834 /locus-tag="SSP0162"  
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 CDS complement(182981..1834 /locus-tag="SSP0162"  
 33)  
 /note="similar to  
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 [Bacillus clausii KSM-K16],  
 percent identity 47 in 137 aa,  
 BLASTP E(): 4e-34"  
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 percent identity 56 in 260 aa,  
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 RESNLALITEKFGIASPEWGRGVS  
 MYIFGTIFGAIFFSIFSGIISILPLSPIAYAMA  
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 /note="similar to  
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 percent identity 38 in 382 aa,  
 BLASTP E(): 4e-67"  
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 /transl-table=11  
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 major facilitator superfamily"  
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CDS	185795..186769	
gene	complement(187067..188257)	
CDS	complement(187067..188257)	/locus-tag="SSP0166" /note="similar to gi 16081118 ref NP-391946.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 46 in 379 aa, BLASTP E(): 1e-92" /codon-start=1 /transl-table=11 /product="putative permease of the major facilitator superfamily" /protein-id="BAE17311.1" /db-xref="GI:72493990" /translation="MDDLKNVYKKGSGQAYIKII VALFISGFIIFSILYSVQPLIPHF TNAFNVSETVASLALSAAITLAIAMLFFGALSE VLGRKPIMIFSVISVSLALVQPF ILDFNTFLIVRLIQGICLAGLPSIAMAYIGEEIS SHNLPEAMGIYISGNAFGGAFGR FTGFISSIIYGYQTGLISIGIISVIAAILFTFLP ASNHFEKQRFVSKALLVSYSKHLK NIRLLKPFMIGFLLGCNIAAFNYIGFVLADEPY LHDSVTSFVYLLFLIGMISSILN AKLRAQLGTNLNALKFSILLIFGIWITLLPLPLF

gene	188370..189257	KILGLAFSVYAFFSGHAIASAVVT
CDS	188370..189257	SRAEDHKAQASSLYLLFFYMGSSVGGTLAGIFYG AIQPGVVLIMITAFMIIAFIIALT IKQK" /locus-tag="SSP0167" /locus-tag="SSP0167" /note="similar to gi 16081119 ref NP-391947.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 32 in 277 aa, BLASTP E(): 5e-40" /codon-start=1 /transl-table=11 /product="transcriptional regulator" /protein-id="BAE17312.1" /db-xref="GI:72493991" /translation="MEWHHEFYFKQLAQTEMNSE CAKMLNVQSSTLSRAIKNLEAELG IPLFNVRGRTIKLNKYGIAFLKTTNNIINEMDIY KSNVLDATNVYNGKLVIGFLHSVG VTYISEFLKSFNLAYPNIQKLKLIHQDAKRILITML DDGEVDMIIITTISETSONTHFEPL IVEKLYVTLHEQHRLSHCSEIAIEALVNEKFILL KPNLLLRQQVDEILKAYQFTPEIS FEGDEVITIATFISSGLGVILPHLRDVRPLPNLK QIPKHNDAKRTIGLCYKNSKNKV PIINKTKKSLIEYFSKIQK" /locus-tag="SSP0168" /locus-tag="SSP0168" /note="similar to gi 26554099 ref NP-758033.1  [Mycoplasma penetrans HF-2], percent identity 23 in 296 aa, BLASTP E(): 1e-12" /codon-start=1 /transl-table=11 /product="putative RNA binding protein" /protein-id="BAE17313.1" /db-xref="GI:72493992" /translation="MKRLFFVIMVMFVLACGT ENDEAKSADKDSKSKATSKMKKF KIGQAVDADGVQVKLTKEIYVNDYDEYSAPENGK VIKVKLKFKNNDQVLMDSDFS MKVNNENYQEWFGNDDTNAGFSHQLNKNGTSGSY ITYDVPDSDNYLEMDATPKFNNV KAKWEIKKTDIKEASVANSNESNDEAETDTNVES EDSEEPKITDESEDTESEETGYS AEMYNALVDEYNALTDGKEMNHVDDVLEIEYDQ LEARVDALYDKKMEEDKALEEM EQDEKEYEEMEAEIDKEYEEMKKEBEDTTDED TSEDDAA" /locus-tag="SSP0169" /locus-tag="SSP0169" /note="similar to gi 28379567 ref NP-786459.1  [Lactobacillus plantarum WCFS1], percent identity 46 in 112 aa, BLASTP E(): 1e-23" /codon-start=1 /transl-table=11 /product="conserved hypothetical
gene	189710..190663	
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CDS	190690..191040	

gene	191299..192045	protein"
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		/note="similar to
		gi 57285324 gb AAW37418.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 68
		in 247 aa, BLASTP E(): 1e-98"
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		TQINLNIELKGVSGSNGIALSESMVTQVAEQLKE
		LDSNIEVLISFNVILVKLAEL
		PEYPRALIFKSAAFQGDWRLLDFCGSNIVNIED
		AKLSQARVKMIKNAGYTLNVVTN
		KSLRANQLANWVGDIPTDHADDMIHLERP"
gene	192302..192763	/locus-tag="SSP0171"
CDS	192302..192763	/locus-tag="SSP0171"
		/note="similar to
		gi 57286554 gb AAW38648.1
		[Staphylococcus aureus subsp.
		aureus COL], percent identity 67
		in 147 aa, BLASTP E(): 1e-53"
		/codon-start=1
		/transl-table=11
		/product="putative transcriptional
		regulator"
		/protein-id="BAE17316.1"
		/db-xref="GI:72493995"
		/translation="MESNSNNNDYENLLFYFAYK
		TFINTADEIIEKYGLNRQHRRFLF
		FIEKVPGITIKDLLKSLEISKQGSATLKKLKDE
		AYIIEKQTATDKRVKALYSTDKGT
		KLVRLELNKKQNDMFQDIQKKVGNWDWYAIMELAS
		YRTGFQEVKYLKDDFNK"
gene	192923..194566	/locus-tag="SSP0172"
CDS	192923..194566	/locus-tag="SSP0172"
		/note="similar to
		gi 27469128 ref NP-765765.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 71 in 547
		aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="putative
		indole-3-pyruvate decarboxylase"
		/protein-id="BAE17317.1"
		/db-xref="GI:72493996"

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/translation="MKKRVGQYLMDCISDVGVDK
VFGVPGDFNLTLDDIISRDDMEW
IGNTNELNASYAADGYARMKGIAAMVTTFGVGEL
SAVNGIAGSYAERVPIQITGAPT
RAVESAGKYVHSHSLGEGNFDDYRNMYASITTAQA
YITPENAQSEIPRVINAALYEKRP
VHIHLPIDVANSEIDVATPFEEIQRPQTDVTKYM
TMVKDKLQSAADKPVIIITGHEINSF
KLHEKLEQFVKQSQIPVVQLSLGKGFNETSPYY
MGIYDASLAEEDIRNYVDQSDAIL
NIGAKLTDSATAGSYQFDDIDVVMINHHHFKMN
ETKDETVSLVDLLDGLNAINYVNN
AEFFPKFKPKAHDYDLTDEPLTQETYFKMMQDFI
REEDVILAEQGTSTFFGAYDLALKH
NNKFIGQLWGSIGYTLPATLGTQMDATSRNLL
LIGDGLQLTVQEIISTMIREKIKP
IIFVINNDGYTVERKIHGENAMYNDIKMWDYKLL
PTVFGGKDEVQVHDVNTSEAFQKV
LLQIEAQPDTHFIEVKMGVHDAPHKLNAGQAF
AKQNG"

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gene complement(194711..1949 /locus-tag="SSP0173"

95) CDS complement(194711..1949 /locus-tag="SSP0173"

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/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17318.1"
/db-xref="GI:72493997"
/translation="MFALSNACSNITSITWILCSN
FWAAKSLFFCLMIWAIFKKSFTSL
RTSKSFLTSTKTEKFSFTSLCIMKMSAKHINHL
SLFRYIEICQRYIVIL"

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gene complement(195140..1963 /locus-tag="SSP0174"

15) CDS complement(195140..1963 /locus-tag="SSP0174"

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15)
/note="similar to
gi|27467289|ref|NP-763926.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 60 in 384
aa, BLASTP E(): e-132"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17319.1"
/db-xref="GI:72493998"
/translation="MTNGLYLDCHAGIAGDMLLS
SLVDLGADVVDYVHQHLLSLPLDQF
SLNFAKKNKQGIQAMGLTIDFEEAHHHRKASDIF
NMINESTLPNRVKERSMLIFDVIA
QAEAKIHGMKIEDVHFHEVGAMDSIIDIIIGSCLA
LEDLGIDEIKSSPVPTGNGKIKIA
HGIYIPAPATAEILKDIPLATFDVQSELTPTPTG
AAFIKALATHIGPLSAVSMNIGY
GCGTKDFEFPNVIRAIQYTATETTPNQVQVLECG
IDDMTPETLGYFIEQVINEGALDA
FYTPITMKKSRPATQLTVISSVTQAEFEDFILK
HTTSLGVRSYAVNRKILHRQFQTI
HTTYGAILVKLAMKDNKIIKAKPEFEDVKNAALH
SGQSFTNVYNDIQNEVRKHQID"

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gene      complement(196333..1970 /locus-tag="SSP0175"
91)
CDS       complement(196333..1970 /locus-tag="SSP0175"
91)
          /note="similar to
          gi|27467290|ref|NP-763927.1|
          [Staphylococcus epidermidis ATCC
          12228], percent identity 68 in 251
          aa, BLASTP E(): e-102"
          /codon-start=1
          /transl-table=11
          /product="putative NCAIR mutase"
          /protein-id="BAE17320.1"
          /db-xref="GI:72493999"
          /translation="MVEKYDAIEQLKAVHANEL
          SVDDAKDQLNHYYDELGFADLHR
          TQRQGFPEVIFGEGKTEQLHDIVHTLIKHDSIV
          LITRIDQEKADHITAKYDQLEYHE
          TARIVSTPIKHIAKTNHYASIIICAGTSDLPVAEE
          AAITAEVMGIQVQRFFYDVGVSGIH
          RLFAHIESIRQSKVSVVVGMEGALSSVVAGLVD
          HPVYAVPTSIGYGANLQGVTTLLS
          MVNSCAPGTSVLNIDNGFGGGYNAAMIINMIESH
          "

gene      complement(197113..1979 /locus-tag="SSP0176"
37)
CDS       complement(197113..1979 /locus-tag="SSP0176"
37)
          /note="similar to
          gi|27467291|ref|NP-763928.1|
          [Staphylococcus epidermidis ATCC
          12228], percent identity 67 in 272
          aa, BLASTP E(): e-105"
          /codon-start=1
          /transl-table=11
          /product="ATP-utilizing enzyme of
          the PP-loop superfamily"
          /protein-id="BAE17321.1"
          /db-xref="GI:72494000"
          /translation="MLTEMITKEQKLETILKDMN
          SVIVAFSGGVDSLSVLKKAIDVLG
          HDHVKAIVIVKSELTRNEEFQDAIALAHQLNAQVI
          ETEIEALKDPHIVENTPDSWYYSK
          RLLYSKLEALRAQLNFNYVADGMIMDDINDFRPG
          LKARTEFNVRSLQEAEVFKSDVR
          AMSKSNHLPVWNKPCSCFSRIPYGEPLSISKI
          NKINEAEKFI LALGLNHVVRVYHQ
          NIARIEVNDADIPSVIHNKDQITVYLKELGFDYV
          TIDLEGYRTGSMNEVIDTHHTH"

gene      complement(197953..1992 /locus-tag="SSP0177"
15)
CDS       complement(197953..1992 /locus-tag="SSP0177"
15)
          /note="similar to
          gi|27467292|ref|NP-763929.1|
          [Staphylococcus epidermidis ATCC
          12228], percent identity 72 in 419
          aa, BLASTP E(): 0.0"
          /codon-start=1
          /transl-table=11
          /product="conserved hypothetical
          protein"

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/protein-id="BAE17322.1"
/db-xref="GI:72494001"
/translation="MKTSILYGKSNVEIDLPHDS
VLIEPTDIDALDDDTNAIRNALAD
PIGTGPLNEMVSANQTVAIVISDITRPTPNHILV
PLILETLSHVPPENFVIINGTGTH
RDQTQEELIQMLGKDVVDQIKIVNHCNDKDTLS
KVGHSKYGCDEVLYLNKDYVEADFKEI
VTGFIEPHFFAGFSGGPKGIMPGIAGIETIMTFH
NAKMIGDIRSTWGNMTDNPVQDMT
REINAMCKPDMFLNVTLNKEKEITAVFAGELYEA
HDKGCAYAKAHAMFKCDNRDFVVI
ASNSGYPDQNLQYQTVKMGMSAAHKVVKEGGSII
LSECSGYPNHGNYAKILKMADSP
QGLVDMISDPNFAMLDQWQVQKQAVIQTFADVYL
YSKLTDKQTTDAMLHPAHEINNTL
KELETKYGTDMTIGVMPLGLTIIPYVES"
/locus-tag="SSP0178"

gene      complement (1992/9..2004
36)
CDS       complement (1992/9..2004
36)

/note="similar to
gi|50122493|ref|YP-051660.1|
[Erwinia carotovora subsp.
atroseptica SCRI1043], percent
identity 48 in 371 aa, BLASTP E():
1e-96"
/codon-start=1
/transl-table=11
/product="glycerate kinase"
/protein-id="BAE17323.1"
/db-xref="GI:72494002"
/translation="MTIVLAPDSFKGMSMSATEVA
RYMSKGISDIFPEADIHTLPVGDG
GEGTMEALVNATNGTFTTLNVTGFLGDTVSAQYG
VLHDKETCVIEMAEASGLKHVPDN
ALNVMQATTYGTGELILDALDSGYTQFILAIGGS
ATNDAGAGMLQALGAKLLDQHHHE
VDLGGGNLHKIQHIDLSHFDARINQCNFTIATDV
QNPLIGTNGASYVFGKQKGATESD
LKQLEHNLTHWADLVAHKKSIRLHDLPGAGAAGG
LGGAFKAFPPSHFEDGIQVVIDYI
KLDQYLENADLVITGEGKIDFQTLYGKTPMGIK
YANRYNVPPVVFIGGSDVDIDQFK
DMGVIGAFSLTDGPMSELEETINQSEKLVKKTQTN
IVSLFFHESAILSKEFSE"
/locus-tag="SSP0179"
/locus-tag="SSP0179"
/note="similar to
gi|52078507|ref|YP-077298.1|
[Bacillus licheniformis ATCC
14580], percent identity 31 in 363
aa, BLASTP E(): 3e-41"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="BAE17324.1"
/db-xref="GI:72494003"
/translation="MSYAILLVNDFIVLFFYYID
LILKIGLKYTKMMLLICMKMIGD
KMMNVLTDELAALIVEETVTRKNTSNINIMNFGE

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gene	202685..205318	IIASFDRRIGQVHEGARKVLASG
CDS	202685..205318	DIVLSEETSYLQGTQPGINLPIIFQDNVVGVI
		GITGDPALVHVADLVKMSPELL
		YQNYFTYELEGQLRSQELLIEELLKSEPSQSFQI
		YLTQQLNVAFITYRKCIINLEKQ
		IFSRSSIVQRLAKIMDKATFAVAFNTYNHIVILA
		TDELQDELNQKIYRIHQVFTSLNL
		DVRIASSLVFTSLNDFKNAYEECELVFMLEENV
		SFASFEDVEEKTLLYQINEEIRER
		YKKRILGELDNQSIETLSKFENDLNIAQTAKYL
		YIHRNTLLYRLECKKLQTLGNPKK
		YSDAIKLQIALWC"
		/locus-tag="SSP0180"
		/locus-tag="SSP0180"
		/note="similar to
		gi 27469078 ref NP-765715.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 73 in 871
		aa, BLASTP E(): 0.0"
		/codon-start=1
		/transl-table=11
		/product="phosphoenolpyruvate
		synthase"
		/protein-id="BAE17325.1"
		/db-xref="GI:72494004"
		/translation="MTKIYAFDEGQKSMKDLG
		GKGANLAEMKRLGLFVPDGFITIT
		EACIEYLNHNSKLPDLLKQLDVELDALSKRIQK
		SFSDDGALLVSVRSRGAKISMPGM
		MDTILNLGLNDENVKLANKTNSRFAYDCYRRL
		LQMGQGVVYGIPMSFDTYFDQYK
		TQHHYESDAEIPAEGLKEICEHFKAIVLDEAYKP
		FPQEPIDQLTEAIEAVFKSWDNR
		ARVYRQLNEIPHDIGTAVNIQEMVFGNSGEKSGT
		GVAFTRNPITGEAKLFGEYLLNAQ
		GEDVVGIRITPKDIETLKEQMPHVHEQFVKVSTQ
		LETHYKDMQDIEFTIENENLYILQ
		TRSGKRTANAAIHIAVDLVEEDVISKEKAVMNVE
		VKSIDQLLHPNFDEQSLKQTSVIT
		KVGLPASPGAASGAIVFSAEMAKQQAEEQGNKVIL
		MRPETSPEIDIEGMVASEAIVTTHG
		GMTSHAAVVARGMGKCCVTCGSDLEINITDKVVH
		YKGSLEYEGDIISVDGAKGDIYFG
		EVEITQAERSHAFEFMQWSEENARLDVRMNAET
		AQDIQAGYQFGAGKIGLVRTEHMF
		FAPERLIEMRRFIFLFTQDKRIAALNTIKYQKN
		DFEEILKLSGERPTIIRLLDPPLH
		EFLPNSNNEKATVAEQNLVTIKELDQYIESLNEV
		NPMLGHRGRLAITYPELYIMQAE
		AIIESALELKAQGVSCOPEIMIPLVSTVAEFTTL
		KAQIISRIETLQOEAKEHIHYMIG
		TMETPRACLIASELAKECDFFSFGTNDLTQLTF
		GFSRDDAGTFIGTYSSELGILEHDP
		FQTLDEVEGIGELIKIASQQAKSANPDITIGVCGE
		LGGDHKSIIQYFNQLDIDYVSCSPF
		RVPGALLSTAQSEVEGGRRLHV"
		/locus-tag="SSP0181"
		/locus-tag="SSP0181"
		/note="similar to
		gi 27469077 ref NP-765714.1
		[Staphylococcus epidermidis ATCC
		12228], percent identity 74 in 262
gene	205311..206126	
CDS	205311..206126	

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aa, BLASTP E(): e-108"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17326.1"
/db-xref="GI:72494005"
/translation="MFDDQQAPQLRLFVISDSIG
ETAQRMIHATLTQFPDISQIEIKK
YPIKNEEELMHILNRAKELNAVVTTLVNPDFN
IAGQHLAKKLQIPYIDYMSDLIGI
IQQTQCNPILESGALRKLDENYFKRIEAMEYAV
KYDDGKHFTDIGEADALIVGVSRT
SKTPLSMYLANKGYKIANIPLVLEVDIPDEVFKH
KHLKVFGLTASPDYILNIRNERVK
ILGLSGPSNYSMDRIREELIHAEVFEKLNATV
INTEYKSIEESAFYIEKCL"
gene      complement(206311..2071 /locus-tag="SSP0182"
74)
CDS       complement(206311..2071 /locus-tag="SSP0182"
74)

/note="similar to
gi|27468686|ref|NP-765323.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 43 in 284
aa, BLASTP E(): 1e-66"
/codon-start=1
/transl-table=11
/product="ferrichrome ABC
transporter"
/protein-id="BAE17327.1"
/db-xref="GI:72494006"
/translation="MMTFEFKHDLTGSELPEdit
SAVALEFSFVDALVALDIDVKGIA
DDGDSTNLISPLREAVGDYVSVGTRLDPDFESIR
SSAPQLIIGDSDRHKEIYEELSEI
APTILFKSFDAGYQETLEVFORIGTAVSKSKDAK
ERLDRHQALVNDNFNNQISIDENKE
TLAAVVSQGVTAHSNSTYVGEFLTKLGFATALN
DKVADTLPAYRESDYLEMSYEQLA
NVNPERLIVMVEDDNDKDLNQNQNQWDDLEAV
KSQRVHFVSRDDWAKRLGLIASED
IVETLANLNEA"
gene      complement(207283..2078 /locus-tag="SSP0183"
28)
CDS       complement(207283..2078 /locus-tag="SSP0183"
28)

/note="similar to
gi|30020510|ref|NP-832141.1|
[Bacillus cereus ATCC 14579],
percent identity 42 in 182 aa,
BLASTP E(): 5e-39"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="BAE17328.1"
/db-xref="GI:72494007"
/translation="MYNIQSIIVAKNIADYRKKHQ
LSLDKVANATGVSKNMLSQIEKGQ
SNPTITTLWKIANGHLISLSQLTSTSTNSDTIDFID
ESDIIPLIDKEVSIYPYPFYDENK

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gene	207922..209106	KFEMFKMEIQPGGKMHSDDHPHGSSEYIIIVNDGV
CDS	207922..209106	LEIEVDGKQYTIHHQAFRFRNSDL PHSYFNPGSTIVALTSTMYQ" /locus-tag="SSP0184" /locus-tag="SSP0184" /note="similar to gi 16800015 ref NP_470283.1  [Listeria innocua Clip11262], percent identity 41 in 381 aa, BLASTP E(): 2e-79" /codon-start=1 /transl-table=11 /product="putative transporter" /protein-id="BAE17329.1" /db-xref="GI:72494008" /translation="MENYRKIKPFNWLLFIGILL VGANLRAPITSIGVALPDIKADLA MSNSAVSVITVVLFAFVLSFAARTSNQFGL KTIFLALCLIFIGIIVRSMTETISW LYIGTVLIGIGIGFGNVLAFAVIKAKFPLHIGIM TGYTVVMNVFGLSSYGTAAPLK SFHYNVAISLIDIVTLVTIIWSFQLKGQEMAT ALPRKSVNVWKSPISWQITILMGG QSLIFYSLINWMPAYLSQSGMSISEAGVYLSVLQ ISIIPFTFITPIFATKMKSQFTLT FVTGLLFIAGVIIMLCVPQLAIIISTILIGVAGGI AFGLVNTFFSLRTEHSQTAALKSG MAQSIGYLFAMGPLLFGVLHDMTGTWIASLSIL LFTAVIITLFGSQAGRNRTIEQSL QK" /locus-tag="SSP0185" /locus-tag="SSP0185" /note="similar to gi 49483510 ref YP_040734.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 56 in 494 aa, BLASTP E(): e-168" /codon-start=1 /transl-table=11 /product="putative cardiolipin synthase" /protein-id="BAE17330.1" /db-xref="GI:72494009" /translation="MQLIFDPGVSPYIRGVLAFF FVINILAFVIVFLDRDRRDATAT WAWLFLFVMPVLFVFFIYIFFGRGIRKKRERGFA HNQIEDGMKRVQAQLQDSTNKISD SDNPVIRKHRDIATLLTKEPSFLSDNNNDIYIT DGHDLFSQMKEDLRNAKTYIHMEY YVLNLDGLGTEIINILEQKAEGLVKKLLYDAVG SKSVHKSFKKFFRENGGQVEAFFQ AKIPLINFRVNNRNRKRVIVDGMTGYVGGFNVG DEYLGNDKFGYWRDTHLRVRGDG VDALQLSFVHDDNSQAKREQLEYNMKYFFDNAYQ GGNVSMQLALSAPSDNWHQIEFGY MKMIMNAKSSIYMHSPYFIPDKGYINALRIAAS GVDVRLIIPNKPDIIFVYWATITS VAQLIRDGVKVYTYENGFIHSMKIIDDEVASVG SSNMDIRSFELNFEVNAFMYDEQI TKQLKAFLLEDLKVSKELTEERYNQRSNWIKFKQ SIKLAASPIL" /locus-tag="SSP0186" /locus-tag="SSP0186"
gene	209327..210811	
CDS	209327..210811	
gene	210972..212357	
CDS	210972..212357	

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/Note="similar to
gi|52078919|ref|YP-077710.1|
[Bacillus licheniformis ATCC
14580], percent identity 43 in 453
aa, BLASTP E(): e-104"
/codon-start=1
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regulator"
/protein-id="BAE17331.1"
/db-xref="GI:72494010"
/translation="MQRDSNLIYYRQLYTQLKED
ILAFKYNSEHKLPKSRVMSKKHDI
SINSVKAAYEQLLAEGYIYTQERKGYIIEPIDKL
IENDKQPSLETYHEHTATEFEYS
FSHMSTDISEFFPVDWTMMKQVFQNYDHYLSSI
PEVKGPMELRQSIKALISYQRGH
CHPEQIVIGSGTNALLTKLIELMTKNITIAVEDP
GYSFRITLLEQTRIHEPIALDRK
GISLEGIKDIQPNNAVITPSSHQFFIGTIMPVSR
IDLLNWASKTHSYIIEDDYDSEFK
YETDNIPSLFSFEKNESVIYLGTFSKTLMPISIRM
SYMILPTKLVRQFELQONTIPDY
SMLNALTNLMIKEGHYEYIKMHQLYGKKREN
LIAHLSMAFGEHIQIKDQAGLHF
IIEVNSPYSYEEIETRAKEQKLELYTINRFKVK
LQKNNGPKILIIIGFSKIEQNHIPE
AVQRLKSVLIE"
/locus-tag="SSP0187"
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/Note="similar to
gi|52078920|ref|YP-077711.1|
[Bacillus licheniformis ATCC
14580], percent identity 63 in 426
aa, BLASTP E(): e-153"
/codon-start=1
/transl-table=11
/product="4-aminobutyrate
aminotransferase"
/protein-id="BAE17332.1"
/db-xref="GI:72494011"
/translation="MSEKYEYYKTQREKYVARGV
GNGNLHVADEAQSATVKDVEGNV
IDFAGAIGTLNVGSHPEITKHLKAQLDKFIHPG
FNVIMYESYLNLAQKLTEITPGHF
DKKSILLNSGAEAVENAVKIARKYTGRQAVVSFV
RGFHGRTNLTMSMTSKVKPYKLG
GPFAPVYQAPYPNISEKSEDLSDELYTOHIINK
LHDFIETVDPSEVSCIVMEPVQ
EGGFIIIPDIQFVKAVKQICEDNGIVFVADEIQSG
FARTGKTFAIEHDFVEDPLITVSK
SLAAGFPLSGVVGRKEIVDSASPGELGGTYAGNP
LACEAALKVIEIENEDLNGKAEQ
LGHQLEAYLTALSQDYEQVKAIRRLGAMVAFEVV
DPETGEPPDKALTAKIKTANEKGL
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VFEKAIEKQTN"
/locus-tag="SSP0188"
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/Note="similar to
gi|16077459|ref|NP-388273.1|
[Bacillus subtilis subsp. subtilis

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gene	212461..213774
CDS	212461..213774
gene	213864..215243
CDS	213864..215243

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str. 168], percent identity 55 in
457 aa, BLASTP E(): e-149"
/codon-start=1
/transl-table=11
/product="succinate-semialdehyde
dehydrogenase"
/protein-id="BAE17333.1"
/db-xref="GI:72494012"
/translation="MTKLEVINPATNEVLRLDY
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AHERSAKLAQWQALIDDHQLDELARLITLEGGKPL
AEAKGEVAYANSYVWYAEAEAKRV
YGRITPANSPSKKIVIDKFPVGVGAIPTWNPFA
AMITRKMAPALAAGCTIICKPAVK
TPLTTIKLVLELAHQAGFPKDAISYIIASGKDAGD
IFTNHSLSISKVFTTGSTAVGKSLI
ESSAQQVKNVTMELGGLAPLIVHNDADIEAAVDG
TIASKFRNAGQTCICANRIYVHED
IAEAYNEKLIKVKVHALSVGDGLKEEVKIGLIDN
QAVEKVLTHIKDAQEKGQQLSRSI
EDIQALGGNFKPVVITNANLDMKAMHEETFGPV
APVMYTSIDLDEVINIANDETFGLA
SYFFTNDYRTGLKLFNELEYGVIGWNDGGPSAAH
APFGGLKESGYGREGGVEGIEPYL
ETKYLISIQE"
/locus-tag="SSP0189"
/locus-tag="SSP0189"
/note="similar to
gi|52078921|ref|YP-077712.1|
[Bacillus licheniformis ATCC
14580], percent identity 66 in 451
aa, BLASTP E(): e-179"
/codon-start=1
/transl-table=11
/product="putative cationic amino
acid transporter"
/protein-id="BAE17334.1"
/db-xref="GI:72494013"
/translation="MKSQFNKSMNIVDVFLAIG
AMLGWGWVLSGEWVSAAGFIGSI
VAFLLIGLLVIVIGLTYAELASAIPEITGGGFVVF
KKAESPGIAFISGWSVLFGYVSVI
TFEAVALPTVIDYVIPFKHHGFMWNIAGWDVYLT
WVLIGSIGSIVLTSNLYFGVKPAA
IMQTVFTIFIVAVGLLLVFGAGFNGFNSNLPFE
NGVGGTMSVLMMPFLFVGFDVIP
QIAEEVKAPSKKIGGILISIIASVIFYLLIVFG
VATGLSPSALNTSSLATADAMVNL
FGHSGFVLLVLGGVAGIITSWNAFIIGGSRIY
AMAKNMIPQWFAYIHPKFKTPTH
GILFLGVLAFAVAPLGRPALSWIVNAGGIGVVLG
YLLVAISFLKLRKTHPNLERPYRI
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WLIVLVWYLIAGVLYLTQKRKTTE
DAYYSIQGDQKQSDYQ"
/locus-tag="SSP0190"
gene complement (216901..2179
08)
CDS complement (216901..2179
08)
/locus-tag="SSP0190"
/note="similar to
gi|15615816|ref|NP-244120.1|
[Bacillus halodurans C-125],

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percent identity 58 in 327 aa,
BLASTP E(): e-101"
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protein"
/protein-id="BAE17335.1"
/db-xref="GI:72494014"
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GWSGILSIGIGTSMQVFNIIKHPMILVPPTIAS
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gene      complement(218088..2189
78)
CDS       complement(218088..2189 /locus-tag="SSP0191"
78)

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gi|49484802|ref|YP-042026.1|
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aureus MRSA252], percent identity
75 in 296 aa, BLASTP E(): e-122"
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SILEELNKLNDQDLVMLKVTIPTK
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FDKILGETVESIYDASVNNK"
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gene      complement(219104..2198
26)
CDS       complement(219104..2198 /locus-tag="SSP0192"
26)

/notes="similar to
gi|52424522|ref|YP-087659.1|
[Mannheimia succiniciproducens
MBEL55E], percent identity 36 in
244 aa, BLASTP E(): 3e-37"
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/transl-table=11
/product="putative SAM-dependent
methyltransferase"
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CDS	220311..221933	/locus-tag="SSP0193" /note="similar to gi 4574118 gb AAD23898.1  [Staphylococcus xylosus], percent identity 89 in 540 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="choline transporter" /protein-id="BAE17338.1" /db-xref="GI:72494017" /translation="MKKNKVMWDTTFIGSSVILL IAVIPMMVFPKASQEVITKMNDV SSALGSVYLFIGLAILIFVLVIAFGKYGNVTLGK ATDKPEFNFSWAAMLCAGIASD ILYWGIIEMAFYYQDPHPHGKGMTDSALNYATMY GMFHWGPIAWATFVLPAICIGYLL FVKKKPIYKVSQTLRPIILKGQTDGLVGKIVDIIF IFGLLGAATSLALGVPMITAGIE RLTGIDGDNMLMRGAILFLVTAIFAYSSYSLGKK GIKVLSDWNVILSFVLLGFLVIVG PTVFIMETTITSMGNMKNFFEMATWLEPFGGIG GRKETNFPQOWTIFYWSWWIVYAP FIGLFIARISKGRTLKEVVLGTIIYGTLCGMLFF GIFGNVAVFLQISQOFDVIONLNT HGTEATIIIEVLHQLFFHNIIIVLFMLSAVLFLAT TFDSGSYILAAASQKKVIGEPLKA NRLYWAFALCLLPFALMLVGGEKALEVLKTAALL ASVPVLVVVFMMVMVAFMRTLINEDR LKLESRADKYREVERRSLRITQVREQKEDDNL" /locus-tag="SSP0194"
gene	complement(222103..222663)	
CDS	complement(222103..222663)	/locus-tag="SSP0194" /note="similar to gi 4574119 gb AAD23899.1  [Staphylococcus xylosus], percent identity 88 in 186 aa, BLASTP E(): 2e-90" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17339.1" /db-xref="GI:72494018" /translation="MAHSNNPEHQLDEAKDIVIN AIGETMDLYGINRSVGNLFGTMLF EDSMTLDEMREQLQMSKPSMSAGVKRLQEFDIVK QQFTRGSRKQHFIAEKDFNFFFSN FFTRKKWRREIVINAEAVHDAVAILNKIINDESTD AAIKTEANETKQQLIDTLPIYYEWL DHLSDALESGEIFKYFPIPENNYKED" /locus-tag="SSP0195"
gene	222866..224359	

CDS

222866..224359

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[Staphylococcus xylosus], percent
identity 92 in 497 aa, BLASTP E():
0.0"
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dehydrogenase"
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AEDSERAILAARRAFKGEWSLETSENRGKKVRA
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EESYADMDDIANVFNYFAGLADKGGELIDSPIP
NTESKVIKEPIGVVTQITPWNYPF
LQASWKLAPALATGCSLVMKPSEITPLTTIRVFE
LMEEVGFPKGVINLVLGKSGEVGE
PLSAHKEVDLVSTGGIKTKGHIMKQAADHVTDV
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ALNGGFFHAGQVCSAGARIIVHNDIKEKFEAALI
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EHREKIENYMEIAKAENATIAIGGKRPEREDLQD
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GPVVTIEGFSTEAELANDSIYGLAGGVFTQD
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/note="similar to
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[Staphylococcus xylosus], percent
identity 95 in 560 aa, BLASTP E():
0.0"
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PMDYEWKAKPEGMSWDYAHCLFPYFKRLEKTFGA
TKDDQFRGHGPIKLRRGPADNPL
FQAFFDAGVEAGYKNTPDVNGFRQEGFGPFDQSQV
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QTRAFVTKLNFEGNKVTGVTFKKNGREHTVNAKE
VILSGGAINSPOLLQLSGIGDSEH
LRLSLGIEPRIHLPVGENFEDHLEVYVQHACKEP
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GAAASNHFEGGGFVRSNEDVDYPNLMFHFLPIAV
RYDGTKAPAAHGYQVHVGPMSNS
RGHLIKISKDPFVKPDEVFNLYLSTEEDKREWVEA
IKVARNILGQKALDPYNGGEISPG
PEVQTDEEIIWVKRDGETALHPSCSCRMGPASD
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gene  
CDS224416..226098  
224416..226098



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CDS	226149..226304	/locus-tag="SSP0197"
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		/transl-table=11
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		/db-xref="GI:72494021"
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gene	226447..227334	/locus-tag="SSP0198"
CDS	226447..227334	/locus-tag="SSP0198"
		/note="similar to gi 48870927 ref ZP-00323644.1  [Pediococcus pentosaceus ATCC 25745], percent identity 57 in 288 aa, BLASTP E(): 8e-92"
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		/transl-table=11
		/product="putative transcriptional regulator"
		/protein-id="BAE17343.1"
		/db-xref="GI:72494022"
		/translation="MELRTLRYFWTVAEEHAISKAAAVLNITQPTLSRQMDLEIELGVELFYRENGKIMLTEEGIFLKNRAEEIISLTNQTTQEFENKKQALSGHIITIGCVFADNSDTLAMILEEMVREHPLITFHVSGIGSEISERLDKGLLDIAILIEPIAMEKYEQVPLPRPRWGLLVSEDSFPRGQSSIHPGDLKKTKLLMSRRPENQKMISEWSQIAVNDLQVIGTYNLIIFNIFSLVRNNGVSAVVIEGVTSNRNLNLAIFIPFKPELYTHCVLVWKKSRITPILKNFIFKRFKEMNHQ"
gene	227460..227780	/locus-tag="SSP0199"
CDS	227460..227780	/locus-tag="SSP0199"
		/note="similar to gi 48826012 ref ZP-00287241.1  [Enterococcus faecium], percent identity 79 in 104 aa, BLASTP E(): 4e-43"
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		/transl-table=11
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		/protein-id="BAE17344.1"
		/db-xref="GI:72494023"
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gene	227804..228217	/locus-tag="SSP0200"
CDS	227804..228217	/locus-tag="SSP0200"
		/note="similar to gi 48826013 ref ZP-00287242.1  [Enterococcus faecium], percent identity 70 in 134 aa, BLASTP E(): 4e-55"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="BAE17345.1"

gene 228381..228971  
CDS 228381..228971

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K"
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/notes="similar to
gi|45533192|ref|ZP-00184184.1|
[Exiguobacterium sp. 255-15],
percent identity 54 in 191 aa,
BLASTP E(): 4e-52"
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LP"
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/notes="similar to
gi|28378584|ref|NP-785476.1|
[Lactobacillus plantarum WCFS1],
percent identity 51 in 127 aa,
BLASTP E(): 8e-32"
/codon-start=1
/transl-table=11
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protein"
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/db-xref="GI:72494026"
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YGN SAYLPPMLEPGFVSATVKIEPK"
/locus-tag="SSP0203"
/locus-tag="SSP0203"
/notes="similar to
gi|15673857|ref|NP-268032.1|
[Lactococcus lactis subsp. lactis
Il1403], percent identity 37 in
456 aa, BLASTP E(): 4e-82"
/codon-start=1
/transl-table=11
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major facilitator superfamily"
/protein-id="BAE17348.1"
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gene 229005..229388  
CDS 229005..229388

gene 229503..230879  
CDS 229503..230879

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[Lactococcus lactis subsp. lactis
Il1403], percent identity 37 in
456 aa, BLASTP E(): 4e-82"
/codon-start=1
/transl-table=11
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major facilitator superfamily"
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		QGIAAALVSPSILAFINLIYDDGPEKKRAVSFYS TIAGIGASGGLIVGGILTSLSVSWR LCFLINIPMCIIIFILLAIKLLPQTTTSSYPFRID LFGALLSVSVSILLIVLGMERLNMA FSLINFVLILIGLILLITFIAYEHKVKYPIELS LFKNKIRSSGYLLRFLFLSTSFSY WYYMSIYFQDSFNLSPLNTGLLICITTG VNFIVA LNIHKKLLKSQTNISVLIKGILISI VGMILLIFCLNHQVGITMFLPLILIGVQGQFIF TPLNLGVYQVTNEQSGIASGLVN LAHQIGSSAGIVFELIATTLHLILNFENNSSL TLISMVIGTVIQIIMLLYVLLVFK KKENKYEI"
gene	complement(231059..2332	/locus-tag="SSP0204"
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gene	233538..233981	/locus-tag="SSP0205"
CDS	233538..233981	/locus-tag="SSP0205"
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		/product="putative acetyltransferase" /protein-id="BAE17350.1" /db-xref="GI:72494029" /translation="MTIRCAKDNEKLKLINKVIPK LFKAMMNVNFDLSDASLRDMSSQL LLQGAKYVYVLIENICKGFVLIDKKTIDYLEQQDY GFYELYVVFEGYRRQGVAKKLIYF VNDFFKRQHGIGEVRLNVNVQNKAQLLEYKVGFOE RNITMSMKVVE" /locus-tag="SSP0206" /locus-tag="SSP0206" /note="similar to gi 52142287 ref YP-084542.1  [Bacillus cereus ZK], percent identity 66 in 108 aa, BLASTP E(): 2e-39" /codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily" /protein-id="BAE17351.1" /db-xref="GI:72494030" /translation="MKNYRYFIITMIIIMTMINY VDRGAISYAQEDIINEFGFDNIW GSILGYFGYGYMLGSLFGGVATDKKGPKFVWLIA GTLWSLFEIGMAFAGEIGMVLFGG SALAG" /locus-tag="SSP0207" /locus-tag="SSP0207" /note="similar to gi 47528555 ref YP-019904.1  [Bacillus anthracis str. 'Ames Ancestor'], percent identity 56 in 255 aa, BLASTP E(): 4e-79" /codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily" /protein-id="BAE17352.1" /db-xref="GI:72494031" /translation="MLFVILGLLGLVWIIIWYKV FTDYPEDNKHVSQEEIESIQSTEE TVHGKTVETEHNAHEKWYHFFKSPTLIFNMVGY FGFQYINFLILLITWPKYLQDEYHF ELHSLWYLGMLPWIGACFTAYFGGRLSDWLRVKT GSLRIARSGLAIFGMTLAAICFLI IPTTNQIGWIMFLMLGNACIFLPNAVNSVVID TAPKKTGTYYGGITHFFVNSATIIA PTLTGLILVTSYGYSSMFISAVVAVIGIIAMCFV KPGIKMKMPTS" /locus-tag="SSP0208" /locus-tag="SSP0208" /note="similar to gi 48825620 ref ZP-00286863.1  [Enterococcus faecium], percent identity 61 in 204 aa, BLASTP E(): 1e-68" /codon-start=1 /transl-table=11 /product="putative nitroreductase"
gene	234158..234481	
CDS	234158..234481	
gene	234661..235452	
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gene	235715..236341	
CDS	235715..236341	

gene	236489..237631	/protein-id="BAE17353.1"
CDS	236489..237631	/db-xref="GI:72494032"
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		/locus-tag="SSP0209"
		/locus-tag="SSP0209"
		/note="similar to gi 27469130 ref NP-765767.1  [Staphylococcus epidermidis ATCC 12228], percent identity 51 in 383 aa, BLASTP E(): e-111"
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		/transl-table=11
		/product="putative enzyme of poly-gamma-glutamate biosynthesis"
		/protein-id="BAE17354.1"
		/db-xref="GI:72494033"
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gene	complement(237727..238668)	/locus-tag="SSP0210"
CDS	complement(237727..238668)	/locus-tag="SSP0210"
		/note="similar to gi 49484498 ref YP-041722.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 68 in 311 aa, BLASTP E(): e-121"
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		/transl-table=11
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		/protein-id="BAE17355.1"
		/db-xref="GI:72494034"
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gene	239002..240399	GQTYIDDVHGRITISVVDDVEHDAFFKYITNLAKK
CDS	239002..240399	VEQ" /locus-tag="SSP0211" /locus-tag="SSP0211" /note="similar to gi 53771630 ref ZP-00183937.2  [Exiguobacterium sp. 255-15], percent identity 55 in 461 aa, BLASTP E(): e-153" /codon-start=1 /transl-table=11 /product="putative proline betaine transporter" /protein-id="BAE17356.1" /db-xref="GI:72494035" /translation="MKFKKEKVNVRVDSQAKKGV VATGIGNAIEWFDFGLYAQLAVIL SANFFGNLPEMQIVSTFAVFAFAFIVRPIGGIF FSLGDKYGRKIVLSTTILLMAAS TLMLGLLPTQDQIGIWAPILLVVRMIQSFSTGG EYAGAMTYIAETAPDKTRGLGSG LEIGTLAGNIMAAIAGLMYSLLSNQQMADWGR IPFILAAPLGIIGIILRSSLDESP AYESTLEEQEELEYSYLDIFKYWKDVVVCFAGV AFLNVANYMVL SYMPSFLNSTNL GGTMGSILSTIITMLVMIPAVFFFGWYSKVGNGR TIIFGLAGFSLFSVLAFLWMSIFM IPFVILGLFIIALFMSIFEGVMPSSLPSMFHTKV RLRTLSLVYNIGAAVFGGLTPFIL STLVETTQQQIAPSYLLMFINVVGLIIFITMFKS TSNKSRLGSYPNVETQEDYDHVVK NPKDALWWEDEVKRD" /locus-tag="SSP0212" /locus-tag="SSP0212" /note="similar to gi 15923270 ref NP-370804.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 43 in 505 aa, BLASTP E(): e-113" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17357.1" /db-xref="GI:72494036" /translation="MSKTVKIVIAVVGVLICG IGGAAYYFTKNTPKNTYLLSEQE TAKQMKAYGEDRFENEFEFQDKMKDESYLINLNA SADVPEALLKSSDIPKSVADASKL GFKLGHDPPKEHSVIALTPTVADNEIGEFAQWAAD KQNYYYAAPILDDVYKAKNNELVD VYKKTITGETSSVEGTNNGTINDSLNLSLLSGTQ ISQDKIDEISKKYSEVITDKLDD NFEKDDVTIKVNGEDKDVKKVTMNVSKGETKAIL TDILEKAKKDDIKAI AEDQFNAK DYKKQLDDILKEVKDITDKAEFSPVKSIVIWEDDQ ILKRNLTMKDEDSGTVKLNGTSQV DDDNLMIDYKLTTDDQEQVALKGKSTKKDDQYKD NYKVTFDNGYRKS DATLTNTESQD GDKRNDKGQIEINANYDKTTIDFNKLDTDTKNN TQKQELSLSTDIDNETVVINIKGD TKLKEDIKPKKANAQDLNTMSDSDFRKLQREISN NTEDIVKDIADIKDKK"
gene	240640..242145	
CDS	240640..242145	

gene	242196..243362	/locus-tag="SSP0213"
CDS	242196..243362	/locus-tag="SSP0213"
		/note="similar to gi 49482516 ref YP-039740.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 55 in 388 aa, BLASTP E(): e-131"
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		/transl-table=11
		/product="hypothetical protein"
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		/db-xref="GI:72494037"
		/translation="MKTIQLFRIYHSFLLKKWHL FFYLILMMCAFLTALLVVQYVNQD DAKFRIGIVDHDNSAETQLILNSMGNGTHLGKDI RIQRYNQQAQKLLKAQKLEGYYV FEKGMKTIFYKHGNLPIAVYTYDQTSTKSLVINQ LTDVYSRLMLSMGGGLTYTTLSF EANKDDKLQLLTDLFTGLNRTGGFDYQPIQIFD TSSYYVVTGYLASIFIFALSLSFI LKMNQAKALKSRLHMYHFSFEKLTLRSLFTLEY TGVWTLGLCLMIQILPNTFEPYN WPTVVIQLVYIILMITGWLTIIDLICFRWFNIVL KIMLALMVLFSGGIPIITYFKHL LNGMFNVQPFVSFTNQMLEILNNYILDTPITFY MSFVITAILLVIIIVWRYR"
gene	243359..244282	/locus-tag="SSP0214"
CDS	243359..244282	/locus-tag="SSP0214"
		/note="similar to gi 21281983 ref NP-645069.1  [Staphylococcus aureus subsp. aureus MW2], percent identity 43 in 304 aa, BLASTP E(): 2e-75"
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		/transl-table=11
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		/db-xref="GI:72494038"
		/translation="MIQSFIFIIILKQWKQLVIF FTILTCTLLIIWAAYSSLNQSFKI PVAVDQDQSQASHTLIQSIEKNDFVKVEKLDQE AIYLDSESVKKEAVALMHIPKDY DKLKNQKLLALTYARDDFIGDITFEMISRSLY EQQIPYIVKKHLDDGQETSLEKV SDTLNQHTPKSAIVHHVNTNSETSSISLVFGI ILFVSSQIVLHQRLKQNGPLTRL FIFQYSKLILFTTYIILHTLILMLVLGITTFIFQ QQLSFTFFAKSLVIIIVYELGVSW LLFKINTLSHRLFMVIFALLMAVLYIFIQL"
gene	244293..244961	/locus-tag="SSP0215"
CDS	244293..244961	/locus-tag="SSP0215"
		/note="similar to gi 49482514 ref YP-039738.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 66 in 219 aa, BLASTP E(): 2e-80"
		/codon-start=1
		/transl-table=11
		/product="putative ABC transporter ATP-binding protein"
		/protein-id="BAE17360.1"
		/db-xref="GI:72494039"

gene	245161..245475	/translation="MIELKNLSKHYRKKCIFESL DMTFENLQLTVLLGENGAGKSTLL RMIAGLEQLTKGEIRYFGEQLSKQRQDKIGYVP QDIALFEHMTVNENIRCFKALCKT PLSNVLIDEYARQLNLNERTMTISNLSGGTKRKV NVLIGLILSNPQILILDEPTVGIIDL KSRFDIHNLLNTMKRERLIILTTTHLDEVEALAD QIKVIGNDPFYREILEDKHWAFEV YNNK"
CDS	245161..245475	/locus-tag="SSP0216" /locus-tag="SSP0216" /note="similar to gi 22127301 ref NP-670724.1  [Yersinia pestis KIM], percent identity 55 in 99 aa, BLASTP E(): 3e-24" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17361.1" /db-xref="GI:72494040" /translation="MSFLGEHLPLISLVIGVGV LFLNIKLKINSILSLIFA AVLGVF MNGMKPLAILDITKEGLGSTLGLALIIGFAVL GKLMVDSGAAQRIASTLIERFGAK YV" /locus-tag="SSP0217" /locus-tag="SSP0217" /note="similar to gi 22127301 ref NP-670724.1  [Yersinia pestis KIM], percent identity 63 in 91 aa, BLASTP E(): 1e-26" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17362.1" /db-xref="GI:72494041" /translation="MILAPLVISIAIEAKTFPMK LAITMVVATTLSHNIFPPQEGPTA LVDAYNADMGVYILGMIVFIPSVIIAGIILPRF MKRIDYPIPLQLQKKKKFYRQ" /locus-tag="SSP0218" /locus-tag="SSP0218" /note="similar to gi 1009388 emb CAA62859.1  [Escherichia coli], percent identity 51 in 217 aa, BLASTP E(): 5e-59" /codon-start=1 /transl-table=11 /product="putative truncated gluconate transporter" /protein-id="BAE17363.1" /db-xref="GI:72494042" /translation="MPSFGLSLFVPLIPAILISI STLSLFIITEDTILHEIVSFIGSA EISLIPIITAI VMFGLRKGKMDTMMKSFETGL KGVATII FIVGAGGAFKEIILEAH VGDIADIMKGTNISPLIMAWLILIRIATGQG VVSAITAGIVGPLIPTFDVSPVL MVLATAVGSNTTITHVNDASFWLFKEYFNISIKDT
gene	245536..245835	
CDS	245536..245835	
gene	245837..246505	
CDS	245837..246505	



gene	246996..248639	FKTWGCVVINDICNRINGCLNTGS IYLK"
CDS	246996..248639	/locus-tag="SSP0219" /locus-tag="SSP0219" /note="similar to gi 27468939 ref NP-765576.1  [Staphylococcus epidermidis ATCC 12228], percent identity 87 in 537 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="BAE17364.1" /db-xref="GI:72494043" /translation="MGQKDESSKINLPQLVLLGL GSLIGSGWLFGAWEASSIAGPAAI ISWIGFVVIGSIAYNYIEIGTMFPQSGGMSNYA QYTHGSLLGFTAAWANNVSLVTII PIEAVSAVQYMSSWPWEWAKFTSGLMDGSTISNA GLFAVFVIIIVIFSLLNYSVKLLT SFTSLISVFKLGVPLLTIIIMLIISGFDIGNYGH VGTFMPYGSAPIFAATTASGIIFS FNAFTIINMGSEIQKPEKNIARGIAISLTLSAI LYIVLQSTFITSMPTMLHENGWS GINFNSPFADMAILGLNLWLAIIYMEAVVSPFG TGVSFVAVTGRVLRAMEQNGHIPK FLGKMNEKYMIPRVAIIFNAIISMVMVSLFRDWG TLASVISTATLVAYLTGPTTVISL RKMAPKMRPFPRANLLKFMAPPFSFVMASLAIYWA MWPTTAEVILIIILGLPIYFFEY KMNWKNKKQIGGSLWIILYLIVLAFLSFIGSKE FKGMNWIHYPDYDFIVIIIALIFY KIGTSSYFESVYFKRAKKINKMDRADLREKRKSE HISEE" /locus-tag="SSP0220" /locus-tag="SSP0220" /note="similar to gi 49482427 ref YP-039651.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 65 in 393 aa, BLASTP E(): e-150" /codon-start=1 /transl-table=11 /product="putative ornithine aminotransferase precursor" /protein-id="BAE17365.1" /db-xref="GI:72494044" /translation="MLDLYEHTDKYSSKNYSPLK LALAKGRGAKVWDIEDNCYIDCIS GFSVVNQGHCHPKIIKALQEQSQRITMVSRLYS DNLGKWEKICKLANKENVLPMMNT GTEAVETAIKMARKWADIKNIDESSEIIMANG NPHGRTLGSLSLSSQDSYKKGFGP LLNNIHYADFGDIEQLKKLINNOGTTAILEPIQG EGGVNIPPTHFIQEVRLCNEYNV LLIADEIQVGLGRGKMFAMEWENTEPDIYLLGK SLGGGLYPISAVLANQDVMVSLTP GTHGSTFGGNPLACAVSMAALDVLEEHVQNAL DLGDRLLKHLQQIESELIVEVRGR GLFIGIELNVAAQDYCEQMINKGVLCKETQGNII RIAPPLVIDKDEIDEVIRVITEVL EK" /locus-tag="SSP0221"
gene	249096..250280	
CDS	249096..250280	
gene	250325..251356	

CDS	250325..251356	<pre> /locus-tag="SSP0221" /note="similar to gi 57285371 gb AAW37465.1  [Staphylococcus aureus subsp. aureus COL], percent identity 69 in 343 aa, BLASTP E(): e-135" /codon-start=1 /transl-table=11 /product="N-acetylglutamate gamma-semialdehyde dehydrogenase" /protein-id="BAE17366.1" /db-xref="GI:72494045" /translation="MIEVGIVGSGGYGAIELRL LIQHPNVNIKYIFSHSKQDQPIKE TFPHLEQLTYHYETLNLSEGIECDVFFATPSNV KHIVPQLLSKRIKIIDLSGDFRLT NRATYETYTYGETAASQEYLNENYSIAEWSNVNA QTTQLIANPGCFPTATLLALHPLI DKDIVKQDNIIIDAKTGVSGAGRSQAQHVHFAEM NENLSAYAIGKHKHKEIEQYLSL LAQQEVKVTFTPHLVPMTRGILSTIYIKLNHAFT NEDLHNLFKDIYEDKPFVIRISLG QFPKTEVYGSNYCDIGIYVDEENQTAILVSVID NLVKGASGQAIQNLNLMYGWKENT GLLQSPVYP" </pre>
gene	251380..252618	
CDS	251380..252618	<pre> /locus-tag="SSP0222" /locus-tag="SSP0222" /note="similar to gi 49482425 ref YP-039649.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 60 in 413 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="arginine biosynthesis bifunctional protein" /protein-id="BAE17367.1" /db-xref="GI:72494046" /translation="MRDIETIDTLNQLNIDLQGD VSSPLGFIAGGLHCGLRKKVDFG WIYSTTPATATGVYTLNQFAAPLKLTEDSINKD KALQAIIVNSAIANACTGEKGMQD ALDTQAWIAEQNLIEQHLVGVASTGVIGSFLPMD KIQYATQHVLKEQYNKSEAFNQAI LTTDTMTKHL5VKVEIDGTTVTIGGTAKGSGMIH PNMATMLGFITTDANIDANTLDYC LKQSIDQSFNMITVDGDSSTNDMVLCMANGQAQH TQIDALHPEWHKFVYALNFCVHYL AKSIAKDGEKATKLVTVKVKGAHDVVEARKIAKS IVSNLVKTVAVHGEDANFGRIVTA IGYASRYIEPSATHVSLCOVSVLEKGMVAVDQE RLKEELASDNILIEATVGNGEA AAYGCDLSYEYVRINASYRT" </pre>
gene	252631..253392	
CDS	252631..253392	<pre> /locus-tag="SSP0223" /locus-tag="SSP0223" /note="similar to gi 57285369 gb AAW37463.1  [Staphylococcus aureus subsp. aureus COL], percent identity 48 in 252 aa, BLASTP E(): 5e-64" /codon-start=1 /transl-table=11 </pre>

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        kinase"
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        IDDIATQLKQDHLPIIIHGGGPFII
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        KVNPLQVSKMNDENIQSIGLNGID
        AKLPDVEPLNEKYGYGEPININTAVIDHLEET
        YIPVIASIGRHKTSRHLYINADTL
        AYKIAQTLNAPIYLLSDIPGVMIDNKVKATLNSE
        HIKNYIEQEIQYGGMIPKQVDAIS
        AIEYGCQKVVIAAGNEAHVVERIRTGKGIGTTIV
        L"
gene      complement(253710..2549 /locus-tag="SSP0224"
42)
CDS       complement(253710..2549 /locus-tag="SSP0224"
42)

        /note="similar to
        gi|27469138|ref|NP-765775.1|
        [Staphylococcus epidermidis ATCC
        12228], percent identity 60 in 408
        aa, BLASTP E(): e-144"
        /codon-start=1
        /transl-table=11
        /product="putative
        succinyl-diaminopimelate
        desuccinylase"
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        GNREQWSYDFFKLTEDNGYLYGRG
        AADMKESGLAALAIALIEMHDAQLLTKGRIFLAT
        TGEEMEQLGSQLNYEKGymDDVDA
        LIIAEPCQDMVMVYAHKGSMDYRIKSQGSASHSSM
        PIFGVNAIKPLIEFIQIDIDNAYQK
        ISKEIKGESLDFTHLLDRMKPSLPATFAVEEIES
        ALQGLVITNTLIKGQVQVNSVPED
        ADADFNIIRTIPEYNNDQVKNLFNNTIEKHANGS
        NLESELYLDLDPVLTGQNSLIDT
        AKTIGKTAFNKDFVAAPIGGVTDASNLLRGKDES
        PFFLVFGPGKPHQVDERVEKAMY
        LKFIDFYKELLITYSKNY"
        /locus-tag="SSP0225"
        /locus-tag="SSP0225"
        /note="similar to
        gi|49485228|ref|YP-042449.1|
        [Staphylococcus aureus subsp.
        aureus MSSA476], percent identity
        59 in 129 aa, BLASTP E(): 1e-41"
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        /transl-table=11
        /product="conserved hypothetical
        protein"
        /protein-id="BAE17370.1"
        /db-xref="GI:72494049"
        /translation="MTLSLNKIHQAHHQYQYTGVD
        FPKLFKAFKDMGIIIVNTVNIQEGET
        SYIHQDGAELTDESVKVAVPIAQQTHLALVKDIL
        QRHQAGETDFPKFCDEMARAGIYK

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gene	255775..256314	WYIDIIAGTCAYIDKENQVLITENIPQS"
CDS	255775..256314	/locus-tag="SSP0226" /locus-tag="SSP0226" /note="similar to gi 46908521 ref YP-014910.1  [Listeria monocytogenes str. 4b F2365], percent identity 52 in 172 aa, BLASTP E(): 4e-45" /codon-start=1 /transl-table=11 /product="putative FMN reductase NADPH-dependent" /protein-id="BAE17371.1" /db-xref="GI:72494050" /translation="MASVAIIAGGNKIESRLTGV VKYAEKYLNDGDIETDVIHVHQLD AEALITANFESINKTHKKIEADGIIIVSPVF KAAYSGIVKTYLDLLPRGAFGTGKT VLPLALGGTFAHVLAIQYSLDPVIKELGADIHK GRFILDKHTSNEDGTGYGDQAEAK DGLNKTLLKKFVSDKAQVIE" /locus-tag="SSP0227" /locus-tag="SSP0227" /note="similar to gi 1280354 gb AAA98144.1  [Staphylococcus aureus], percent identity 50 in 188 aa, BLASTP E(): 5e-51" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17372.1" /db-xref="GI:72494051" /translation="MPKVVDHEKKQQIIQYAWQ SIVSNGAKGATVRNI AKLARMTPG QIRYYYPNHHDLLKAVSVEVDSKVRGRKAVYND GSLSPLDKVIQAMLKAMPLDEERY ADMEVWLAFQYELHEVGKDSMGNEIFTLIKASMS FLEEHDLLDTSLNQYVVAIMKMHAL LDGLALHKLNLNPEQMINEDEHLEIESEVKS WLRR " /locus-tag="SSP0228" /locus-tag="SSP0228" /note="partial similar to gi 49478076 ref YP-037308.1  [Bacillus thuringiensis serovar konkukian str. 97-27], percent identity 54 in 156 aa, BLASTP E(): 1e-45" /codon-start=1 /transl-table=11 /product="truncated conserved hypothetical protein" /protein-id="BAE17373.1" /db-xref="GI:72494052" /translation="MISRYVLRMKQVGLILLAMT PVIDILLIITMSVDLLNGAKATVP HGIAAVYIGVSIAFRKQMIQWADERFKYYVLKEG NLPEKKTGIAAYAKAYFVSWLHRVL AYLIGTGLLWLIINIVQGQSVAALYHVIKIWTV ILGIDLITLSYFIWPKPKKV"
gene	256481..257065	
CDS	256481..257065	
gene	257136..257609	
CDS	257136..257609	

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gene      complement(257707..2583 /locus-tag="SSP0229"
66)
CDS       complement(257707..2583 /locus-tag="SSP0229"
66)

/Note="similar to
gi|15614705|ref|NP-243008.1|
[Bacillus halodurans C-125],
percent identity 30 in 213 aa,
BLASTP E(): 3e-21"
/codon-start=1
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/product="hypothetical protein"
/protein-id="BAE17374.1"
/db-xref="GI:72494053"
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EETLECPVEVINQDTFIVQIGETQ
LQFCRSEDVIQPYHFAIDIPYNHFYDMKEHYQN
ILFLLMEDGHHTTYFESFVAHAHY
FNDSGNIIVELIARVSNITDEPEFSRISEIGFVC
NETNIAIYQALS DYKIETFEHAHFE
PYALNFLGDTSDSYILLTPEDRRWSFSEKHSIA
YPIDIKTETFHLSYDTRHQWHLKQ S"

gene      complement(258607..2601
96)
CDS       complement(258607..2601 /locus-tag="SSP0230"
96)

/Note="similar to
gi|23097823|ref|NP-691289.1|
[Oceanobacillus ihyenssis HTE831],
percent identity 59 in 528 aa,
BLASTP E(): 0.0"
/codon-start=1
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/product="L-lactate permease"
/protein-id="BAE17375.1"
/db-xref="GI:72494054"
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RMSALKGMIISAFIVTFLGVFVWG
MQGHVISASLLQGTHKTLTILYILFGALVLLNTL
RQTGAVTRINEGFKKLSGDMRVQV
IIVAFLFGLSIEGASGFGTPAVVTAFLMVALGFR
PMIAVVITALIADSVAVSFGAVGTP
VLVGLSTLNDADSSLFOATERITLDDLSSGIFI
PIILIAITLIIFPGTKNLKSIVEM
IPWLACIGFIYVASSFAFVLFGEFVAILGSLT
GLIVAVVTASKGWL LPKNEWKDG
DDSYTPTKSEHMDPLLTAWSPYLMVVILLT
VPLIKDFTTQVLDLSWNQILGFET
ISSDWEFLYSPGTILLLSALFAILIQRSFKDLS
QASVESLNTIKTTGITLVATLVMV
HVFINSINTS DLSIMPEYIAENMSKYLGPWLF
VAPFLGALGSFITGSATVSTLTFS
PIQLNIAQSIGAEPTVLAQAIIGAAGNMICVH
NVVAVCAVNMMPKEGFSVIRKTLG
PALLYCLLVGLSAYIITSIFF"
/locus-tag="SSP0231"
/locus-tag="SSP0231"
/Note="similar to
gi|56965377|ref|YP-177109.1|
[Bacillus clausii KSM-K16],
percent identity 55 in 418 aa,
BLASTP E(): e-138"

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gene      260590..261843
CDS       260590..261843

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gene	262531..263505	/codon-start=1
CDS	262531..263505	/transl-table=11
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		/protein-id="BAE17376.1"
		/db-xref="GI:72494055"
		/translation="MNKKLAKMGMPPTLLWGYIG VLIFMMDGGLAWISPYLHDHGL SVHQTAILTTCYGVIIAIGSWFSGVLVEIIGPRK VMLLGTLLYIIGHMIFVGLALPSM NYGLMIPSYAIRGFGYPLFAYSFLVWVAYRSPQR RLGAAGWFWFVFVTGGLSVLGSFY SSMAIQIFGHIFTLWTAILWVIVGTFLAVFVNDR KFEIENKNGFKTHLKEMGAGITI LKREPRVAVACIVRIINQAAQYAPFLPLPIYLST KGIATTTWLNINGTIFIANIIFNL IFGALSDKIGWKNITISYIGGIGCAVFTLGLYFIP EIFTGNVFI VGTGVLWGMCLAGF VPISALVPSLVHDGDKGPAMAILNLGAGLCVFAG PGLVALFYDSIGVQGMMLIFGLY VASAIMTRFLKTPEERGILNEKEAT"
		/locus-tag="SSP0232"
		/locus-tag="SSP0232"
		/note="similar to gi 48824874 ref ZP-00286199.1  [Enterococcus faecium], percent identity 61 in 321 aa, BLAST E(): e-112"
		/codon-start=1
		/transl-table=11
		/product="ornithine carbamoyltransferase"
		/protein-id="BAE17377.1"
		/db-xref="GI:72494056"
		/translation="MKTCDFSADLHLLIDFTGE LKEKKRGIPHPYLGKGNLAFLE KPSRTRRSFSAAYDLGAYPEYFGQGDHILGVK ESSED TAKVLGRMYDGI EFRGHQ KDVEALAKNAGVPVWNLITNEWHPTQMIADFFTL KEHWGTLQGGKTLTYVGDARNNAH DLLITGAILGVNIHVAAPKALQPDEDIQVMAQKY AAESSDILITDDIQQAIIYQTDAL YTDVWFSGMGEDQSLEPRINQLLPYQVNKEMLIN TMNPDVIVLHCLPAFHDVNTQVQG QIYETYGLTEMEISDDVFKEHAVIFDQSENRLH SIKAIMAVTLGDIF"
gene	263960..264418	/locus-tag="SSP0233"
CDS	263960..264418	/locus-tag="SSP0233"
		/note="similar to gi 57286687 gb AAW38781.1  [Staphylococcus aureus subsp. aureus COL], percent identity 87 in 87 aa, BLAST E(): 6e-37"
		/codon-start=1
		/transl-table=11
		/product="truncated phosphotransferase system glucose maltose N-acetylglucosamine-specific IIC component"
		/protein-id="BAE17378.1"
		/db-xref="GI:72494057"

gene 264213..265496  
CDS 264213..265496

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/translation="MSKLFEKAQQFGKSFMLPIA
ILPAAGLLLGIGGALSNPNTIKAY
PVLDIALLQNIFILMSAAGNIVFQNLPIVIFAVGV
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RCIWRYYHRRYDSFVT"
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/note="similar to
gi|15923232|ref|NP-370766.1|
[Staphylococcus aureus subsp.
aureus Mu50], percent identity 80
in 421 aa, BLASTP E(): 0.0"
/codon-start=1
/transl-table=11
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phosphotransferase system glucose
maltose
N-acetylglucosamine-specific IIC
component"
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VIFFIWPTVQGWIFGIGGLVDKTVIGITFFFGFI
LRLGPFGLHHIFYLPFWQTAGDG
SLEVKGHMVQGTQNIFFAQLGDPDVTKYFSGGSR
YMSGRFITMMFGLCGAALAIYHTA
KPERKKVVGGLMLSAAITSLTGTITEPLEFSFLF
VAPMLYVIHAVLDGLAFMMADIFN
ITVGQTFSGGFIDYLLFGVLQGNKTNFLWVIPI
GIVWFVLYYVIFRYLITKFNFKTP
GREDEGVTTETVEATDRAKTI IQALGGKENIDVVD
CCATRLRVTLNSDKAVDKTMLTFT
EARGVIQKGNQVQVIYGPHTTIKNEVEELLEND
K"
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gene 265664..266293  
CDS 265664..266293

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/locus-tag="SSP0235"
/note="partial similar to
gi|49482798|ref|YP-040022.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity
60 in 198 aa, BLASTP E(): 2e-62"
/codon-start=1
/transl-table=11
/product="putative truncated
glucosamine-6-phosphate isomerase"
/protein-id="BAE17380.1"
/db-xref="GI:72494059"
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NVVTFNLDEYVGLSAEHNQSYHYV
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EQLRGEIGSADIQLGIGENGHIG
FNEPYSSESFVTRVVDLTPSTINANSQHFENIED
VPKQAISMGLSSIMKAKRIILLAF
GKNKQQAIAKALLEGEVSEALPASILHKHPNVEVI
IDDEIFTSLIEDGTL"
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gene 266539..267387  
CDS 266539..267387

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/locus-tag="SSP0236"
/note="similar to
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gi|16119885|ref|NP-396590.1|
[Agrobacterium tumefaciens str.
C58], percent identity 37 in 273
aa, BLASTP E(): 2e-58"
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/transl-table=11
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quorum-quenching N-acyl homoserine
lactonase"
/protein-id="BAE17381.1"
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HEFPITYTVFIDHPDAKILFDACPNAMGDSGRW
ISATQKAPPYFADEACHLPNRLEQ
INVDPKEVDVFIASHLHLDHAGCLEYFTNATIIV
HDELSGAMKTYARNQQEGAYIWA
DIDAWVKNNLKWRITIKKEEDNLKLVGVRILNYG
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DAITYKESIEDTLKPPGILYDSIGWTKSVEKIQR
LAKEKNAQIWFHGDGEQFEGFRKS TEGYYE"
/locus-tag="SSP0237"
/locus-tag="SSP0237"
/note="similar to
gi|23100256|ref|NP-693723.1|
[Oceanobacillus ihayensis HTE831],
percent identity 66 in 375 aa,
BLASTP E(): e-147"
/codon-start=1
/transl-table=11
/product="putative Zn-dependent
alcohol dehydrogenase"
/protein-id="BAE17382.1"
/db-xref="GI:72494061"
/translation="MKTRA AVLREMGKDAPYTES
HPLTIETLELQGPQSNEVLKIGA
VGLCHSDLSVINGSRPRFPMVLGHEAAGEIIEV
GENVAEFEVGDHIVCTFIPSCGHC
IPCREGRPALCENGAAANEKGEMLEGGFRYESDR
DEVMMHHHLGVSGFADYAVVSTNSI
VKVDKKIPFEKVAIFGCAVITGIGAVINTARINA
GSTVAVVGLGGI GLNAILGARLAG
ASEIIALDINEEKFALAKSLGATAVFNSGEAHTI
EDIKQYTQGGVDYAFETAGVVPAM
DVAYQITRRGGMTTITGLPDPKHQFSFPQVTLAA
EERTIKGSYVGSVCPDRDIPRFIN
LYHQGRLPVNELLTDTLPLEHINEGFDRLARGEA
ARLVVKMD"
/locus-tag="SSP0238"
/locus-tag="SSP0238"
/note="similar to
gi|42519794|ref|NP-965724.1|
[Lactobacillus johnsonii NCC 533],
percent identity 56 in 435 aa,
BLASTP E(): e-137"
/codon-start=1
/transl-table=11
/product="phosphotransferase
system cellobiose-specific
component IIC"
/protein-id="BAE17383.1"
/db-xref="GI:72494062"

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gene	267443..268573
CDS	267443..268573

  

gene	268584..269900
CDS	268584..269900



gene	269919..270815	/translation="MSRFNDTLEKYLLPVASKLG SNKILISLRDGIIVAMPLIIIGSL FLVISGIAIPGWIEWLEAQGIQPYLMKAVNGTFG LMGLVASFGVAHSIARQYDTDGVS AGIISMAAFLVVTNPMVTGGKTSSEAIPQMYMGS QGFLVALIIGIFSGLIQFQWFINRN IRIKMPDQVPPAVAKSFSALIPGAVIILLWLIY IALDNLFPFGNIHDLIVNTLGVPLS LMGSTLIGTIILVGLNSAFVFWGIHGAVNVNAV QPIWLKNIDENRIVYQANPHGDL HIITQPFIDNFVFMGGGGSTIGLVIVIAILAFKK RSSKITKTMAPLTLMPGIFNINEP TLFGLPVVLNVRLIVPFIAPMINATITYFAMAS GLVHLTNGTAMPWTIIPPIISGFLA TGHVSGSLVQMVCIIVDILLYPPFYRTMEKYNLQ LEQKEADETKEI"
CDS	269919..270815	/locus-tag="SSP0239" /locus-tag="SSP0239" /note="similar to gi 42519793 ref NP-965723.1  [Lactobacillus johnsonii NCC 533], percent identity 60 in 300 aa, BLASTP E(): 1e-97" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17384.1" /db-xref="GI:72494063" /translation="MVKRLLSANASEIVEMTATE LKQSIKASDGRVVLSENVVTRTPV IPDITNAELARAFGADLILLNGLDAFDPKVVND EDKQVINELRRLVCRPIGVNLEPV DKTATMSEKLNIVEGRQASSKTVKALEKLGINF ICMTGNPGTGVNDRKIVNAISETR KHFTGLIIAGKMHSAGVDEPVITETIYVDQFIDAG ADIILVPSIGTVPGFDEEQLKNI KAVHRRGLVMSAIGTSQESSDPSTIRDFAIRNK ICGVDIQIHIGDAGYCGLAPVNNIF ELSKAIRGERHTVSMIARSIQR" /locus-tag="SSP0240" /locus-tag="SSP0240" /note="similar to gi 48826183 ref ZP-00287408.1  [Enterococcus faecium], percent identity 64 in 104 aa, BLASTP E(): 1e-30" /codon-start=1 /transl-table=11 /product="phosphotransferase system cellobiose-specific component IIB" /protein-id="BAE17385.1" /db-xref="GI:72494064" /translation="MAEKTIMLVCAAGMSTSMVLV QKMKEAEKQKQLDRDIFAVSTSEA DQKIESDNIDVLLGQVRFKKDEYTKKCEKDI PVAVIEMRDYGTMMGENVLNTAEQ LMTK" /locus-tag="SSP0241" /locus-tag="SSP0241" /note="similar to gi 48869880 ref ZP-00322617.1
gene	270852..271172	
CDS	270852..271172	
gene	271183..271509	
CDS	271183..271509	

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[Pediococcus pentosaceus ATCC
25745], percent identity 57 in 107
aa, BLASTP E(): 9e-28"
/codon-start=1
/transl-table=11
/product="phosphotransferase
system cellobiose-specific
component IIA"
/protein-id="BAE17386.1"
/db-xref="GI:72494065"
/translation="MSEAENSELEFAMSLIAYSGD
AKSHAMEAIYAAKKNAFEEAEKKL
KLAEVSLLEAHHIQTNNMLTKEAQGDEIKMSLLTI
HSQDHLMTAITFKDMAAEMIDLYK KMDSKA"
/locus-tag="SSP0242"
/locus-tag="SSP0242"
/notes="similar to
gi|57285143|gb|AAW37237.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 68
in 264 aa, BLASTP E(): e-103"
/codon-start=1
/transl-table=11
/product="ABC-type amino acid
transport system periplasmic
component"
/protein-id="BAE17387.1"
/db-xref="GI:72494066"
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GTSDDKNDNDNKNKTASENKTFFVVG
TEGTYPFFSYHDKQDKLTGYDIDVMKAVAKEMGY
KVKFKETQWDSMFAGLDSGRFNVI
ANQVGINDERKEKYKSEPTYSEAVLVVNKNNK
DIKSFDDVKGKKLAQTFTSNYKGL
AKSKGAELTKVDGFNQAMDLLQSNRVEGTFNDNI
SYLDYKKQKPNADVKIIEGNAEKS
QSALTFSKKEDDATIEKVNKAMKKLDNGELAKI
SKKWFGEDVSKS"
/locus-tag="SSP0243"
/locus-tag="SSP0243"
/notes="similar to
gi|49484629|ref|YP-041853.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity
89 in 239 aa, BLASTP E(): e-117"
/codon-start=1
/transl-table=11
/product="ABC-type amino acid
transport system permease
component"
/protein-id="BAE17388.1"
/db-xref="GI:72494067"
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APMLEGLVKFSIPITLVTFLLGLV
IALLTALMRISTSRILRGIARFYISIIIRGTPMIV
QLFIIFYGIPELGRLLTNNSENQW
TLAPVIAAIIIGLSLVNGAYASEIIRGGIMSPKG
QTEAAYSIGMNYRQTIQRIILPQA
IRVSVPALGNTFLSLIKDTSLLGLILVAEMFRKA
QEVASTTYEYLTIIYLLVALMYWVV
CFIISIAQNFIYESYLERGYRS"
/locus-tag="SSP0244"

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gene	271743..272537
CDS	271743..272537

  

gene	272521..273240
CDS	272521..273240

  

gene	273237..273968
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CDS	273237..273968	/locus-tag="SSP0244" /note="similar to gi 15925402 ref NP-372936.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 83 in 242 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="ABC-type polar amino acid transport system ATPase component" /protein-id="BAE17389.1" /db-xref="GI:72494068" /translation="MIELKNIKKSFDDKEVIKGI DLNVNQGEVVTFIGRSGSGKTTLL RMINALELPTEGAVVYVNGETYSNADKKSQIKVRK QSGMVFQSYNLFPHKTALENVMEG LITVKKTKKDEAKQALALLEKVDLTAVKQDRPN ALSGGQQQRVAIARALAMNPKVML FDEPTISALDPELVNDVLRKIDLANEGMTMIIVT HEMRFAKEVSNKIVFIHDGVIGES GPPEQIFNHPQSAELQRFNLMIREV"
gene	274312..274827	
CDS	274312..274827	/locus-tag="SSP0245" /locus-tag="SSP0245" /note="partial similar to gi 57286778 gb AAW38872.1  [Staphylococcus aureus subsp. aureus COL], percent identity 42 in 135 aa, BLASTP E(): 1e-23" /codon-start=1 /transl-table=11 /product="putative truncated transcriptional antiterminator" /protein-id="BAE17390.1" /db-xref="GI:72494069" /translation="MLSKRQYHILMFIECETFV QIHHLATHFNVTERTIQYDLEYIE DMASNLGLIIQRTKQEGVKITTTPEQLKRFHKS THTTIHYAKEERLLYITLKLEAN TPTSSQVLATTVSVSRRITVEDLKSQVQNWLEQHD YLAIAECAFDVLAHLNKFVKYRYG VTAYQYMSKLLK"
gene	complement(274922..275839)	/locus-tag="SSP0246"
CDS	complement(274922..275839)	/locus-tag="SSP0246" /note="similar to gi 47527176 ref YP-018525.1  [Bacillus anthracis str. 'Ames Ancestor'], percent identity 59 in 303 aa, BLASTP E(): e-102" /codon-start=1 /transl-table=11 /product="putative 2-dehydropanoate 2-reductase" /protein-id="BAE17391.1" /db-xref="GI:72494070" /translation="MRILVLGAGGIGGYFGGRLA ESGQNVTFLVRPKRKSFLERNGLA IHSEQGDYHFNPLQITKDDRVAFFDVILLSSKSY HLEQAMTDLKPFDGHTAIIPLLN GVAHIPQLQSIFGDKVMGGYCVIETTLDSMGEI

gene 276053..276808  
CDS 276053..276808

IQTSPFDKLFFFGELDGSKSERAQK  
IAQAFSETKAEFKLSTSI EQGMWHKYLMITVLSS  
ITTLMHAPIGP IRSDSGGINFVRS  
LYNEVASIMRAHRAPLADDIVSQYMTSFNQLSYH  
FKTSMQORDMEKGLNIETGHLQGYL  
LNLADTYQIDAPLLKCVYQNHKVYKEMLK"  
/locus-tag="SSP0247"  
/locus-tag="SSP0247"  
/note="similar to  
gi|27468804|ref|NP-765441.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 37 in 252  
aa, BLASTP E(): 4e-41"  
/codon-start=1  
/transl-table=11  
/product="putative metal-dependent  
membrane protease"  
/protein-id="BAE17392.1"  
/db-xref="GI:72494071"  
/translation="MSFKNDHKYQWKDMQGGKDFL  
LPFIYLIGNFCLSIIVILTIMIGIN  
ETQGGNNANFNANFSGTGPGLIMEMIAFIIIFALW  
ILFHRHSFRQSWKQGLQNIKQHWK  
LIVITFIVIIIVFKEIYPYLVNAFAPEHWKFETQ  
NDKMVEEMFATPVSTILAFFSIVI  
IAPMTEEFLEFRHLIIGELGKKLNFYVMSVISIIV  
FASLHVTEAKSPLEIVMYLAIAGV  
IVYVYMKSQRSRLAVAIALHALNNLLAYIFMIIM"  
/locus-tag="SSP0248"  
/locus-tag="SSP0248"  
/note="similar to  
gi|27467520|ref|NP-764157.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 63 in 270  
aa, BLASTP E(): 1e-96"  
/codon-start=1  
/transl-table=11  
/product="ABC-type uncharacterized  
transport system periplasmic  
component"  
/protein-id="BAE17393.1"  
/db-xref="GI:72494072"  
/translation="MRKWFI LGSFLVLTIIILAAC  
GKSNGEKEDKEITIAASPAHPGVV  
LEHAKEEMKKKG YDLKIKTVNDYKVPNKLLDKGD  
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EAGKVFTTPMGVYSKKYKDIKIDIPKGSTIYVSNH  
PAEEGRFLSFFVDKGLIKIKKGV  
IEDAKFDDIVENKKDLKFNNKQGAFLPKTYNSK  
EGAAVIMNSNYAIDNGLTPHKDAI  
AIEGKSSPFANIVAVQEGHKNDKKFKELMKVLQS  
KEMKKFITDKYQDVIPYEK"  
/locus-tag="SSP0249"  
/locus-tag="SSP0249"  
/note="similar to  
gi|15896788|ref|NP-350137.1|  
[Clostridium acetobutylicum ATCC  
824], percent identity 36 in 308  
aa, BLASTP E(): 2e-54"  
/codon-start=1  
/transl-table=11  
/product="lactate dehydrogenase"

gene 277150..277968  
CDS 277150..277968

gene 277150..277968  
CDS 277150..277968

gene 278012..278944  
CDS 278012..278944

gene 278012..278944  
CDS 278012..278944

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/locus-tag="SSP0250"
/locus-tag="SSP0250"
/notes="similar to
gi|57286566|gb|AAW38660.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 41
in 184 aa, BLASTP E(): 2e-36"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="BAE17395.1"
/db-xref="GI:72494074"
/translation="MSMGGVMMLEHRHVKLIRLML
INRNQFLNADEIARYLNVSNRTAR
NDIQYINSEILDDLIVSVKGRGYKLNQSLYSMQQ
IETIVTDFTNKESELLIKLGYQLL
MYQQPLTSEAIGKTFHLTKAEVTDYINKIKAWCI
SFDVNIQITKKKGITVNGSEMNI
NAILHLNLQSENKVTVDAFILAEHQYMKHQTEDF
IYLTISTGVGMAYIRKGLSVGVN
GNFGEIGHTIIKGDSDYQCPVCKQYVCVENEISG
LAISRKASHILNKHVS TREAIEMY
LHQAHSEITEMIDEVLILTQQLCTNLFSIFNINN
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/locus-tag="SSP0251"
/locus-tag="SSP0251"
/locus-tag="SSP0251"
/notes="similar to
gi|56418819|ref|YP-146137.1|
[Geobacillus kaustophilus HTA426],
percent identity 68 in 419 aa,
BLASTP E(): e-161"
/codon-start=1
/transl-table=11
/product="O-acetylhomoserine
sulfhydrylase"
/protein-id="BAE17396.1"
/db-xref="GI:72494075"
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DFS KARAVPIYQTSSYVDNTEHA
RKLFALEEDGNIYTRIMNPQTQNVFEERIAALEGG
VGALATSSGQAAIHLALLNIVESG
DEIVASSNLYGGTYNLLNITFKLGIKVHFVDP
HPDNFKNAITDKTKAVYAETIGNP
RIDVLDIEAVADIANNHNIPLIVDNTFTPTYLLR

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		PFEFGADIIVHSATKFIGGHGTSI GGVIVDSGKFNWDNGKFPGLVEPDESYHGISYAK DVGEAAIYITKARVQLLRDLGSAVS PPNVHEFLIGLETLHLRLRHSINALRVAQYLEQ HPKVTVWVNYPLKNNAYHQLAQKY LPDQGQAILTFGIDGTVDIAKFDGLNLFSLHA NVGDSKSLIIHPASTTHLQLSPED QKASGVVPELVRLSVGTENINDIIADLNGPKES LGN" /locus-tag="SSP0252" /locus-tag="SSP0252" /note="similar to gi 27469242 ref NP-765879.1  [Staphylococcus epidermidis ATCC 12228], percent identity 67 in 299 aa, BLASTP E(): e-110" /codon-start=1 /transl-table=11 /product="cysteine synthase" /protein-id="BAE17397.1" /db-xref="GI:72494076" /translation="MIAFDLIGNTPLVLLESFSN KDVQIYAKLEQYNPGGSVKDRLGK HLIETAIRENIIQKGDVVVEASAGNTGIGVAIAA NHYGVSAVIFAPEGFSEEKISIIK ALGAEVIRTDQTLGMAQAQAARDYELQTGAYYL NQFESYRNPETYKSTIGKEITDKL KDIDYFVGGVSGGTFGTGVAEHLAATYHTESVIV EPEGSILSGGNAHSHDIEGIGSEK WPSFLPKALVSDIIKVSDDAAFNQVKLLARQEG LVGSSSGAALQGALEIKKHINKGV IVTIFPDGSDRYMSKQILNYKETIK" /locus-tag="SSP0253" /locus-tag="SSP0253" /note="similar to gi 27469241 ref NP-765878.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 380 aa, BLASTP E(): e-176" /codon-start=1 /transl-table=11 /product="cystathionine gamma-synthase" /protein-id="BAE17398.1" /db-xref="GI:72494077" /translation="MNKKTQLIHGGQTTDPYTGA VTTPIYQTSYMQDGIQDMRQGYE YSRANFTRSALEGLIADLEQGESGFAGSGMAA ISAVIMLLDKGDHLLINSVDVGGT YRALTKVFNRFIDAEFIDTNNIEAVEQYIKPET KMLYIETPSNPLLRVTDIKKSAEI AKKHHLISVDNFTMTPYFONPLTLGIDIVLHSA TKYIGGHSDDVAGLVATSDAEALAE RLGF IQNSTGGVLPQDSYLLIRIGIKTLGLRMEQ VQRNTLAIIDMLQQHSAVKQVFHP SISDHLNHDIEAQSEGHTGVVAFEVADIESAKK VISESHYFTLAESLGAVESLISVP ALMTHASIPKDIREKEGIADGLVRLSVGIETDKD LVEDLEQSLNALG" /locus-tag="SSP0254" /locus-tag="SSP0254"
gene	282093..282998	
CDS	282093..282998	
gene	282995..284140	
CDS	282995..284140	
gene	complement(284238..>284900)	/locus-tag="SSP0254"
CDS	complement(284238..>284900)	/locus-tag="SSP0254"

900)

/note="Start codon is not  
identified similar to  
gi|23097745|ref|NP-691211.1|  
[Oceanobacillus ihayensis HTE831],  
percent identity 42 in 156 aa,  
BLASTP E(): 3e-31"  
/codon-start=1  
/transl-table=11  
/product="putative truncated sugar  
phosphate permease"  
/protein-id="BAE17399.1"  
/db-xref="GI:72494078"  
/translation="RYFCKHTYRHCLYTARYIYC  
TIWTFKPIVQLTGNYSIDIALSIF  
WILIGIFGVVGIGSGSIIDKKGIHFAFNFGVIAL  
ACASVLLAYTPSIWLLPFIASSLF  
GLSYIFLTGVLVWGIKLFVKNASLGIGIPFLLL  
AVGQVIGSSIAGIVIDILNYEYSF  
IIFGIIGLPLLIYPKVEVTENKIPKGRYSKLQK  
TNSDILNDTYAQHQTSTNSNNDKYN HI"  
/locus-tag="SSP0255"

gene complement(284804..2854  
87)

CDS complement(284804..2854  
87)

/note="similar to  
gi|23097745|ref|NP-691211.1|  
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percent identity 42 in 223 aa,  
BLASTP E(): 2e-41"  
/codon-start=1  
/transl-table=11  
/product="putative truncated sugar  
phosphate permease"  
/protein-id="BAE17400.1"  
/db-xref="GI:72494079"  
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GRFSFGLFLPDITNDLSLSASQAG  
LISSLFYLAYCFTIVYSTLTQDTIGPKRMILAG  
ISVVIGLITIGVSSNAIILSIGVI  
FTGASTGLVSPFYGYTISLWINLQDQKANTLIN  
SGTSMGLMFTGITAMLVFLDWRDT  
YLIYALIALVVLFWNYIVIPKLOKDIKHTGSLN  
IRDISASTRIVTASTLLGISTAFF  
GLSQNPLSN"

gene complement(285621..2861  
75)

CDS complement(285621..2861  
75)

/note="similar to  
gi|23097744|ref|NP-691210.1|  
[Oceanobacillus ihayensis HTE831],  
percent identity 37 in 181 aa,  
BLASTP E(): 5e-29"  
/codon-start=1  
/transl-table=11  
/product="putative transcriptional  
regulator"  
/protein-id="BAE17401.1"  
/db-xref="GI:72494080"  
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FKGVGLKQIIQEANVATMTLYNHF"

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ESKDNLVAQVLKQRETRYWHYLDSHVEQHPEKPF
ISAVTAHCQWLNDYSYKQDMFMRA
IEDYADTDNEIESTARGHKERLLHYLEKLADDAG
IENGYDLAVQYITLLLEGTTSM TAL
LGSKDATSHAITMAKLLNEAHNQ"

gene      complement(286349..2868 /locus-tag="SSP0257"
19)
CDS       complement(286349..2868 /locus-tag="SSP0257"
19)

/Note="similar to
gi|57285077|gb|AAW37171.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 44
in 152 aa, BLASTP E(): 2e-30"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17402.1"
/db-xref="GI:72494081"
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STDYRHSQDVTMFVSAHISFLKELLDESFYIK
VHIYDYDAKRVLFLIMYNSNDER
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/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="BAE17403.1"
/db-xref="GI:72494082"
/translation="MVLVALILFIISIVFLIYSI
TLLMGKDGIMFSLFTKEEKALTKG
QKLIYILITIVLFVASLVWLLNLI"

gene      complement(287290..2881 /locus-tag="SSP0259"
32)
CDS       complement(287290..2881 /locus-tag="SSP0259"
32)

/Note="similar to
gi|57286412|gb|AAW38506.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 66
in 277 aa, BLASTP E(): e-112"
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/transl-table=11
/product="urease accessory protein
Ured"
/protein-id="BAE17404.1"
/db-xref="GI:72494083"
/translation="MSNNKQAWTGQLDLSVFNNG
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LTSQGATKIYKTLNDHVEQYQTFN
IKNNGYAEYVGDPIIAFENAKFYQHNVFNLESTA
SLFYTDILTPGYSKSDKRFSYTYM
HLLNEIYVDDALVTFDNMLDLPQKQNVDDLGYME
DYTHLGCYFIHPSVNOQKFIQVY
EEIKHFQHKYDCRFGITHLPTHGFSRLRILSNKTQ
VIESIITAVQCXVVKQIFDRDVF LRLKY"

gene      complement(288133..2887 /locus-tag="SSP0260"

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47) complement(288133..2887 /locus-tag="SSP0260"
47)
/note="similar to
gi|511070|emb|CAA84509.1|
[Staphylococcus xylosus], percent
identity 97 in 204 aa, BLASTP E():
e-109"
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/transl-table=11
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ureG"
/protein-id="BAE17405.1"
/db-xref="GI:72494084"
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IEKIVKRLAKDMSIGVITNDIYTK
EDEKILVNSGVLPEDRIIGVETGGCPHTAIREDA
SMNFAAIDELKERNDIELIFIES
GGDNLAATFSPELVDFSIIYIIDVAQGEKIPKGG
QGMIKSDFFVINKTDLAPYVGASL
DRMAEDTKVFRGNRPFFTNTLKTDEGLDEVIQWI
EQDVFLKGLA"
gene complement(288761..2894 /locus-tag="SSP0261"
50)
CDS complement(288761..2894 /locus-tag="SSP0261"
50)
/note="similar to
gi|15925282|ref|NP-372816.1|
[Staphylococcus aureus subsp.
aureus Mu50], percent identity 75
in 229 aa, BLASTP E(): e-100"
/codon-start=1
/transl-table=11
/product="urease accessory protein
UreF"
/protein-id="BAE17406.1"
/db-xref="GI:72494085"
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LKLDRILFVQNLPKETROGSKQMG
NRMVKLASELYSDWINWYHAQMKDKKASLHPAI
CFTMLGHHLGVDIETIIDYLYQN
VSSLTQNAVRAIPLGQTAGQRIVHKMIPIMKETR
DHIMTIPASQLGITAPGLEINQME
HENVNVIRIFIS"
gene complement(289443..2898 /locus-tag="SSP0262"
95)
CDS complement(289443..2898 /locus-tag="SSP0262"
95)
/note="similar to
gi|27468782|ref|NP-765419.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 88 in 150
aa, BLASTP E(): 5e-73"
/codon-start=1
/transl-table=11
/product="urease accessory protein
UreE"
/protein-id="BAE17407.1"
/db-xref="GI:72494086"
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LPAQFTETETMLVQYDYLVESLLKDLGIPYEHDR
KVNKAFRHHIGHSHD"
gene      complement(289906..2916 /locus-tag="SSP0263"
21)
CDS       complement(289906..2916 /locus-tag="SSP0263"
21)
          /note="similar to
          gi|410516|emb|CAA52680.1|
          [Staphylococcus xylosus], percent
          identity 96 in 571 aa, BLASTP E():
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          AGNPDIMDNVDIIIGATTDIISAEGKIVTAGGID
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          GGTGASEGKATITVTPGFWHLHRMLLAAESLPLN
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          GLKVHEDWGATPSALDHALQVADDYDVQIALHAD
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          TEGAGGGHAPDLIKSAAYANILPSSNTNPTLPYTV
          NTIDEHLDVMVITHHLNASIPEDI
          AFADSRIRKETIAAEDVLQDMGVFSMVSSDSQAM
          GRVGEVITRTQVAHRMKEQRGILL
          DGDSEYNNNRIRKRYIAKYTINPAITHGISDYVG
          SIDEGLADIILWEPAFFGVKPDV
          IVKGGLINAAINGDANGSIPTSEPLKYRKMYGQL
          GGNLQSTSMTFVSTTAYENDIGKL
          LGLKRKLRPVHNIRKLSKKDMKNNNATPDLDVDP
          QTYEVFVDGEKITSEPA TELPLTQ RYFLF"
gene      complement(291627..2920 /locus-tag="SSP0264"
31)
CDS       complement(291627..2920 /locus-tag="SSP0264"
31)
          /note="similar to
          gi|410515|emb|CAA52679.1|
          [Staphylococcus xylosus], percent
          identity 86 in 134 aa, BLASTP E():
          1e-63"
          /codon-start=1
          /transl-table=11
          /product="urease beta subunit"
          /protein-id="BAE17409.1"
          /db-xref="GI:72494088"
          /translation="MKPGEIIVKRTEIEVNQGHN
          ATILNVKNTGDRPIQVGSYHFFFE
          ANPALQFDHEKAYKRLDIPAGAAVRFPFGDEKE
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gene      complement(292047..2923 /locus-tag="SSP0265"
49)
CDS       complement(292047..2923 /locus-tag="SSP0265"
49)

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/note="similar to
gi|581787|emb|CAA52678.1|
[Staphylococcus xylosus], percent
identity 99 in 100 aa, BLASTP E():
3e-49"
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EMEIATFPDGTGLITVHHPIV"
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/note="similar to
gi|27468778|ref|NP-765415.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 52 in 294
aa, BLASTP E(): 3e-88"
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protein"
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KFVNADVNILPNAIQEIQFSGHHI
QFINAFLSGFSEIFLLKSVLAGTLILIGIFIASR
KAGVYAIVANLIGFLAVIVLGANH
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/locus-tag="SSP0267"
/locus-tag="SSP0267"
/note="similar to
gi|57286681|gb|AAW38775.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 62
in 485 aa, BLASTP E(): e-175"
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diptide oligopeptide nickel
transport system periplasmic
component"
/protein-id="BAE17412.1"
/db-xref="GI:72494091"
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SGNESKGKTLNVELPLKTTISIAPY
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SPTQLDLKLKDDIKFQNGKKVTGQ
AVKASLEESIKKSDLVRGSLPIKEIKVDGQNVSI
TTKEAYPELVSELASPFSAIYDTK
ADSDVTKAPVGTGPYQIKDKQSQNIKLDQFKDY
WQGPKLHDHVNVTYQEDGNARSSD
LSSGKADVITDPVEKEKTLNQGDKTTTSSVSGF

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gene	292565..293467
CDS	292565..293467
gene	293559..295037
CDS	293559..295037

gene	295034..296014	RTSLIMYNHTSKKMTKPVREALDK
CDS	295034..296014	VVDRESIAKNVSKNHATPATGPNTKLFIDKQQ VQKQDIDEAKKIMAAQGYTKAHL KLTVSTYNGRPELPKMAQVQLQSDAKKANIDITIR NVDDIEGYLKDQSDQDASMSFGT IPRGDTGYFFNQAYKPEGAINAGGYDNAKVTKLI DQFNKTVDKTERNRLTNEIIDITD KDKANSYLTMDNIVGMNKKVKNLKATPEGIYLI DYKVDKAK" /locus-tag="SSP0268" /locus-tag="SSP0268" /note="similar to gi 27467981 ref NP-764618.1  [Staphylococcus epidermidis ATCC 12228], percent identity 60 in 308 aa, BLASTP E(): e-10 <sup>7</sup> " /codon-start=1 /transl-table=11 /product="putative ABC-type oligopeptide transport system permease component" /protein-id="BAE17413.1" /db-xref="GI:72494092" /translation="MILKNILSRIGQMIIIVFLV LSTITFILMKLTPGDFIDKILHLDV ANVSSDQIEATKAKLGLDQPVIIQYVQVLGQIIQ LNEGTSYQIGEPVIKELIYYTPPT LFIAVMTIIVVVFVAIPLGMIAAKYYHTWLDSL RSVTSFTVSIPIFFLGTILIIYVFA QKWNLLPSSGLDTMAGYILPVIALSVGMSAYYVR LMRSNLVELYQSKEVEAARLRGMS ERYILWQDLFKPAIIPIITVLGMSVGSIGGTVV IENLFGIPGIGHFLVDSIQARDYP VVOGAVIMIGFFVVLANTMSDLLLWIDPKRRYN KPTDIERMKRQDGESL" /locus-tag="SSP0269" /locus-tag="SSP0269" /note="similar to gi 27467980 ref NP-764617.1  [Staphylococcus epidermidis ATCC 12228], percent identity 65 in 269 aa, BLASTP E(): e-10 <sup>2</sup> " /codon-start=1 /transl-table=11 /product="putative ABC-type oligopeptide transport system permease component" /protein-id="BAE17414.1" /db-xref="GI:72494093" /translation="MKQINRRNMIFYAFVAVYFV LIIAQFFVSSYSAYEVNLGSSLET PNLTHWLGTDYGRDLFSRVIIGARYTLIIISLIT LFITVIIGVPLGLLAGYKKGIVDT FIMRLIDIGLSIPEFVLMIALASFFKPSIWNLVI AITIIKWMYTRLTRSVSSEINK PYIQMARLFHVPTHVIFKHFMPQVMPSSIIVLMT VDFGKIILYISSLSFGLGQAQPPS PEWGAMLVNVRDRISSYPLLIIVPACLITVITILL FNLGADALRDLRLKQORDVND" /locus-tag="SSP0270" /locus-tag="SSP0270" /note="similar to
gene	296011..296832	
CDS	296011..296832	
gene	296825..297604	
CDS	296825..297604	

gene	297597..298286	gi 27467979 ref NP-764616.1
CDS	297597..298286	[Staphylococcus epidermidis ATCC 12228], percent identity 49 in 254 aa, BLASTP E(): 2e-66"
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		/transl-table=11
		/product="putative ABC-type oligopeptide transport system ATPase component"
		/protein-id="BAE17415.1"
		/db-xref="GI:72494094"
		/translation="MTNILEITNLSIADRFGNKL IQHVDLGLKKSKVNVLIGESGSGK SLTARAMVQQIPNTLDMQYDCMTYEHSEMSDMHN LLGKEIGFISQNYTHSFNDHTKLG KQLISIYRQHYKTKDKGAQKIVEQALS NVELNPS QMMSKYRFSLSGGQLARVQIASVL MLNPKVIIADEPIASLDAVTGVSIMNLIKHLAEV HKVTLLLIITHNLSHVLD FSDWIHV IKNGEMVESNHIDAFKNNVDKPYSLKLFNSRSRL KKG DYHA"
		/locus-tag="SSP0271"
		/locus-tag="SSP0271"
		/note="similar to gi 27467978 ref NP-764615.1  [Staphylococcus epidermidis ATCC 12228], percent identity 46 in 230 aa, BLASTP E(): 2e-55"
		/codon-start=1
		/transl-table=11
		/product="putative ABC-type oligopeptide transport system ATPase component"
		/protein-id="BAE17416.1"
		/db-xref="GI:72494095"
		/translation="MLNLTDVFSYKHEAILKKI QLSIQADEIVGIVGESGSGKTTLA KIMLGLLQPTHGEVITHKERVLP IFQHAVDSFNP KFKIRKSMEEPIKYQRRGESQKAA QRLSDL MAYQLDTKLM DRLPEELSGGQLQRFNT IRTLML EPDILICDEITASLDVIA EQRMIDILRHYYKTHKGMILISHDLAFLNQIVN RFIVMKNGEIVDDFETKDLFNVIR HEYTKTLLSIY"
gene	298529..299440	/locus-tag="SSP0272"
CDS	298529..299440	/locus-tag="SSP0272"
		/note="similar to gi 57286403 gb AAW38497.1  [Staphylococcus aureus subsp. aureus COL], percent identity 55 in 302 aa, BLASTP E(): 5e-91"
		/codon-start=1
		/transl-table=11
		/product="putative ferrichrome-binding lipoprotein precursor"
		/protein-id="BAE17417.1"
		/db-xref="GI:72494096"
		/translation="MKKLIFPLALMLLILACGN NSSDDASKDKKKEKTYQDSGKKV KIPDKPRIVVLGATYAGGKELDANIVGVANIV DSKVLKDKFKVDKVDKVAENVESV

		AKLPDLIITYNTDKNLKLNKVAPTIAFDYMKH DYKEQHKLKGIVGKEDKAEDWIK DWEETKDDGNEIKDAIGEDTTVSIIKDFDKKIY ALGKTYGHGSEILYDSFGLKMPK VEKATKKNLDADISEEQIPEMSGDYVVPVAKGA DLSFENKDIWKNTEAVKNGKTFKV DEGIYWLNDPYSLSDYERKDLKEKLNH" /locus-tag="SSP0273" /locus-tag="SSP0273" /note="similar to gi 54022168 ref YP-116410.1  [Nocardia farcinica IFM 10152], percent identity 31 in 114 aa, BLASTP E(): 2e-11" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17418.1" /db-xref="GI:72494097" /translation="MKKQKIDNWVQLTKYVNYI DTMIEKKLKQEYNLSVKEFYVLYE IYKAKGKKYKINDLIKIVDLSQSAMSRLIVRIEK PTKALVVRQECLEDHRAMYIYLTE EGQDITEKALNTYESLISKVSFSNIRKLSQIDSI D"
gene	299742..300155	/locus-tag="SSP0274"
CDS	299742..300155	/locus-tag="SSP0274"
		/note="similar to gi 57286524 gb AAW38618.1  [Staphylococcus aureus subsp. aureus COL], percent identity 80 in 472 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="BAE17419.1" /db-xref="GI:72494098" /translation="MKGFFNKILKREDPSVYQVK DAHLNRTLRLVKDFLALGVGTIVST SIFTPLPGVVAAQHTGPAVALSFLLAADVAGLVSF AYAEEMSSAMPPFAGSAYSWINVVF EVFGWVAGWALLAEYFIAVAFVASGFSANLRGLV SPLGIELPKSLSNTLTGDDGGIIDI VAAVVILLTACLSSYGVSAAARIENILVVIKVL VLLFIVVGLTAIDLSNYVPFPIEH KVTETSGFGWQGIYAGVSMIFLAYIGFDSIAAN SAEAINFQKTMFRGILGSLAIAVI LFVAVSLVLVGMFTYSAYADNAEPVGWALRQSGF GVVAAIVQAISVIGMFTALIGMML AGSRLLYSFGRDGLLPsWLGKLNKLNPNRSLII LTVIAVVIIGSMFFFAFLAQLISAG TLVAFMEFVIGIFGLRPREGKDIPMPAFKMPFPY VMPITTFVSVVVVFWGLGAEAKLY TLIWFIIIGLLIYLLYGKHSKKRQS" /locus-tag="SSP0275" /locus-tag="SSP0275" /note="similar to gi 57286497 gb AAW38591.1
gene	302176..302556	
CDS	302176..302556	

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[Staphylococcus aureus subsp.
aureus COL], percent identity 46
in 123 aa, BLASTP E(): 3e-23"
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/protein-id="BAE17420.1"
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FFENIGFTIKKNEAVLDKMRGIET
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KEAAEVDLLNHVETAGGKVLQRG
TKHEGFYGGFLFSDIDGHLFNIIAM"
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/notes="similar to
gi|16799517|ref|NP-469785.1|
[Listeria innocua Clip11262],
percent identity 48 in 269 aa,
BLASTP E(): 8e-69"
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/transl-table=11
/product="putative hydrolase"
/protein-id="BAE17421.1"
/db-xref="GI:72494100"
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TAHYFDQQLIFEVLEMIHQTYHIS
DVLVSGIHSAYVDESSDEFLNFIRNYYDIKKV
ASFNEITEDHFVKIALRIKDEDLV
KQVTEIEQRYKGIKIRAVTSGNDSVDLILPSVKN
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/locus-tag="SSP0277"

gene      complement(303493..3039
15)
CDS      complement(303493..3039
15)
/locus-tag="SSP0277"
/notes="similar to
gi|27467028|ref|NP-763665.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 41 in 144
aa, BLASTP E(): 6e-27"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
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/db-xref="GI:72494101"
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LTVTVKFSAGYIKQAILTEVKENA
YDIIVMSNTREKSDIKNILGNVTHKIASNVDPV
LIVN"
/locus-tag="SSP0278"

gene      complement(304025..3050
92)
CDS      complement(304025..3050
92)
/locus-tag="SSP0278"
/notes="similar to
gi|15925579|ref|NP-373113.1|

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[Staphylococcus aureus subsp.
aureus Mu50], percent identity 71
in 353 aa, BLASTP E(): e-151"
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dehydrogenase"
/protein-id="BAE17423.1"
/db-xref="GI:72494102"
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ENAGFGSIELGGITPKPOPGNPKP
RMYRLVEDQALINRMGFNNLGMNKALSYLRKHRY
QIPVGLNVGVNKSPTPEARYEDYI
KVIDTFKNDVTFFTVNISSPNTENLQSFHDKDEF
SQLCEAIQTYKYESLNVPFIFIKL
TSDLSLDGLGAMLTPIQTQFDGIIILANTTQOREA
LHSNHRREETGGLSGKPLFERNLKL
ISYAYKQTDGQFLIIGTGGIFNAEDVIKMMRQGA
SLVQIYSALVFEFGPLTQKLNKQL
AHYLKSNNGYNNVNEIIGLDVK"
/locus-tag="SSP0279"
/locus-tag="SSP0279"
/note="similar to
gi|49487367|ref|YP-044588.1|
[Staphylococcus aureus subsp.
aureus MSSA476], percent identity
71 in 283 aa, BLASTP E(): e-117"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17424.1"
/db-xref="GI:72494103"
/translation="MNQAWSQLPLSHIKNIVPV
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KRKSTFFDAEIIAGLNLFKEVGITAPRVIDSGEIE
DDAYLLLTYLDEGVSGSQEALGQL
VARMHSEQQADNQFQFDLPYEGGDISFDNSWTNS
WITLFVEKRLDKLDRLVQOGLWG
DADVTQYQAVRRVIVNELESHNSKPSLLHGLDWG
GNYMFLTGDGSPALFDPAPLYGDRE
FDIGITSVFGGFTQAFYDAYHKHYPLSEGADVRL
EFYRLYLLMVHLVKFGEMYAGSVD
RSMQKILNQ"
/locus-tag="SSP0280"

gene      complement(306535..3067
68)
CDS       complement(306535..3067
68)

/note="similar to
gi|57286496|gb|AAW38590.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 69
in 72 aa, BLASTP E(): 1e-23"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17425.1"
/db-xref="GI:72494104"
/translation="MTLLDRINELANKEKIETLS

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		IEEKEEQQTLRQEYLMIRGQVIH TFSTLKVVDPLGEDVTPDKVYQLREEMGTLDDID"
gene	complement(306746..3077	/locus-tag="SSP0281"
	23)	
CDS	complement(306746..3077	/locus-tag="SSP0281"
	23)	
		/note="similar to gi 26989208 ref NP-744633.1  [Pseudomonas putida KT2440], percent identity 42 in 312 aa, BLASTP E(): 1e-64" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17426.1" /db-xref="GI:72494105" /translation="MTTIQKHNGFKRTFQQGHLT LGLMLPFDNSENIALSFENQVDLA QYAE NLGFTSLFVRDNPLYSPHLGNVITNYDPFV FLSYLSAKTSKIALGTSSIVATLR HPIHTAKAATSLDLISDERFLLGLATGDRPFEPF AFKIKETQLSKQFQDAIYAMNDLW QSHSPKISNSIFELYEDSGQLLPKHNHIFMAT GYSRQELSWIKKNMDGLMFYQPF QKQKALLKEWHNNDVFKPFMHPLVIDLSLNPNEL VKPIKGGYRLGRNTLLNILKSYEK IGTNHMLHLTSDNRPYKSLLEVGDIYIIPHFPP HLSQEEKNNDITRON" /locus-tag="SSP0282" /locus-tag="SSP0282" /note="similar to gi 9968803 emb CAC06168.1  [Staphylococcus warneri], percent identity 44 in 264 aa, BLASTP E(): 4e-56" /codon-start=1 /transl-table=11 /product="glutamyl endopeptidase precursor" /protein-id="BAE17427.1" /db-xref="GI:72494106" /translation="MLKRRLRGGLIFIIALLCTV ISINGNTYAATQTHQSTDQSAQSE DAKVGINQIKTRVLPNDRTQIENTTNGHYQSV GYISIGDNIATGVVIDKNTVLTK HVANLSEGNMNFSPAAQNENTMPTGYTFSEKEIEV YPGNEDLALIHNLKNKDEQSGVDV VQPATLKDASAVTKDMPITVITYPGDKSLATMWE SKGQILNTNTTEFEYNASTFGGNS GSPVFNENNEVIGIHQGGIEGESNSAVAMTDDVL SFINKNS" /locus-tag="SSP0283" /locus-tag="SSP0283" /note="similar to gi 57286494 gb AAW38588.1  [Staphylococcus aureus subsp. aureus COL], percent identity 50 in 185 aa, BLASTP E(): 2e-48" /codon-start=1
gene	complement(308808..3093	/locus-tag="SSP0283"
	71)	
CDS	complement(308808..3093	/locus-tag="SSP0283"
	71)	

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regulator"
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SSELNETTLSSSFITITSYIQETH
NECKLNSEAYGQVVEKRVKEELEDIFLTLLVQQH
PNETRESLAASARFLSWGLYGTAK
HWFHSSQLSANDYIEGALPFLMKQILK"
gene      complement(309542..3102 /locus-tag="SSP0284"
94)
CDS       complement(309542..3102 /locus-tag="SSP0284"
94)

/note="similar to
gi|45358682|ref|NP-988239.1|
[Methanococcus maripaludis S2],
percent identity 46 in 239 aa,
BLASTP E(): 1e-62"
/codon-start=1
/transl-table=11
/product="truncated conserved
hypothetical protein"
/protein-id="BAE17429.1"
/db-xref="GI:72494108"
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LVQIPQVSHIEIQVFIMSVPLII
GAFCYPLGNRKMMLVDNQLNTLERIYGMTLVTL
PIWVVVIFICGVLKSGPPSSNQLLQ
TFIVAVFSGIIATTLFFYATNMVKHNQAKLGAVE
STQATEIIFTLIGEMLLLDLPLFS
TVSMIGIIITLIGIFYFSFMNSIIKENNNMIL"
gene      complement(310347..3105 /locus-tag="SSP0285"
05)
CDS       complement(310347..3105 /locus-tag="SSP0285"
05)

/note="similar to
gi|16078291|ref|NP-389108.1|
[Bacillus subtilis subsp. subtilis
str. 168], percent identity 63 in
44 aa, BLASTP E(): 3e-08"
/codon-start=1
/transl-table=11
/product="truncated conserved
hypothetical protein"
/protein-id="BAE17430.1"
/db-xref="GI:72494109"
/translation="MRAILIGILGALFFSVFII
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gene      310801..312078 /locus-tag="SSP0286"
CDS       310801..312078 /locus-tag="SSP0286"

/note="similar to
gi|27468290|ref|NP-764927.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 66 in 421
aa, BLASTP E(): e-175"
/codon-start=1
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/product="D-serine D-alanine
glycine transporter"
/protein-id="BAE17431.1"
/db-xref="GI:72494110"
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VLLMSFNLLSTKLFGELEFWFAIKVTVIALI
IVGIVMIIMAYKTPFGHASVSNIIY
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GETKNPHKTIPQAINNVPLRILLE
YIGALAVIISIIIPWNELDPEGSFPVKVFALVGP
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NSRTLFGLSDRKQAPPKFQATNRKGVVPVAILVT
CALLLFAVLNNYFIPNATTVFVYI
STVSTVLNIFIWTIIMIAVRYTKARPDLHKQSR
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/note="similar to
gi|57286688|gb|AAW38782.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 74
in 311 aa, BLASTP E(): e-135"
/codon-start=1
/transl-table=11
/product="putative inosine-uridine
preferring nucleoside hydrolase"
/protein-id="BAE17432.1"
/db-xref="GI:72494111"
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IKEPNITQHIESITIMGGGTFGNW
TPTAEFNIWVDAEAAKRVFECGVCINVGLDVTH
QVLATDHWIDRFKQIKNFIANFVV
ELLEFFKSTYKTHFMDGGPIHDACTILYLMQPD
LFTMQHTHIDIEHQSPLTYGTMSV
DLNDIMNKEKNAYFATAVDVSAWTLMENMLASY
EKHTH"
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/locus-tag="SSP0288"
/note="similar to
gi|15923202|ref|NP-370736.1|
[Staphylococcus aureus subsp.
aureus Mu50], percent identity 58
in 188 aa, BLASTP E(): 1e-59"
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/product="putative peptidase"
/protein-id="BAE17433.1"
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DVKAGDTIALSGNTGEQTTGAHLH

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gene	312137..313084
CDS	312137..313084

  

gene	313270..313854
CDS	313270..313854

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 95)

CDS complement(314030..3146 /locus-tag="SSP0289"  
 95)

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 [Bacillus halodurans C-125],  
 percent identity 34 in 204 aa,  
 BLASTP E(): 9e-32"  
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 DNA-3-methyladenine glycosidase"  
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 /db-xref="GI:72494113"  
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 VLFVAVRNGQLNFQELYKMDNSVINALTQIKGIG  
 RWTAEVFLFTLQKRNILPIYDVG  
 LQRAAQWLYQTTKAERKKQLTICKEQWQGCASIG  
 AFYLWEAIIHQDLLQYDSIYDIPKD HKN"

gene complement(314706..3150 /locus-tag="SSP0290"  
 59)

CDS complement(314706..3150 /locus-tag="SSP0290"  
 59)

/note="similar to  
 gi|49482472|ref|YP-039696.1|  
 [Staphylococcus aureus subsp.  
 aureus MRSA252], percent identity  
 70 in 118 aa, BLASTP E(): 1e-42"  
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 /transl-table=11  
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 protein"  
 /protein-id="BAE17435.1"  
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 VDRVWPRGISKEDANLDFWLKELA  
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 DEQHNQAVVLQDLLN"

gene 315191..315619 /locus-tag="SSP0291"  
 CDS 315191..315619 /locus-tag="SSP0291"

/note="similar to  
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 [Bacillus cereus ATCC 14579],  
 percent identity 29 in 148 aa,  
 BLASTP E(): 6e-14"  
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 tetrahydrobiopterin synthase"  
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gene	316134..317177	AIWIWHQFNKHLPENNSLQKLEFFETDTQGLVLT TELMDK"
CDS	316134..317177	/locus-tag="SSP0292" /locus-tag="SSP0292" /note="similar to gi 27469047 ref NP_765684.1  [Staphylococcus epidermidis ATCC 12228], percent identity 63 in 342 aa, BLASTP E(): e-125" /codon-start=1 /transl-table=11 /product="putative regulatory protein" /protein-id="BAE17437.1" /db-xref="GI:72494116" /translation="MIKVSPKQFLYNVLGVAIA IVAGLIPNAILGELFKLFAPKSSV FTLLQVVESIQFTVPLLVGALIAMRFKLSPLAT AVVASSAFVSGGAAQFKDGVWLLV GVGDLINTMLTAAIAVFLILLVGEKFGSLTLIIL PTIVGVIASVIGVFTLPYIQMITT GIGNLVNSTELQPVLMSEMLIALVFSFIIISPIS TVATALAIGINGLAAGSASLGIVA CEGALVAGTLKINRAGVPLTIFLGGVKMMIPNMV RHPILLPIFTNALITGLVGGLIG IGGTKESAGFGIIGLVGPISAFRMEHSIILNLV FVFIAFFVVPFVMGYLINTLYMKI LKIYDREIFKFLA"
gene	317703..318434	/locus-tag="SSP0293"
CDS	317703..318434	/locus-tag="SSP0293" /note="similar to gi 57286492 gb AAW38586.1  [Staphylococcus aureus subsp. aureus COL], percent identity 47 in 240 aa, BLASTP E(): 2e-48" /codon-start=1 /transl-table=11 /product="similar to immunodominant antigen A" /protein-id="BAE17438.1" /db-xref="GI:72494117" /translation="MKKTILASSLAVALGVTGYA ATADHNQAHASEENIDQAHADLA QNNPEQLNEKPLHAGAYNYDFVLGGNEYTFTSDG QTWSWNYTTAGAQSSANTIQDVT AQATITHNETSANEVTRTQQQSSNTEVAAVEAPKA SSNTNVQTAQTSTSTKSTTTTTTT STSSIDAIAINQMAERTGVSAQWKGVIQRESGGN ANAVNASSGAYGLFQLLGHGEHAG MSVQDQMDKAVEVYNNQAGAWVAW"
gene	318702..319859	/locus-tag="SSP0294"
CDS	318702..319859	/locus-tag="SSP0294" /note="similar to gi 57286483 gb AAW38577.1  [Staphylococcus aureus subsp. aureus COL], percent identity 73 in 384 aa, BLASTP E(): e-169" /codon-start=1 /transl-table=11 /product="putative aminotransferase" /protein-id="BAE17439.1"

gene	319885..320883	/db-xref="GI:72494118"
CDS	319885..320883	/translation="MVISDRLAQVPDSYFAKTMG QPVEHGPLPLINMAVGIPDGETPT GIIDCFDTALREPNQKYVAFHGKETFFKQAIIVDF YQRQYDVVLDDKDEVCILYGTNG LVALPSCIVNPGENVLLPDPGYTDYKAGVLLADA HPQPLVLEPPYYLPQWDKVDRLIL KNTRLVYLTYPNNP TGSVATQAVFDEAVAQFKGT KTKIVHDFAYSAFGFDHKNPSILO TEGAKDLAIEVFSLSKGYNNMSGRVGFVAVGNKDM IQALKKYHTHTHAGMGALQDAAT YALNHYYDDFLDEQSNIFKQRRDTEAKLKEENIP FEPMKGGIFLWLKTPPNFDGESFV DYLLQEQSILVAPGIPFGEHGKNYVRISLALDDE QLKVAERIQSLRHLYE"
		/locus-tag="SSP0295"
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		/note="similar to gi 21284209 ref NP-647297.1  [Staphylococcus aureus subsp. aureus MW2], percent identity 63 in 332 aa, BLASTP E(): e-123"
		/codon-start=1
		/transl-table=11
		/product="putative D-specific D-2-hydroxyacid dehydrogenase"
		/protein-id="BAE17440.1"
		/db-xref="GI:72494119"
		/translation="MTRIKLFGVRNEDKAFIEAW SNKHKVEVDLDEDLLTCETVSRVK GFDGVSISQQIPLDETIYKQLHDFGIKQIAQRSA GFDIYDFELAEKYNLIISNVPSYS PHSIAEYTVSQALNLVRNNDIQOKTAEYDFRWQ PDILSRSIDLKVAVIGTGRIGSI VAKIFAQGFDAEVTAYDIAPNDDYRSFLTYASTI NEAIQNADIVTVHIFASKENDYLF DETILFNEFKPGSVF INCARGTIVKTSALIDALDR GLIKGAALDTYEGEKGLFPDQRH TAFNDDMLKQLIERPDVIVSPHIAFYTDAAVENL IVDALDATMEVIKTDGTRLRVN"
gene	complement(320934..321140)	/locus-tag="SSP0296"
CDS	complement(320934..321140)	/locus-tag="SSP0296"
		/note="similar to gi 57286481 gb AAW38575.1  [Staphylococcus aureus subsp. aureus COL], percent identity 65 in 67 aa, BLASTP E(): 6e-19"
		/codon-start=1
		/transl-table=11
		/product="putative copper chaperone"
		/protein-id="BAE17441.1"
		/db-xref="GI:72494120"
		/translation="MATETIQVEGMSCDHCKHAV ETALTELDGVSTADVSLAAGNVKV DFDDDKVTMPQMKDAIEDQGYDKV"
gene	complement(321186..323570)	/locus-tag="SSP0297"
CDS	complement(321186..323570)	/locus-tag="SSP0297"

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/note="similar to
gi|49487336|ref|YP-044557.1|
[Staphylococcus aureus subsp.
aureus MSSA476], percent identity
73 in 795 aa, BLASTP E(): 0.0"
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/transl-table=11
/product="copper-transporting
ATPase"
/protein-id="BAE17442.1"
/db-xref="GI:72494121"
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AQPKKEVAEKSSQKELELRSLVK
LIISAVLAAPLLLMLVHLFGIIPSIFMNPWFQ
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MPHLYFETSAVLITLILFGKYLET
RAKTQTTNALSELLNQAEARVLRDNKEQMIPL
NDVVEGDYLIKPGEKIPVDGKII
KGKTSIDESMLTGESMPVEKQVDNVIQSTMNKN
GSITVKATKVGKDTALASIIKVVE
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WIAFVQQGQFEPALVAAIAVLVIA
CPCALGLATPTSIMVGTGKAAENGILFKGGEHIE
RTHQIDTVVLDKGTITNGKPVVT
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NIKLLDITDFEAVPGRGIIKANISG
KNLIVGNRQFMNDENVDIKDSIEDIMTQFEKSGKI
AMLIAINQEYRGMVAVADTVKDS
ATAIKQLHDLNLIKVVMLTGDNERTAQAIA NEVGI
DTIIAQVLP E E K A A K I K S L Q T Q D K
TIAMVGDGVNDAPALVQADIGIAIGTGTEVAIEA
ADVTILGGDLLLIPKAIAKASKATI
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/locus-tag="SSP0298"

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gene complement(323745..3251  
96)

CDS complement(323745..3251  
96)

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/note="similar to
gi|32470568|ref|NP-863238.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 70 in 482
aa, BLASTP E(): 0.0"
/codon-start=1
/transl-table=11
/product="sulfate permease"
/protein-id="BAE17443.1"
/db-xref="GI:72494122"
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IVVALALIP E A I S F S I I A G V D P M V
GLYSSFIIAVVISFVGGRPAMISAATGSVALVIV
PLVKDHGVQYLLAATILMGIIQII
FGILKIGRLMKFIPNSVMIGFVNALAIMIFTQI
KHIFGISIPTYLEFVISTLLIIYLL
PRVFNKVPAPLVAIIILLTITYLITGAKVETVGD
L GAINRSLPQFFIPDPFENLQTLQI
IFPYSLSMAIVGLVESLTLTARIVDQATDTYSSKN

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gene 325396..326157  
CDS 325396..326157

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IGQSVINVRSGATTRLSTFTAGIFLIILIIIFGD  
WVVQIPMPILAAIMVMVSIPTFDW  
RSFKFIKKAPRTDAFVMILTVAIVLISNNALGV  
IVGVVVSALCFATKISNVVVYEE  
EDDTIHYYITGQIFVVSIDSLMQLDLELRHKT  
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/note="similar to  
gi|27469318|ref|NP-765955.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 69 in 253  
aa, BLASTP E(): 9e-98"  
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/transl-table=11  
/product="ABC-type transport  
system involved in lipoprotein  
release ATPase component"  
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KENIMLPLSIQKMSKEEKENYKEVTEALGIQEL  
GDKYPNEISGGQQORTAAARASVH  
KPAIIFADEPTGALDSKSAQDLHRLLEDLNKNMN  
ATIVMVTHTDPAASYSNRVIMLKD  
GNIHSEVYQGEDTNQAFYKNIHMQTALGGVAHE  
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gene 326147..328042  
CDS 326147..328042

/locus-tag="SSP0300"  
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gi|27469319|ref|NP-765956.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 53 in 633  
aa, BLASTP E(): 0.0"  
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/product="ABC-type transport  
system involved in lipoprotein  
release permease component"  
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MLIEQIAMFLVTSVIGIVGVFGSKILLMIVLK  
ILDISTSVSLTFQFFAVTQTIVLV  
IVAMCLIMIQSFIFLRKRSILSMNDSKSEATK  
NNISIAEIVSGILGIAMIFGYIM  
STEMFGKFASGMMFTPFIIILFLTVVGAYLFRSS  
VSVIFKTIKNAKHGKVSITDVVFT  
SSIMHRMKKNALSLTIIATISAVTVTVLCFAGIS  
KATIDNVKLSPQDFNFTQKQA  
EAFENKLDEAHIGYDEQYKELERVVTKDSFFKE  
SGGTGNMMPTEMFITSNQYFKDKD  
ITGNKAKITNLAAAGGFAQNDQGIILKLSKPDQ  
SIKVIDSNEDVHFSSEVSAYAGPVL



gene	328213..329082	IVSEDKYNQLKQSAVETKHQYGYNLEKQSDWKAA NKIAKSINPDIQSQKTQRQDMNDS VGILLFVTAFLGLAFLVAAGCIIYIKQMDETEDE IPNFRILRKIGYTHQDMLKGLGLK VIFNGLPLIVSLLHAYFAAKAFMFLMGGSTMT IYIVMIAYSIVYGFVAVMAFVHSS RIVRHSI" /locus-tag="SSP0301" /locus-tag="SSP0301" /note="similar to gi 27469035 ref NP-765672.1  [Staphylococcus epidermidis ATCC 12228], percent identity 80 in 289 aa, BLASTP E(): e-134" /codon-start=1 /transl-table=11 /product="putative dehydrogenase" /protein-id="BAE17446.1" /db-xref="GI:72494125" /translation="MNLLEFHKQIKGYTQDRQPG IQKDMNPQPISTEMESYKSGGKLKG KVALITGGDSGIGRAIAVLVYAKEGANVAIGYYDE HEDAEAVVEQISSLGVTAKAYAHD LKKVEDSQKLEKVVADFGEINILVNNGGVQFPQ DHFEDIAPEQIKETFEINIFGMMF LSQAAVPHLKEGDAIINTSVTAYRGS AHLIDYS ATKGAIVAFIRSLATILMSKGI NAVAPGPIYTPLIPATFSEDKVENQGETPMERR GQPAELAPSYVFLASYADSSYITG QVIHVNGGDYITS"
CDS	328213..329082	
gene	complement(329318..329587)	/locus-tag="SSP0302"  /note="partial similar to gi 49398117 ref YP-031716.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 51 in 82 aa, BLASTP E(): 8e-19" /codon-start=1 /transl-table=11 /product="truncated hypothetical protein" /protein-id="BAE17447.1" /db-xref="GI:72494126" /translation="MLLTVAFFSFDKFDRFNPLL KKETSYAIVKLNLTQYYQDLSIYSK QGEKRSYKVSFNGYNPSEQYVCLKHKGYVEHIE YIIKQSFPSLK"
CDS	complement(329318..329587)	/locus-tag="SSP0302"
gene	complement(330076..330282)	/locus-tag="SSP0303"  /note="similar to gi 27469036 ref NP-765673.1  [Staphylococcus epidermidis ATCC 12228], percent identity 41 in 68 aa, BLASTP E(): 2e-10" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17448.1" /db-xref="GI:72494127"
CDS	complement(330076..330282)	/locus-tag="SSP0303"

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/translation="MKFLIKGAIIVVILGVVKT
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SIENVNFDGIKNLDFEKLIPSDFF"
gene      complement(330419..3318 /locus-tag="SSP0304"
40)
CDS        complement(330419..3318 /locus-tag="SSP0304"
40)

/note="similar to
gi|52079191|ref|YP-077982.1|
[Bacillus licheniformis ATCC
14580], percent identity 57 in 466
aa, BLASTP E(): e-149"
/codon-start=1
/transl-table=11
/product="putative di- and
tricarboxylate transporter"
/protein-id="BAE17449.1"
/db-xref="GI:72494128"
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ITESIPIPATSLIPLILLPLTGGTDEVIAASAYA
DPIVFMYMGGFIIALAEKWNLHK
RIAMTIIISMGTSSNRILGTMIATAFISMWISN
AATALMMLPIALALIQEIKDAQFL
KPASAKFSKALLLTVAYSASIGGLATLIGSVPN
AVFAAVASSSLDRKVSFAQNMIFA
VPLTVILLAILYLLTKWLFKIEDADQISSDFAK
KALHDLGPMSEKELTGIVFLVS
LLWIFGGLLPETLHITDTIAMEFVALLFLIPAK
NAKGGLLVWDDMNKLPWGILLFEG
GGLSLAAAFEDSGLTKWFGMGLGIVKPLPFILIV
IVLTAILFLTEVMSNTAVSNMLM
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LNIFAIIVISLFAYFWLPIAFGL"
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/note="similar to
gi|16078255|ref|NP-389072.1|
[Bacillus subtilis subsp. subtilis
str. 168], percent identity 52 in
391 aa, BLASTP E(): e-118"
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/transl-table=11
/product="hypothetical protein"
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IGGGVNFALSSKLETPSEMISST
VVADNSVMALYFMLLIAPLSPLIKKQFKSDYES
KSTPESQQAYWEPKKIQLLDIAFS
IASAVTLVAVSPKADLIQQWMPQHNVVTLIVS
FLGDPYLLLTTLTLLIVAVVWDF
ESLAGASEIGTFLYIFFVVGITPASFATIITTA
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gene      331996..333192
CDS        331996..333192
gene      333221..333784

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CDS	333221..333784	/locus-tag="SSP0306" /note="similar to gi 49484756 ref YP-041980.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 59 in 187 aa, BLASTP E(): 2e-62" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17451.1" /db-xref="GI:72494130" /translation="MSEKEKMLAGDWYDANFDES LDAERMKAKDLCFELNHIKPSDKE SRHTILTLLNYPEKALELLSPFQTDYGYNIFLG ERIFINHDCYFMDGGKIFIGDDVF IGPSCGLYTAVHPLEYKERNIGLEQALPIRIESN VWLGANVVVLPVGTITIGESVIGAG STVAKDIPPNVLALGTAPKPVSDIKNQ" /locus-tag="SSP0307" /locus-tag="SSP0307" /note="similar to gi 49482542 ref YP-039766.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 74 in 338 aa, BLASTP E(): e-144" /codon-start=1 /transl-table=11 /product="putative regulatory protein" /protein-id="BAE17452.1" /db-xref="GI:72494131" /translation="MDILIGTLEFIVLVALFTLF TYRAPMGMRAMGALANAAIATFLV EAFHKYVGGDLLGISFLGLGDAAGGLGGVAAAG LVALAIGVSPVYALAIASCGGLD LIPGFVAGYVIGYLMKYAERKVPDGVDLIVGILI IAPLARLVAVGVTPLVNNSLLKIG DIIQSSTEVSP IIMG IILGGVITVVGTA PLSSMA LTALLGLTGMPMAIAAMVSFASSF INGTMFNKLKLGDRKSRIACVIEPLSQADVVSAN PVPIYTANFIGGALAGAVIASSGM INDATGTATPLAGFLVMFGFNDPIKIFIYGAIIIG LIGLIVGYVCSVLFKNYPIVSKED IETR" /locus-tag="SSP0308" /locus-tag="SSP0308" /note="similar to gi 52078945 ref YP-077736.1  [Bacillus licheniformis ATCC 14580], percent identity 54 in 258 aa, BLASTP E(): 7e-83" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17453.1" /db-xref="GI:72494132" /translation="MNIQDAQPSTLREMIKQKGL TGHTSGMAKGYVQANVVILPSKCA YDFLLCFCRNPKTCLLDVSEKGNKSFTKYGVTA
gene	334244..335260	
CDS	334244..335260	
gene	complement(335308..336093)	
CDS	complement(335308..336093)	

gene	336273..336854	DISTEVAAYRIYQYGELIETRANV
CDS	336273..336854	DDLYTDDMVSFLIGCSFTEHALLAEGIPIRHLE ENHNVPYMTNIPANPSGQFKNGI TVSMRPMITMTQAIKATEITTRFKNVHGTPHIGN PTEIGITDLALPDFGEPVTINENE VPVFWGCGVTPQSVALDAKPDLMITHAPGHMFIT DIPDSQLSD"
		/locus-tag="SSP0309" /locus-tag="SSP0309" /note="similar to gi 27469109 ref NP-765746.1  [Staphylococcus epidermidis ATCC 12228], percent identity 29 in 203 aa, BLASTP E(): 9e-16" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17454.1" /db-xref="GI:72494133" /translation="MKRTAEKILIWIGIILQFIL IFLMAIVAPFFNDVSVKNELIEVI NQSNINYNQNASQMDPANIVDLVSNLFILALIVVI VCTVIAIIFAILTNKLSKFVGIIIF ILLGLVTVLTLNWIITAILWLWVAGILLVRKKQKS YDRYQPAKGNRKKEQAKHHNNQK RNTETTYHEEDDHKSEEQDKAPTQLSRKARYKK" /locus-tag="SSP0310"
gene	complement(336965..338035)	
CDS	complement(336965..338035)	/locus-tag="SSP0310"  /note="similar to gi 16077903 ref NP-388717.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 36 in 356 aa, BLASTP E(): 3e-43" /codon-start=1 /transl-table=11 /product="similar to intercellular adhesion protein C" /protein-id="BAE17455.1" /db-xref="GI:72494134" /translation="MKTYTSVIFWMMRTIACLSIV LIHSITTTFSKMDFLGHGTAIRVF QLMLMFSTPLFVFISEFLAKNYQVKTKPGFFKN KLIYLGIPIYIIINIGIALFYFESK TFDQFMTHLGDITMFHGGAVTYFIVIIIFQFYILHI LFAKYLKWKVPVVIIGAVIFATI YWAFRQYAPQSEHPILGLFWEREGWMLFLGWISY FLLGFYTGIYYETFMKKIKKYTW IIIGAIATSILVDNYLFGISTWVESKRFDIPFY VKMVILVFFLFAASYVKYVVKPILF ISNYSFCIYLIHYFFVHELGLLRAASSLRNIAPN FIITLTVSICLAYIFNLISKYGF VGGIGHIKYDKVYESYKKGKMD" /locus-tag="SSP0311" /locus-tag="SSP0311" /note="similar to gi 27469034 ref NP-765671.1  [Staphylococcus epidermidis ATCC 12228], percent identity 82 in 514 aa, BLASTP E(): 0.0" /codon-start=1
gene	338276..339820	
CDS	338276..339820	

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/transl-table=11
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e dehydrogenase"
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gi|49487332|ref|YP-044553.1|
|Staphylococcus aureus subsp.
aureus MSSA476|, percent identity
53 in 182 aa, BLASTP E(): 7e-54"
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regulator"
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gi|49487331|ref|YP-044552.1|
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aureus MSSA476|, percent identity
70 in 842 aa, BLASTP E(): 0.0"
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of the RND superfamily"
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 aureus MRSA252], percent identity  
 33 in 748 aa, BLASTP E(): e-123"  
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 HQIGLIELTPPRSTINFTQYYQLTYLLEHIFN  
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gene	343395..345677
CDS	343395..345677

gene 345996..347393  
CDS 345996..347393

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70 in 457 aa, BLASTP E(): 0.0"  
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PLLLIVGRVIQGLSAAAMPSTLAIMKTYFEGKE  
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MVATFVGWRWIYILSIIALLAMYLIKGTPEKTS  
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VVITQSGTFGITSPLILGLIIIFIVATIIIFLKVE  
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/note="similar to  
gi|15923092|ref|NP-370626.1|  
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aureus Mu50], percent identity 76  
in 391 aa, BLASTP E(): e-176"  
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/transl-table=11  
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amidase"  
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gene 347483..348658  
CDS 347483..348658

gene 348919..349383

CDS	348919..349383	/locus-tag="SSP0317" /note="similar to gi 27469030 ref NP-765667.1  [Staphylococcus epidermidis ATCC 12228], percent identity 51 in 153 aa, BLASTP E(): 7e-41" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17462.1" /db-xref="GI:72494141" /translation="MNGDKKISELLDNYKKPLKK LFKYDKSKARAFDKDSRSKVEGQK GIFVIFNNKQPIFVGQVGGYMTGYKITQKDLNDK LGQFNKSDSGTARFRRVFAEQNS LDEAETKEIKAENYGLKFQFIKVGKNSMINILE ILALEYAKENDINLYNFL" /locus-tag="SSP0318" /locus-tag="SSP0318" /note="similar to gi 52078856 ref YP-077647.1  [Bacillus licheniformis ATCC 14580], percent identity 31 in 237 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="putative esterase" /protein-id="BAE17463.1" /db-xref="GI:72494142" /translation="MSIRELSLSFHHQEIKIKLP KNYFKTNGKSYPLVIVQDGDYLFK DVKKDVI FVGIVPNNRKKDYTPWKS VVGDI EYGG QADAYITTVADAVIPYLRKCFRIS QDRKDIGIAGASFGGLVSLYALFKHADTFGHYIL ISPSVWYPDFVKFMKSQPIINSTH HIYWYVGQLEGKQSNHNLNQYMPQTEAAVDILNE LLVSETSVFYFDNRKGLHRQYYF KKYFNRAINKLF" /locus-tag="SSP0319" /locus-tag="SSP0319" /note="similar to gi 27467114 ref NP-763751.1  [Staphylococcus epidermidis ATCC 12228], percent identity 56 in 138 aa, BLASTP E(): 2e-40" /codon-start=1 /transl-table=11 /product="putative truncated permease of the major facilitator superfamily" /protein-id="BAE17464.1" /db-xref="GI:72494143" /translation="MTRIALILSIIGSLMLIISG NVTLLLLGRIVQGFSAAIIMPATII SIVNDFEGDDRRQKALSFWSIGAFGGTGLSSFFA GAMATFISWQSIFVLSILLSLVAL LLVKNLPESKQVKAQSNHFDYIGLTI FVIMIASI SL" /locus-tag="SSP0320" /locus-tag="SSP0320" /note="similar to gi 27467114 ref NP-763751.1
gene	349426..350118	
CDS	349426..350118	
gene	350589..351005	
CDS	350589..351005	
gene	351053..351766	
CDS	351053..351766	



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[Staphylococcus epidermidis ATCC
12228], percent identity 46 in 224
aa, BLASTP E(): 1e-50"
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permease of the major facilitator
superfamily"
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gene      complement(351863..3521 /locus-tag="SSP0321"
35)
CDS       complement(351863..3521 /locus-tag="SSP0321"
35)

/note="similar to
gi|52081185|ref|YP-079976.1|
[Bacillus licheniformis ATCC
14580], percent identity 50 in 56
aa, BLASTP E(): 4e-09"
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/transl-table=11
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VHDLHLAFKRRQ"
gene      352256..352789 /locus-tag="SSP0322"
CDS       352256..352789 /locus-tag="SSP0322"

/note="similar to
gi|49484748|ref|YP-041972.1|
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aureus MRSA252], percent identity
54 in 177 aa, BLASTP E(): 1e-49"
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methyltransferase"
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gene      352935..354512 /locus-tag="SSP0323"
CDS       352935..354512 /locus-tag="SSP0323"

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gi|27467949|ref|NP-764586.1|

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[Staphylococcus epidermidis ATCC
12228], percent identity 66 in 520
aa, BLASTP E(): 0.0"
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transporter"
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ATVIGVAVSLGVGAIQINGLHYL
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LQSWTIYYWGWMSWSPFVGTFIA
RISKGRSIREFIIAIVGVVVISIIWFSAGVTG
ITVGQSHSSILKMPETQLFGIFN
ELPFGFILSIVALALIASFFITSADSATYVLGMQ
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gene      complement(354768..3559
37)
CDS       complement(354768..3559 /locus-tag="SSP0324"
37)

/note="similar to
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percent identity 77 in 386 aa,
BLASTP E(): e-175"
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yl CoA synthase"
/protein-id="BAE17469.1"
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RYNKSADFKSLCFHVFPFTKMGKALDSILTDDI
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gi|9937369|gb|AAG02428.1|
[Staphylococcus haemolyticus],

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percent identity 74 in 381 aa,
BLASTP E(): e-159"
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acetyltransferase"
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STLKTIFKEDGTVTGGNASSINDGASTIILMDEV
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LMGYAPYHAVTKLLNQADKAIEDFDVVMTEAFA
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/notes="similar to
gi|9937370|gb|AAG02429.1|
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percent identity 80 in 425 aa,
BLASTP E(): 0.0"
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VISSERLMIGQIVFDGVSDEILSQIYNLETQI
KQIADEVYPSIIERGGGYRKIDID
TFPNEGGLSLKVSVDTKDAMGANMLNTILEGITA
YLNELKDQVDILMSILSNHATASV
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TLVGTIEVPMTLATVGGGTQVLPFI
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/locus-tag="SSP0327"
/notes="similar to
gi|49484883|ref|YP-042107.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity
73 in 323 aa, BLASTP E(): e-141"
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/protein-id="BAE17472.1"

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CDS	357196..358479

  

gene	358668..359642
CDS	358668..359642

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DDPVFDSKGGFYFTDFRGYSTNLK
GGVYVYVSPDFKSIPTVIONLAVANGVALSTDEKT
LWVETNANRLHRIDLLEDGVTIA
PFGASIPYYFTGHEGPDSCCIDSDDNLYVAMYGQ
GKVLVFNKKGPSIGQILMPGRDQG
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gene      complement(359873..3603 /locus-tag="SSP0328"
04)
CDS       complement(359873..3603 /locus-tag="SSP0328"
04)

/note="similar to
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[Staphylococcus epidermidis ATCC
12228], percent identity 61 in 143
aa, BLASTP E(): 8e-48"
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antigen precursor"
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gene      360487..361833 /locus-tag="SSP0329"
CDS       360487..361833 /locus-tag="SSP0329"

/note="similar to
gi|30018581|ref|NP-830212.1|
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percent identity 66 in 422 aa,
BLASTP E(): e-166"
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/product="Na+ H+ antiporter"
/protein-id="BAE17474.1"
/db-xref="GI:72494153"
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LDTMQNHFLITPWLLIPLIVIAL
VVLKVPAPAIACMGIVLGGFAQIFVQGGTITEAL
TALQTGYTIDS GNKLVDELFNRRG
LESMFYTIISLTIVAMTFGGVLEYS GMLKALITQI
LKIAKSTGTILIASVIVSCIGTNI
CSEQYISIIIVPSRMVINAFKEKELHPKNLSRALE
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		/note="similar to gi 27469024 ref NP-765661.1  [Staphylococcus epidermidis ATCC 12228], percent identity 65 in 291 aa, BLASTP E(): e-109" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17475.1" /db-xref="GI:72494154" /translation="MDIKHMKYFVEVVDQKGMTN ASKHLFIAOPTISKAIKDLEQELD MTLFDRSKRQLVLTDAISIFYKKCKEILTLYNDV PKEINSLLGLETGHISIGLSAVMN MNQFINILGEFHQKYPNVVYSLVENGGMKIETQL INDEIDIGITITLFPVDQSIFHSVTL YQEDLKLVLNKEHHLANETHVDMMSMLKDEDFILF NEDFYLNDKIIIEAAKNAGFIPNTI SKISQWNFIENLLNAHLGVSILPENIVHLLDSSF SNKTLEDPGMRWELGVINWKKDKYL SHATKQWIDFMKERL" /locus-tag="SSP0331" /locus-tag="SSP0331" /note="similar to gi 49484742 ref YP-041966.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 60 in 123 aa, BLASTP E(): 3e-37" /codon-start=1 /transl-table=11 /product="holin-like protein" /protein-id="BAE17476.1" /db-xref="GI:72494155" /translation="MMLLQQFKKIITVLIQVLVI MGITYLGNVIQRYMHPIAGSIVG LLLFLLLLQFKVIPAKWVNEGSNFFLTMTMVEFFV PSVVGIMDVVPMINLNFILFFSMI LLGTCCVALISGFIAEKMVKNKQDGNVGN" /locus-tag="SSP0332" /locus-tag="SSP0332" /note="similar to gi 27469022 ref NP-765659.1  [Staphylococcus epidermidis ATCC 12228], percent identity 70 in 225 aa, BLASTP E(): 1e-86" /codon-start=1 /transl-table=11 /product="holin-like protein" /protein-id="BAE17477.1" /db-xref="GI:72494156" /translation="MLILEAIIIMILTIAMIYIGA KKLQKQKFQTPFLNPALIASIGIII VLLLFVRVDYKTYMLGGKWYNILNCTVVCLAFPL YQNRHKILKYARVIFSSVLMVAML NFWVFVSILKLFYGSKETIVTMLPRSITAAGVIE VSHQLGGIDTITVMFIITTLGLIGS ILGAYLLRLGRFRSSIAKGMTYGNASHAFGTAQA LDIDSETGAYSSIGMILTAVLSSI VLPILILFLY"
gene	363184..363579	
CDS	363184..363579	
gene	363580..364266	
CDS	363580..364266	

gene 364478..366220  
CDS 364478..366220

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[Staphylococcus aureus subsp.
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KDEVREFIEAFKIPTIVTLPAKGIADDPYNLG
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GIIGDSKALQQLTDSAKHVKNRD
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DEIPPMSTAVKRF"
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gene 366554..367948  
CDS 366554..367948

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gi|53771340|ref|ZP-00183037.2|
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percent identity 51 in 452 aa,
BLASTP E(): e-141"
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protein"
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ENGVNKAMQSLGKYKVLMIPLTMTIFSILGFSIG
LAEETIIFVPIGIIARTLGYDAL
TGAAMVILGAASGFMGMLNPFITVGVAQTVAELP
MFSGWGLRSIIYIFILIAAITVM
LYARKVKHDKTKSYVYELEQSEGHVTVSMHIARF
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YGWSFNEMSANFILAGLLAGFIGGLGLNGTFDAM
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CDS       complement(368198..369196) /locus-tag="SSP0335"

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identity 49 in 332 aa, BLASTP E():
2e-77"
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IRLLRHRGKTRHTKSHQENRGRIR
ISYSIHDRPQIIINDRERIGDWEADTVMGKTGKSC
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CDS       369346..371334 /locus-tag="SSP0336"
gene      369346..371334
CDS       369346..371334

/note="similar to
gi|27469020|ref|NP-765657.1|
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12228], percent identity 81 in 658
aa, BLASTP E(): 0.0"
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transporter protein IIABC
component"
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FYNISLPSYLGFFAGKRFVPIIMMA
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gene	371509..372054	ETDDRVHKGQVLMQIDLDYITAHA
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gene	372210..373196	
CDS	372210..373196	
gene	373322..373723	
CDS	373322..373723	



gene 373838..374164  
CDS 373838..374164

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/note="similar to
gi|57285232|gb|AAW37326.1|
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aureus COL], percent identity 67
in 107 aa, BLASTP E(): 1e-36"
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/note="similar to
gi|15895774|ref|NP-349123.1|
[Clostridium acetobutylicum ATCC
824], percent identity 36 in 164
aa, BLASTP E(): 4e-26"
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acetyltransferase"
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/note="similar to
gi|27469013|ref|NP-765650.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 57 in 321
aa, BLASTP E(): e-107"
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/transl-table=11
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LYIHGGAWFQNPPLYKHFDFIDSLAGELGAKVIMP
IYPKVPHATYKETFTLLETLYTQL
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YEKIDPMLAIDGSKYFIKLWANGLDLTDWRVSP
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gene 374595..375086  
CDS 374595..375086

gene 375253..376227  
CDS 375253..376227

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CDS	complement (376471..376791)	/locus-tag="SSP0343"
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gene	complement (376861..377379)	/locus-tag="SSP0344"
CDS	complement (376861..377379)	/locus-tag="SSP0344"
		/note="similar to gi 57285230 gb AAW37324.1  [Staphylococcus aureus subsp. aureus COL], percent identity 62 in 167 aa, BLASTP E(): 4e-56" /codon-start=1 /transl-table=11 /product="putative truncated permease of the drug metabolite transporter" /protein-id="BAE17489.1" /db-xref="GI:72494168" /translation="MKQQSRLGIIILAILGASFW GLGGTVSDYLFKHQNDIDINWYVTA RLIISGLLLLTIFKILNPRQSIIFVFRNVTNTIQ LLIFSTLGMLLVQYAYMASINYN AAIATLQYIAPVYITLWFIIRKKETFKLFDVIA ILLTLTGTFLLLANGSLDSLMVSS SMWIIGIISGLS"
gene	377483..378364	/locus-tag="SSP0345"
CDS	377483..378364	/locus-tag="SSP0345"
		/note="similar to gi 16077582 ref NP-388396.1  [Bacillus subtilis subsp. subtilis str. 168], percent identity 28 in 295 aa, BLASTP E(): 1e-32" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="BAE17490.1" /db-xref="GI:72494169" /translation="MYKGIIIEDNGEERIQYPDE YWRHIVLKTRLDQAFMEQIPIHHW SALQVFVFLRGKLTIRISDKNIVLNTGDFGINF"

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 YIHKHFQDKITLGHLSQNIYLSEA  
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 /locus-tag="SSP0346"

gene complement(378537..3796  
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 CDS complement(378537..3796 /locus-tag="SSP0346"  
 94)  
 /note="similar to  
 gi|27469138|ref|NP-765775.1|  
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 12228], percent identity 44 in 411  
 aa, BLASTP E(): 8e-95"  
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 succinyl-diaminopimelate  
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 FNIRTIPEHDNDQFITYFNEILKQ  
 VETDKTDIEIDTYMSRPPVYTTGENKLASLAHDL  
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gene complement(379890..3802  
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 CDS complement(379890..3802 /locus-tag="SSP0347"  
 19)  
 /note="similar to  
 gi|27469012|ref|NP-765649.1|  
 [Staphylococcus epidermidis ATCC  
 12228], percent identity 40 in 96  
 aa, BLASTP E(): 2e-11"  
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 /db-xref="GI:72494171"  
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gene 380655..381812  
 CDS 380655..381812  
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 gi|27469011|ref|NP-765648.1|  
 [Staphylococcus epidermidis ATCC  
 12228], percent identity 74 in 385

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aa, BLASTP E(): e-173"
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synthesis protein PgsB"
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QKANALVNECMVNPDYQITFQKELVKANIGVIV
NVMEDHMDVLGPTLDEVAEAFAT
IPYKGHLIVMKDDYTDFFAKVAKRRKTKLIVVNK
EEVPESFLRKFGYIVFPDNVAIAM
GVAEALGIDRDIALQOMLNAPPDVGAVEVKYYNA
NNSINVYVNAFAANEPOSTKAILN
KVEYNYFPYNKIVLLNCRSDRIDTRQFCEDFI
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gi|27469010|ref|NP-765647.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 88 in 150
aa, BLASTP E(): 3e-71"
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synthesis protein PgsC"
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CITYVILFFYSFIN"
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gi|27469009|ref|NP-765646.1|
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12228], percent identity 59 in 357
aa, BLASTP E(): e-124"
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MTKFSDDRKTNISKNLENVFLKGLNLKSLNVIN
QVTDNITARDFMKSVEAQTYGNYL
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KENNDYVVVNVWDGITTDRSVTTTRQREYAHSLSE

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gene	381814..382266
CDS	381814..382266
gene	382282..383352
CDS	382282..383352

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/note="similar to
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12228], percent identity 61 in 52
aa, BLASTP E(): 5e-13"
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12228], percent identity 65 in 538
aa, BLASTP E(): 0.0"
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/note="similar to
gi|57286525|gb|AAW38619.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 80
in 445 aa, BLASTP E(): 0.0"
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/transl-table=11

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gene	383342..383500	
CDS	383342..383500	
gene	383503..385095	
CDS	383503..385095	
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CDS	complement(385354..386691)	

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gi|57286701|gb|AAW38795.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 73
in 238 aa, BLASTP E(): e-100"
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4-diphosphocytidyl-2-methyl-D-
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DDDVIIITHDAVRPFLTRRIKENIESVLKYGA
VD
TVITATDTIITSADGDSIQSIPVR
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/notes="similar to
gi|57286702|gb|AAW38796.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 74
in 342 aa, BLASTP E(): e-150"
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dehydrogenase"
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DLSTIAYSSELVSVSWHALQRFERK

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gene	387201..387917
CDS	387201..387917
gene	387910..388938
CDS	387910..388938

gene 389014..390702  
CDS 389014..390702

SISNKSFGIWDGDNGLGYITAILLSKLYPQAKIY  
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PANVTDFDHAFECVGGKGSQSAVNQIIDLVSPGET  
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gi|57286703|gb|AAW38797.1|  
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aureus COL], percent identity 69  
in 562 aa, BLASTP E(): 0.0"  
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glycerophosphate transferase  
involved in teichoic acid  
biosynthesis"  
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LEETALEQYSDEMTQNGKNLLLLDHFTEFTFKKGG  
NSSKTEYTVKPMISSEVNEFVLNI  
IFKAPMPKMNPPVKKRITDLKLKYNKYSFNVRNFI  
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ISVRRNFIDKFKFPYLLGKADYIF  
VDDFHPLLYTVKFRKSQEIIVWHAAGAFKTVGY  
SRTGKKGPPFNSVNHRYNTKAEV  
SSETDIPFYGEAFGIKEQNIPTGVPRDILFDQ  
DYEKAIVADMEALPIVKGQVIL  
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IVLFKMHPPVKNKLNIPREYQEYF  
VDVSDFREVNILFITDILISDYSSLVYEFVFK  
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/note="similar to  
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aureus COL], percent identity 54  
in 572 aa, BLASTP E(): 0.0"  
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glycosyltransferase"  
/protein-id="BAE17502.1"  
/db-xref="GI:72494181"  
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SDAVTLANSRIIYTLSPTKFYRTS  
LLRDHAIEFPEDLRSADQLFTMKAYVNAKRIAV  
LADKPIYYATKREGHMSSAYVSP

gene 390853..392577  
CDS 390853..392577

gene	392762..393346	EDFYKVMSLITEEILNSPLENKNEVLGYFIDRHF SFSRTNNFSLKIADDKKEAWMDAL GDFIQKVP TVVDELVNSDFKPLLHYARLKDMMKY QMVEESYKNGKFHSYSAQEGTLKI QFDEGEPYFVFKLVKPDIRMSHFENDQGFLE LEFISSIINPNHVASMIQLKLLSR NKKEFIYIPLTMNDQTRFKFADLNDLMPYLIKE KVWDAHLEMRVDNMTIEKRIGNRR VKYPYSKETSTITQYNNQYRFTPYFTKDFDNLS FYITSNKLNEMLAVEIKDKQTIQL RSLEFNYYLSEGMAVILPHMFTYGYLTSVTTKD TLTYHLSVGEKVKDKDLKKNFKIE TPHLVLYK"
CDS	392762..393346	/locus-tag="SSP0358" /locus-tag="SSP0358" /note="similar to gi 23114979 ref ZP-00100256.1  [Desulfitobacterium hafniense DCB-2], percent identity 39 in 188 aa, BLASTP E(): 3e-41" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17503.1" /db-xref="GI:72494182" /translation="MTKSKIDVKDLINIGLFTAV YFIFIAPPGILGIPIFMLLLPAM IGLVGGIPVMLLITKTQKFGALTICGVVVSLLLA IMGHPWMALILSVPIVVIADMVMA MGQYKSWKLNSIGYIIFSWPIGNLLPFYFMRNS YLAFIQDKYGTDYEATVEGLFSIG MIPILITTIIGAWIGAYIAKGILKKHFKRAGII " /locus-tag="SSP0359" /locus-tag="SSP0359" /note="similar to gi 23114980 ref ZP-00100257.1  [Desulfitobacterium hafniense DCB-2], percent identity 37 in 218 aa, BLASTP E(): 9e-39" /codon-start=1 /transl-table=11 /product="ABC-type cobalt transport system permease component" /protein-id="BAE17504.1" /db-xref="GI:72494183" /translation="MYNQVLSQNHIFNFDPRIKI GLMLIISLISLTGGVTGQGFIRL IIMVIPVLLLIVIGKYKIGIACIVLTVAAWYGEA FVSIEQSQVATLLVFPVSGIITRF LPSLAMGYIYFKTTQVEVILGLERMKLSRKITI PIAVMFRFIPTIRMESASIKDAMK IRGISLRFAFKKPMQYIEYRIVPLLNSVIKIGNE LTIASITRGLNLTHRSSIVTLKI RWLDWLFIVGTLILLCITYIYIV"
gene	393348..394067	
CDS	393348..394067	/locus-tag="SSP0360" /locus-tag="SSP0360" /note="similar to gi 23114981 ref ZP-00100258.1  [Desulfitobacterium hafniense DCB-2], percent identity 45 in 486
gene	394077..395531	
CDS	394077..395531	



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aa, BLASTP E(): e-111"
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/transl-table=11
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transport system ATPase component"
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VSQVSGSVFQNPQRSQFFCLNTTSE
LAFEPENFGVEPNEINTQIANAYEFNIEHLLDR
GIFNLSGGEKQLIACCTTIQVSGHD
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IAEHRLHYLMDVVDRIILAQGTM
RKQYDKDTFNKLSHETLAELGLRTHLDMKPKV
HHNVACGTLILKDFNFKYKPRPL
SINIPKIELNKGKVTAVIGHNGSGKSTFARCLTG
VERFKGKVDNDEVTLKRGHRLNN
VYLVFQDVNNQLFAESVGEELRLSHADLDDDETQ
KQLQYYGISQHIERHPLSLSGGEK
QRLAIAASAVETSRDILFDEPSSGLDGQRMREIS
GIIDDLATNGHTIIVITHDYELL
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gene complement(395654..3977 /locus-tag="SSP0361"  
26)

CDS complement(395654..3977 /locus-tag="SSP0361"  
26)

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/note="similar to
gi|27468879|ref|NP-765516.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 25 in 691
aa, BLASTP E(): 1e-60"
/codon-start=1
/transl-table=11
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regulator"
/protein-id="BAE17506.1"
/db-xref="GI:72494185"
/translation="MISSLSIRNHYYTELKRCIN
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CLSTSYDFDNHKLVEQFRNLILE
NLHLPLQDENTASLYISNIIDFLIKEAKVLTNTV
YIPPLNTKHPLLQQITEYIHNNIY
HKISTKNVSKAFYISQSYISILFSSILNMNFKHY
TTSRLIALSLFDLIQNDSQSIYDVA
IKYQFTNVSTYSKHFHYIQMPPKKYIYNFRQEY
YNEPKQIDIDQAKTIHYFAQIQKS
AKRVDHIAKTLNLSLFSSTFNEPHTFIQLERL
DDLVDHFMISEQNDILVFPKVINI
SILDTQIIHLNAFKLQQVLTSIHQLIDRNYHITL
KITSKFLTNQSTFLRKLLLELKN
NLNHITLQLDLTFNEAKSMTESINNIRKQSPQIK
IGVIIDKIIENSANILQIRRFMSL
LETDLFYINLDSLAELETQKISPIQQDLDLKA
RIVLFIHSLGSKHAKKLIFNHLTH
SAIKSCYHYSKQETHVAITQFLIEFNQLIGGFGY
PYYSDDYDRIMLFNQYQSAMPVVH
IYGLLSPYYKQPITTLPIAIVTKTKTHYHILLFN
NLSESTISVINHHFIKSPFISS

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gene 398064..399080  
CDS 398064..399080

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YPRKLTMHYFKDPLIFKLTKSAL LNMIMISIN"  
/locus-tag="SSP0362"  
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/note="similar to  
gi|20806727|ref|NP-621898.1|  
[Thermoanaerobacter tengcongensis  
MB4], percent identity 31 in 337  
aa, BLASTP E(): 1e-43"  
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regulator"  
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TEVLTEISHECQKHHLHVAVASSE  
ENEDKQODLIETFVSQNVSAIILVPVSKQFMKR  
EWLKIPIMTLDDRELESTSLPSITV  
DNEEAAYIATKRVLESTCKEVGLLLANPNISTTI  
GRKNGYNKAISEFDLNVNPSLIHY  
SDQQLGTNAQIYSGYEATKTLLSKGIKIVATNH  
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gi|53611566|ref|ZP-00342323.1|  
[Azotobacter vinelandii], percent  
identity 57 in 57 aa, BLASTP E():  
9e-12"  
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permease of the major facilitator  
superfamily"  
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/db-xref="GI:72494187"  
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FAALIAIFIMTGDGIEQAFLSKN  
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SMVREK"  
/locus-tag="SSP0364"  
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/note="similar to  
gi|53611566|ref|ZP-00342323.1|  
[Azotobacter vinelandii], percent  
identity 50 in 348 aa, BLASTP E():  
e-104"  
/codon-start=1  
/transl-table=11  
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permease of the major facilitator  
superfamily"  
/protein-id="BAE17509.1"  
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VIWLVFHILFLVFLGLVNYSMML  
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gene 399165..399419  
CDS 399165..399419

gene 399374..400456  
CDS 399374..400456

gene 400473..401957  
CDS 400473..401957

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HIGFMGTLWMSVIWIGVGGLIAFYVVGKRNKPN  
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QQWLWTWGTMHITCIVGDVVWGIV  
ADKIGWKRQVMLFGCIGCGITTLFFYYLPILSGD  
IFAIAILCAVLFGITQSAFVPIFA  
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/note="similar to  
gi|27469003|ref|NP-765640.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 60 in 493  
aa, BLASTP E(): e-178"  
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SGQMHGLVALNHQGEPIRNAILWN  
DTRTTQQCQSIKNQFGETLLKNFIEGFTLPKLL  
WLQENEPHWQALDVFLLPKDYVR  
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LAIGDIYPKLINSHDFVGNLTEDV  
KAALGLDNDVAVFAGGADNACGALGAGVINEAQA  
LCSIGTSGVVLTCQOENEKSLGNN  
IHYFNHALPQMTYTMGVTLISAGDSLNLWKRTMFD  
DESFDDIVQQAESQIGANGLFA  
PYLQGERTPHGDAYIRGSGFIGLSSNTVKADFARA  
TIEGITYSLYESYRIMMQANSNSN  
RVISIGGSKSNFWLQLQADVFNAEVTPCLKYEEG  
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TLTQQLLTIK"  
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/locus-tag="SSP0366"  
/note="similar to  
gi|16077682|ref|NP-388496.1|  
[Bacillus subtilis subsp. subtilis  
str. 168], percent identity 59 in  
352 aa, BLASTP E(): e-121"  
/codon-start=1  
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/protein-id="BAE17511.1"  
/db-xref="GI:72494190"  
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CEYCKSGKYNLCPDVEFLATPPVDGAFSQQYISHP  
EGFLFHIPEALSYEATLNPEPFSV  
GVQACKRANVQPGSTTVIMGMGPVGLMAVVAKA  
FGATKIIVSDLEKIRLDEALKLGA  
THAINIKEEGVATRINEITKGKGVNYAFETAGNP  
IALQNALAALNNGGTLAIVGLPQQ

gene 401976..403046  
CDS 401976..403046

gene	403921..404595	ENIENLNPFIANHEINIVGIFRYANTYDMGLEML ASTSADLNTMFTDAYDLNEAKEAM EQARTNKSGSLKVMVYPNGKPE"
CDS	403921..404595	/locus-tag="SSP0367" /locus-tag="SSP0367" /note="similar to gi 53771322 ref ZP-00182843.2  [Exiguobacterium sp. 255-15], percent identity 42 in 217 aa, BLASTP E(): 4e-47" /codon-start=1 /transl-table=11 /product="putative 2-haloalkanoic acid dehalogenase" /protein-id="BAE17512.1" /db-xref="GI:72494191" /translation="MYKAIIFDVYGTIFDISSLE KHMDQFDEAQASSISQLWRKTLQ HMFLLQIMQRYITFDDLTkdALRYTLDEHKVQYN REDINQLFADFLLDYFKEIPRVF SDLKAKNIDIGVLSNGNDSMLMPLVDNSKISEYI DTVMSVDEIKQYKPSASALILN YYHLTREELFVSSNSWDITGAANFGFDTVWINR DKVQFDYNGQSPMTIVSNLNLVK WLEMNK" /locus-tag="SSP0368"
gene	complement(404785..405774)	
CDS	complement(404785..405774)	/locus-tag="SSP0368"  /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 46 in 359 aa, BLASTP E(): 7e-86" /codon-start=1 /transl-table=11 /product="putative truncated succinyl-diaminopimelate desuccinylase" /protein-id="BAE17513.1" /db-xref="GI:72494192" /translation="MVAEIGSGKPVVGVSGHMDV VTGDTGEQWNYDPFKLTEDDQGRLL HGHGSADMKSGLAALAI SLIEIKKAGTINQGTIR FMATAGEEVTISNGAALLHEKG YMD DVEALLIAEPSQDGIVYTHKG TMDIQVISKGKSA HSSMPELGFNAINPLVD FIIHNLV EYNKVDVRSKLLGTPTMNSTIINGGDQVNSIPEY AESLFNMRTIPAYDNKKFESLFNS IKEKEDNADITVNPYVNRDPVYTTGDNEFLKLAK SLGD EYFNRLDVTSS TATT DASY LMKKKGEDFSFVMYGPGETQAHQVDEYVYKDTY LTFIDLYTQMLPQYLNDFK" /locus-tag="SSP0369"
gene	complement(405823..405939)	
CDS	complement(405823..405939)	/locus-tag="SSP0369"  /note="similar to gi 27469138 ref NP-765775.1  [Staphylococcus epidermidis ATCC 12228], percent identity 72 in 37 aa, BLASTP E(): 5e-08" /codon-start=1

		/transl-table=11 /product="putative truncated succinyl-diaminopimelate desuccinylase" /protein-id="BAE17514.1" /db-xref="GI:72494193" /translation="MSVLSNEERVKILSDIIEIQ SVNEKELDVAHYLQKLFK" /locus-tag="SSP0370"
gene	complement (406040..406531)	
CDS	complement (406040..406531)	/locus-tag="SSP0370"  /note="similar to gi 15925519 ref NP-373053.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 69 in 161 aa, BLASTP E(): 6e-61" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17515.1" /db-xref="GI:72494194" /translation="MIRHATKSDLENILDIYNDA ILNTTAVYSYKPQTLASREIWFEN KSQNNPEIFVFEQQGEAVAFATYGSFRDWPAYQY SIEHSIYVNEHHRGKGIAQSLLKQ LINHAQVEGYKTLVAGIDATNDNSIYLHKKFDFQ HSGTIQNVGYKFDKWLDLAFYQLD LSK" /locus-tag="SSP0371" /locus-tag="SSP0371" /note="similar to gi 15925518 ref NP-373052.1  [Staphylococcus aureus subsp. aureus Mu50], percent identity 65 in 205 aa, BLASTP E(): 1e-72" /codon-start=1 /transl-table=11 /product="sortase A" /protein-id="BAE17516.1" /db-xref="GI:72494195" /translation="MKKKGNRLITLIGVLFLAA IYLFAPKHIDQYLHEKESSEKIET YDKDAANKKENKQEIIPDKSEMVGILTVDPAEIK TPVYGPATPELLDRGVSFAEADE SLDDQNIAIAGHTNIGSSDYQFSNLKEAKGSEV RFKVGKNKNVYKITKIFDVKPEDV QVLDEHKSSKKQLTLITCDNYNEQTNTWEDRKIF IAEAV" /locus-tag="SSP0372"
gene	complement (407430..408098)	
CDS	complement (407430..408098)	/locus-tag="SSP0372"  /note="similar to gi 49485199 ref YP-042420.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 81 in 221 aa, BLASTP E(): 5e-99" /codon-start=1 /transl-table=11 /product="putative N-acetylmannosamine-6-phosphate

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/db-xref="GI:72494196"
/translation="MLPQGLIVSCQALPDEPLHS
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ESLSELVSYIRNKAPNVEIMADISTLEEAKNADE
LGFDPYVGTTLRGYTSYTKGHILYE
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/note="similar to
gi|57285427|gb|AAW37521.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 73
in 264 aa, BLASTP E(): e-108"
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regulator"
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ISDEKIQSFVNVQIMRSQIIYAGLGSSSGLSATEF
YYRMMRMGLKGSVSTDAHQMCKIFG
SLLTSDTFLAISNSGETAELIAAAEVAHARGAY
VVAITNYEGSTLTCEADLVLTITD
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NVYQHTKKTIVLNE"
/locus-tag="SSP0374"
gene complement(409147..4100
19)
CDS complement(409147..4100
19)
/locus-tag="SSP0374"
/note="similar to
gi|49482548|ref|YP-039772.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity
57 in 284 aa, BLASTP E(): 7e-90"
/codon-start=1
/transl-table=11
/product="putative ROK family
protein"
/protein-id="BAE17519.1"
/db-xref="GI:72494198"
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GIGGAFYNQTLGLYNGTRHRANEI
GYLLYRSEDQLTFEQRASRTALKSLMKSKSFPYS
DDVPMFLFKLADQDNELALDILNEW
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gene 410343..411161
CDS 410343..411161

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/note="similar to
gi|57285425|gb|AAW37519.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 82
in 272 aa, BLASTP E(): e-126"
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lyase subunit"
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FELIEATQNNLIIYAIPDLTGVNISIEQFGELFN
HEKIIQVQYIAPNFFLLERIRKAF
PDKLILSGFDEMLVQAAVSGVDGAIGSTYNVNGV
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/note="similar to
gi|57285424|gb|AAW37518.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 81
in 510 aa, BLASTP E(): 0.0"
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family protein"
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KLKVTSAEYLEARFRPSVRVIGSLLFVLFHLGR
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SLVGILCILYTLFGGFEGVWSDFIQGIILLGGA
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MNGVLALISAPLFYGMGTMLYSFYTHESALPEGF
NTSSIVPYLILTEMPFFIAGLLIA
TIFAAAQSTISSSLNSISACLVDIKHRIFGKKG
EKDEVTFARWMIILSGLFGFGMSI
YLIASDSNDLWDLFLITGLGVPLAGVFAVGIF
TKRNTLGVICGLALGIIIFAYIFN
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KDIVGLTIPDIKEKSNYVSKIHVK K"
/locus-tag="SSP0377"
/locus-tag="SSP0377"
/note="similar to
gi|42525870|ref|NP-970968.1|
[Treponema denticola ATCC 35405],
percent identity 45 in 182 aa,
BLASTP E(): 2e-43"
/codon-start=1
/transl-table=11
/product="putative NADPH-quinone

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gene	411187..412716
CDS	411187..412716
gene	413085..413615
CDS	413085..413615

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gene	413873..414679	
CDS	413873..414679	
gene	414769..415431	
CDS	414769..415431	
gene	complement(415472..415813)	
CDS	complement(415472..415813)	



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BLASTP E(): 2e-42"
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beta-glucosidase"
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/db-xref="GI:72494204"
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KALIQSNARDL"
gene      complement(415815..4161 /locus-tag="SSP0381"
53)
CDS       complement(415815..4161 /locus-tag="SSP0381"
53)

/notes="similar to
gi|15613344|ref|NP-241647.1|
[Bacillus halodurans C-125],
percent identity 50 in 89 aa,
BLASTP E(): 5e-20"
/codon-start=1
/transl-table=11
/product="putative truncated
transcription antiterminator"
/protein-id="BAE17526.1"
/db-xref="GI:72494205"
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SRFMTHLKFFSQRLINHESLNEVTDSELLQVLQQ
KHVKS DACVDKSKLLRSIRLGLAN
RFNWTSQSRK"
gene      complement(416354..4166 /locus-tag="SSP0382"
17)
CDS       complement(416354..4166 /locus-tag="SSP0382"
17)

/notes="similar to
gi|15673443|ref|NP-267617.1|
[Lactococcus lactis subsp. lactis
Il1403], percent identity 41 in 86
aa, BLASTP E(): 3e-11"
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beta-glucoside operon
antiterminator"
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17)
CDS       complement(416808..4176 /locus-tag="SSP0383"
17)

/notes="similar to
gi|57285216|gb|AAW37310.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 60
in 268 aa, BLASTP E(): 6e-95"
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GDHLVSEALYFADPEGNGIEIYDRPKAGWIWND
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TMYFEGTQGDIIKFGSGFFSRVKTESNQEIMQ
TKSERFKFASRHDVYIETETYHPA
MLILLFQVYEFQEKQRKNAN"
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/locus-tag="SSP0385"
/notes="similar to
gi|15614899|ref|NP-243202.1|
[Bacillus halodurans C-125],
percent identity 54 in 576 aa,
BLASTP E(): 0.0"
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/transl-table=11
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protein lipid transport system
ATPase component"
/protein-id="BAE17530.1"
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LSIFGTSQKLGKILRTYLYKKYTE
MSAIFQNRRTGDLMAHATNDIRAVQNAAGAGIL
MIADSLITGGTVIITMATTVSQWL
TLIAMIPLPFMVLLTSIYGSLLSKGFKKAQAAS
KLNDKQTQESVAGIKVTKTFGYEPS
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GMSYFLSIAFGAQMVFHNDISLQO
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IEEIGELPNIDITSYVIDERPQGD
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GRTGSGKSALIRLLREFDQHAQ
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EEAILNLERLRSGKTNIIATHRMSAVKHADLII

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gene	417805..418350
CDS	417805..418350
gene	418585..420366
CDS	418585..420366

gene	420359..422122	VMNEGRIIERGNHATLMSKKGWYY DTYQAQALQEQLSRNLSLTKGDGEND"
CDS	420359..422122	/locus-tag="SSP0386" /locus-tag="SSP0386" /note="similar to gi 56419871 ref YP-147189.1  [Geobacillus kaustophilus HTA426], percent identity 53 in 581 aa, BLASTP E(): e-177" /codon-start=1 /transl-table=11 /product="ABC-type multidrug protein lipid transport system ATPase component" /protein-id="BAE17531.1" /db-xref="GI:72494210" /translation="MTENANLTAKDQGSALIRLF KYTLPYKWIIVLAFITLILSTIAS MMTPYMWKIFIDYLTTPRHFPKETMWVLIVIFIS IQLIGAITLYFSQYLQFYLAFAKVI QQLRIDAFNKLKGLGMRYPDKVPGGSIVSRLTND TETIVDMIVGVFSTFIMAFFMMIS SYIMMFVLDVKLALIALIFLPIIMIILASYSRKYS AFLFSKSRQRLSDLNSKLAESIEG MKIIQAFNQERRLNKEFNKINDEHYQYMLKTVKL DSLRLRPAISSISIFAVVMILGYF GVISFTTIGITAGVVFVAFVQYMERFFEPINQVSQN LNILQQALVSASRVFALINDDTYE PQQEANNNDNAIETGEIEFDNVFSFYDGETDVLKN ISLTAKPGEMIALVGHTGSGKSSI INLFMRFYEFNRGDIKIDGNSIKKIPKTELKEKI GLVLQDAFMFYGTIASNIKLYHPS MTFEQVKAAAEFVNANHFIEKLPNQYQHKVIEKG SAFSSGERQLIAFARTIATNPKIL ILDEATANIDSETEEQIQSSLNKMKGRTTLAIA HRLSTIQDADQIFVLNKGIEVERG THAQLIAQKGIYHNMYLLQNG"
gene	complement(422220..422498)	/locus-tag="SSP0387"
CDS	complement(422220..422498)	/locus-tag="SSP0387"  /note="similar to gi 27468987 ref NP-765624.1  [Staphylococcus epidermidis ATCC 12228], percent identity 65 in 91 aa, BLASTP E(): 3e-31" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17532.1" /db-xref="GI:72494211" /translation="MAEIKQGTNKFYIGDDENN QAQITFNQNDNQIDIDHTGVPEE MGGQGIGSQLVKAVVDYARDNNLKVSATCPFAKS VIEKHDEYQDVVVG" /locus-tag="SSP0388" /locus-tag="SSP0388" /note="similar to gi 27468986 ref NP-765623.1  [Staphylococcus epidermidis ATCC 12228], percent identity 54 in 320
gene	422676..423671	
CDS	422676..423671	

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aa, BLASTP E(): e-103"
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/transl-table=11
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transport system periplasmic Mn
Zn-binding protein"
/protein-id="BAE17533.1"
/db-xref="GI:72494212"
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EMVNIASDLFIYSNQMDMPVAKK
TAGSINNEHLKLPVAANLKQADLLSNHEHEHDHE
HEGHEAHEEHDEHEGHDHEEGSKD
PHIWLDPVLNKKMKVKAIKDDLKVKDSRHKAYYEK
RYKQLIADLDDINHEMKDITSNPK
RDTVVISHDSIGYLANRYGFKQEGVSGMNNNEEPS
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/locus-tag="SSP0389"

gene      complement(423824..4252
48)
CDS       complement(423824..4252 /locus-tag="SSP0389"
48)

/notes="similar to
gi|27468985|ref|NP-765622.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 79 in 472
aa, BLASTP E(): 0.0"
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AVITGCSVVIKPEATSLITLKIAELLRASTIPA
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VIVTSNADLDKAVNYIVTARINNA
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LEDsafKEEIfGPVLPiVtYSEFE
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/notes="similar to
gi|57285214|gb|AAW37308.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 64
in 143 aa, BLASTP E(): 3e-45"
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/transl-table=11
/product="putative transcriptional

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		regulator"
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		CVVRQRNEKDKRVTNASLTDKGRS
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		LSAQPIE"
gene	425990..426946	/locus-tag="SSP0391"
CDS	425990..426946	/locus-tag="SSP0391"
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		gi 57285213 gb AAW37307.1
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		aureus COL], percent identity 80
		in 318 aa, BLASTP E(): e-152"
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		FNKIHGEGIQSLFGTKVLPFEEVDGQSYQLVSDHE
		NKGVPAGKPKWNGPVPMDKAIYGL
		GPIEITVSFYFEDFMKILEDFVGMTVLTKEDGVVI
		LEVGEKGNGQGVILRKDDTGPEAR
		QGYGEVHHVSFRLKDHAIAVQWLEKYQTLGIGNS
		GLVDRFYFEALYARIGHILIEVST
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		IRPFDTSR"
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		gi 52141900 ref YP-084931.1
		[Bacillus cereus ZK], percent
		identity 43 in 302 aa, BLASTP E():
		2e-64"
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		TDAQSIIGFHGVTLLSSHPKATLN
		TLVNDMGLHKVNEDDNVVHVETKGHWQHHVIAIKK
		ESAQMNVNRWGVGVVHHIAWSVPTD
		KVQREWLVKMTGKGYHVDVKNRNYFKAIYMKEQ
		GGIIIFEATGEGPGFTVDERFETLG
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gene	427964..428566	/locus-tag="SSP0393"
CDS	427964..428566	/locus-tag="SSP0393"
		/note="similar to
		gi 15925508 ref NP-373042.1
		[Staphylococcus aureus subsp.

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aureus Mu50], percent identity 65
in 195 aa, BLASTP E(): 6e-68"
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LNNIFK"
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gi|57286571|gb|AAW38665.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 49
in 180 aa, BLASTP E(): 2e-44"
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to nicotinamidase"
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/db-xref="GI:72494218"
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ESTQIVEALNRQAKEPLVTKHRLS
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VEAADKDYKLTLLSDAMADQDVEK
HQFLINKILTRYADVTTVEAWCNS"
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gi|49487472|ref|YP-044693.1|
[Staphylococcus aureus subsp.
aureus MSSA476], percent identity
76 in 471 aa, BLASTP E(): 0.0"
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tricarboxylate transporter"
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gene	428695..429249	
CDS	428695..429249	
gene	complement(429340..430755)	
CDS	complement(429340..430755)	

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gene      complement(431075..4321 /locus-tag="SSP0396"
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CDS       complement(431075..4321 /locus-tag="SSP0396"
24)

/note="similar to
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12228], percent identity 68 in 349
aa, BLASTP E(): e-138"
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protein"
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gi|27468982|ref|NP-765619.1|
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12228], percent identity 72 in 592
aa, BLASTP E(): 0.0"
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CAVMIIILVRPISILLSTMNTEISK
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gene      complement(434306..4362 /locus-tag="SSP0398"
58)
CDS        complement(434306..4362 /locus-tag="SSP0398"
58)

/notes="similar to
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12228], percent identity 77 in 653
aa, BLASTP E(): 0.0"
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/notes="similar to
gi|27468505|ref|NP-765142.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 75 in 510
aa, BLASTP E(): 0.0"
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permease"
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LQLSGLDTFTQTAEKPTNLDLFKGTTVIGIISF
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12)
CDS       complement(438504..4391 /locus-tag="SSP0400"
12)

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gene      440719..441003

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gene	441515..443440	
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gene	complement(443569..444780)	/locus-tag="SSP0404"
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43)
CDS       complement(444780..4459 /locus-tag="SSP0405"
43)

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CDS	448416..449096	/locus-tag="SSP0410" /note="similar to gi 57285200 gb AAW37294.1  [Staphylococcus aureus subsp. aureus COL], percent identity 68 in 225 aa, BLASTP E(): 8e-89" /codon-start=1 /transl-table=11 /product="gluconate operon transcriptional repressor" /protein-id="BAE17555.1" /db-xref="GI:72494234" /translation="MKYDYPEQWLEGVSKGEMIA AEIRLRIVDGKIAFDTLTLENQIA KEYNVSRSPVRDAFKLLKQDQLIHLRMGAEVL FEDKEKKELYDLRIMLESFAFSRI KNLNHEQIVKEMRKQLEMMKVAVQFEDAEAFTEH DMKFHEVTIMASKHQYLTTFWNNL RPVMESLILLMSKRMNENLEDFERIHHNHEIFI EAIEQQDAQKLLNKAFLHNFDDVGE DIDSFWLT"
gene	449133..450680	/locus-tag="SSP0411"
CDS	449133..450680	/locus-tag="SSP0411" /note="similar to gi 57285199 gb AAW37293.1  [Staphylococcus aureus subsp. aureus COL], percent identity 80 in 515 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="gluconokinase" /protein-id="BAE17556.1" /db-xref="GI:72494235" /translation="MKYMIGVDIGTITSTKSVLYD EKGQFIMKHNIGYPLHTPNVEVSE ENPDELFDVAVLMTIKYIMREADIAKEDLKLISFS AQMHSLIAMDASHQRLTENLTWAD NRASRYAEAIAIKTHNGDAIYQRTGPIHPMSPLS KIFWMKHEQQEIFNQATATFADIKT YIFYQLFETFVIDQSMASSTGMLNLESLEWDKEA LSLLGITESQLPEIVPTTHILKGM KRRYAALMGIDENTPVVVGASDGVLSNLGVNAFK KGEVAVTIGTSGAIRTVIDKPRTD YKGRIFCYVLTEDHYVIGGPVNNGGVLRWL RDE LLASEVETAKRLGVDSYDVLTKIA NNVKPGADGLIFHPYLAGEAPLWNADARGSFPG LTLSHKKEHMIRAALEGVLYNLYT VYLALIEVMNETPKTIKATGGFAKSEVVRQMMAD IFDIDLIVPESYESSCLGACVLGM KALGEIDDFSIIEDMVGTTNKHHPNEDNVRTYQQ LISIFINLSRSLEARYTEIAAFQR EHMTEDE"
gene	450870..452228	/locus-tag="SSP0412"
CDS	450870..452228	/locus-tag="SSP0412" /note="similar to gi 27468962 ref NP-765599.1  [Staphylococcus epidermidis ATCC 12228], percent identity 85 in 452 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="gluconate permease" /protein-id="BAE17557.1" /db-xref="GI:72494236"

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CDS	452464..452583	/locus-tag="SSP0413" /locus-tag="SSP0413" /codon-start=1 /transl-table=11 /product="putative truncated 2 deoxy-D-gluconate 3-dehydrogenase" /protein-id="BAE17558.1" /db-xref="GI:72494237" /translation="MTKFSLESFSLKGKNAIVTG GARGLGKYYTIALTMYGQM" /locus-tag="SSP0414" /locus-tag="SSP0414" /note="similar to gi 48865615 ref ZP-00319474.1  [Oenococcus oeni PSU-1], percent identity 53 in 235 aa, BLASTP E(): 7e-67" /codon-start=1 /transl-table=11 /product="putative truncated 2 deoxy-D-gluconate 3-dehydrogenase" /protein-id="BAE17559.1" /db-xref="GI:72494238" /translation="MKAYVKQHEGNVSFLQODLT ESGSAAKVITNAVGTWGSILDILVN NAGVQIRNNILDYKNVSFLQODLTESGSAAKVIT NAVGTWGSILDILVNNAGVQIRNNI LDYKDEDWQNVIEINLNATYYMAHEAAKVMTEQG SGKIIINIGMSQSYRAGKNIPFYAA SKHGVVGITRAYADALAPYNIQVNALSPGYIRTD MTKVLEEDPIRGREIKGHIPIPSGEW GVPENLMGPLIFLASEASDYVTGISLPVDGGYLL R" /locus-tag="SSP0415" /locus-tag="SSP0415" /note="similar to gi 23100678 ref NP-694145.1  [Oceanobacillus ihyenssis HTE831], percent identity 71 in 351 aa, BLASTP E(): e-141" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17560.1" /db-xref="GI:72494239"
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gene	455760..455951	
CDS	455760..455951	
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CDS	complement(456154..456423)	
gene	456628..457332	

CDS	456628..457332	<pre> /locus-tag="SSP0419" /note="similar to gi 49487262 ref YP-044483.1  [Staphylococcus aureus subsp. aureus MSSA476], percent identity 65 in 234 aa, BLASTP E(): 6e-79" /codon-start=1 /transl-table=11 /product="putative short chain dehydrogenase" /protein-id="BAE17564.1" /db-xref="GI:72494243" /translation="MVELQDKVAVVTGASSGIGA SIAETLANQGKVVLTGRDESRLA EVAKRIQDNKQAVVETSIVDVTHKEEVELVEKT KEKFGQIDILVNSAGLMLSSAITE GDVEAWEAMIDVNIKGITLYINAVLPFMLNQSSG HIINIASISGFVTKKSTLYSASK AAVHSITQGLEKELAKTGVRVTSISPGMVDIPLS GDTDWGARKKLDPKDIAEAAIYAL QQPSHVNVEVTRPV" </pre>
gene	457581..458081	
CDS	457581..458081	<pre> /locus-tag="SSP0420" /note="similar to gi 38049248 gb AAR10419.1  [Enterococcus faecium], percent identity 38 in 167 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="BAE17565.1" /db-xref="GI:72494244" /translation="MEMRYLTERDVKQYRAIRLK SLQTDPKGFVSTYEREKSLPEDEF KARLKLNDTHFTIGTFDSGELICIATFYSERMEK VKHKGNLTVYCDPRYRGQGITAQ MIQHIINDVSVGVVKIIGLCVLSSENTQAIRLYE KLGFKRYGREPKSIFDGHRYYDED LMYLEV" </pre>
gene	complement(458177..458545)	/locus-tag="SSP0421"
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CDS       complement(461089..4617 /locus-tag="SSP0425"
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64)
CDS       complement(461768..4623 /locus-tag="SSP0426"
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gene      complement(462361..4629 /locus-tag="SSP0427"
39)
CDS       complement(462361..4629 /locus-tag="SSP0427"

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39)

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[Staphylococcus aureus subsp.
aureus COL], percent identity 77
in 192 aa, BLASTP E(): 2e-82"
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ate dehydratase"
/protein-id="BAE17572.1"
/db-xref="GI:72494251"
/translation="MIFQKKRRKTAETLSIILAD
DKRTSEINTGVGFLNHMLTLTFH
SGLSIIIEANGDTEVDHHDVTEIGIVLGQLLLD
MIRERKSFQRYGVSYIPMDETLSR
AVVDISGRPYLSFNATLSKEKVGTFDSELVEEFF
RALIINARLTTHIDLRRGGNTHHE
IEAIFKSFARALKMALSENDND

<-----User Break----->
64 in 685 aa, BLASTP E(): 0.0"

/codon-start=1
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/product="putative NhaP-type Na+
H+ and K+ H+ antiporter"
/protein-id="BAE17620.1"
/db-xref="GI:72494299"
/translation="MLLEAFLIFIIAIVISSII
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IPLHFEFDSVEFMMAVIAPLLFVEGTHVSRKLL
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IAWIWPELPMPPAAFAIAAILCPTDAVAVQAITKG
KILPKGALSILEGESLLNDAAGII
SFKIAVTALVTGAFSAFDAIEQFIISTILGVVIG
IVIGMLIVRLRIYLSMNKGLKDN
TMIFIQLLTPFAVYFVAEMLHASGIIAVVIAGLI
HGFERDRLIRAQTELQMNYNQIWS
TLSYVLNGFVFVVLGFIVPKVSEIINKEPENIK
FLITTTLLIALAIYVFRFIWVIL
FKQFYYPNNIQSYLNDNQETPPKRVHYAFIMTC
GIHGTISLSMALTLPILLAQQQTF
TYKNDLLFIASLMVLIISLVMAQIVLPLITPSEQR
KASTMSYVAAKVLIVQNVIKHEK
VKSKEDESINYNTVISEYFDELFFLLQMSPEDNN
AKEMKRLEDIANEESEETLERLVS
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LQMLILIRAKKHADTSQIKQPKS
NFQEVKKIMIRIVNHNVALRLKSEQTSDNVLEVNI
VLNQYVNRHLIRKRNQNNQTPA
SITEAHKLEGLYMQRAFLDKLVQNNKLDHAHSQ
VRENINYNIWVASK"
/locus-tag="SSP0476"
/locus-tag="SSP0476"
/Note="similar to
gi|27468921|ref|NP-765558.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 57 in 264
aa, BLASTP E(): 6e-91"
/codon-start=1
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/product="conserved hypothetical
protein"

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gene 512423..513232  
CDS 512423..513232

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/protein-id="BAE17621.1"
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/translation="MNIGVISDLHIDRHKSLKPK
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SNNYKLTQAFIKSVEAQAIKVLFIIPGNHDFWSA
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YHLNDAWAIVNGTWGYDYSYASPEFSLERIARRK
YYGATWQDKVKIDWFMDRKLRSRI
AANQAIKDIEKVKDKQIILMTHTIVTHPKFAVPMF
HRLFDYFNAFIGTSDDFDEIYKKYP
IRYSIMGHVHFRNRFRDEQGVTYICPCLGYQREWR
SDDVTRIEDHALNIIQI"
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76)
CDS       complement(513368..5139 /locus-tag="SSP0477"
76)

/note="similar to
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in 202 aa, BLASTP E(): 4e-77"
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/transl-table=11
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MGCEGVSAAAMILQFNHLNIPATEI
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HIIDOGQPVVIYHTVLGKRPRYRTYKLDNQPTKL
VANIHVTVLVGYDAQHYYYIDPLW
SHLGKSFILPAIPTKYQLMKIKKSKLEQSYDAP
GRMSFHLIS"
gene      514156..514620 /locus-tag="SSP0478"
CDS       514156..514620 /locus-tag="SSP0478"

/note="similar to
gi|15925425|ref|NP-372959.1|
[Staphylococcus aureus subsp.
aureus Mu50], percent identity 34
in 155 aa, BLASTP E(): 1e-24"
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/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="BAE17623.1"
/db-xref="GI:72494302"
/translation="MNYIIIELEPTLSVIGEKKIY
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VPESIKKAMQINKDILPKLDYEIRHAPFFELYK
EGAIREDDDYVTEIWLPIV"
gene      complement(514944..5161 /locus-tag="SSP0479"
49)
CDS       complement(514944..5161 /locus-tag="SSP0479"
49)

/note="similar to
gi|49484651|ref|YP-041875.1|
[Staphylococcus aureus subsp.
aureus MRSA252], percent identity

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66 in 387 aa, BLASTP E(): e-148"  
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/transl-table=11  
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major facilitator superfamily"  
/protein-id="BAE17624.1"  
/db-xref="GI:72494303"  
/translation="MDKTSNPRLPIMIIIMLGIM  
TTEGPLTIDMYVPSLPNVQNAFDI  
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VALIIISLYVIASLIAVFTTSLSI  
LLTLRLIQGLTGGGVIVIAKASIGDQHKGKALAK  
GLASLLVVGNIISIIAPLIGGYAL  
TIANWKAIFLILTIISFAILLFAFFKMEETRSRH  
LSKLNFSIAIFKDFGSLKKPAFII  
PMLLQGLTYVMLFSFSSAAPFITQKIYDMTPQQF  
SILFAINGIGLIIVSQLTATLVEY  
INRYLLILLTLIQIAGVILICFTLIFHLPLWVL  
VIAFFLNVCPTVGIGPLSFTLAME  
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SFTFKNSSN"  
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/note="similar to  
gi|27468915|ref|NP-765552.1|  
[Staphylococcus epidermidis ATCC  
12228], percent identity 71 in 127  
aa, BLASTP E(): 3e-51"  
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IAPFAGLIITIPITFVLSKYLRDE"  
/locus-tag="SSP0481"  
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/note="similar to  
gi|57285147|gb|AAW37241.1|  
[Staphylococcus aureus subsp.  
aureus COL], percent identity 79  
in 285 aa, BLASTP E(): e-127"  
/codon-start=1  
/transl-table=11  
/product="putative cation efflux  
family protein"  
/protein-id="BAE17626.1"  
/db-xref="GI:72494305"  
/translation="MTQSENKIAQKGAYLSLIV  
YIILSIVKYFVGYYVDSAAVRADS  
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SENISTLLVSFIIMEVGIQVVIEN  
FPRIFSGAHATPNAITTYVSVISGVIMIIVFFIN  
QKLAKRTNSSSLNSAAKDNLSDAL  
VSIGTAIGLVFTQIGFSIVDILATILGLLIYIT  
GFGIFKESIFTLSDGFNEQELDAY  
KNYVLEIEEVIDVQSIKGRYHGSSIFVDVTIVVE

gene	516423..516806
CDS	516423..516806

gene	517066..517935
CDS	517066..517935

		SDLSLEEAAHHICDKVEHHMHEKGI SSVYVHPEPVSIIQ"
gene	complement(518225..5185	/locus-tag="SSP0482"
	93)	
CDS	complement(518225..5185	/locus-tag="SSP0482"
	93)	
		/note="similar to gi 2735514 gb AAB94658.1  [Staphylococcus carnosus], percent identity 50 in 114 aa, BLASTP E(): 1e-25" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17627.1" /db-xref="GI:72494306" /translation="MKKLLLASFASITIAATGYG VTSTADAAETFPQQSSQSNSDVYS QFIEAGGTKALWDNIVMPESGPNPDVAVNELGYRG LGQTEAWGKGSVEEQTGKMIKYA EDRYGSIDAAIDFRLANGWW" /locus-tag="SSP0483" /locus-tag="SSP0483" /note="similar to gi 49484632 ref YP-041856.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 75 in 228 aa, BLASTP E(): e-101" /codon-start=1 /transl-table=11 /product="putative phosphoglycerate mutase" /protein-id="BAE17628.1" /db-xref="GI:72494307" /translation="MPKLILCRHGQSVWNAENLF TGWADVLDSEQGENEAITSKKLK AQGIEIDIVYTSLLERAIKTTYHLLNESNQLFIP IISKWRLNERHYGGLQGLNKDDAR KKFGEDQVHIWRRSYDVAAPPQDEAQRESYLNDR KYEHLDRRVMPESSESLKDTLVRVI PYWNDQISQQLLDGKTVLVSAHGNLSRALIKYLE NVSDDEDIVGYEIKTGAPLIYELTD DLQVIDKYYL" /locus-tag="SSP0484"
gene	complement(519913..5200	
	17)	
CDS	complement(519913..5200	/locus-tag="SSP0484"
	17)	
		/note="similar to gi 57285145 gb AAW37239.1  [Staphylococcus aureus subsp. aureus COL], percent identity 91 in 34 aa, BLASTP E(): 9e-10" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="BAE17629.1" /db-xref="GI:72494308" /translation="MKLDLQTARRNLSNPNIKTR KRARKIIQQHKRSK" /locus-tag="SSP0485" /locus-tag="SSP0485"
gene	520237..521700	
CDS	520237..521700	

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note="similar to
gi|49484631|ref|YP_041855.1|
|Staphylococcus aureus subsp.
aureus MRSA252|, percent identity
69 in 473 aa, BLAST E(): 0.0"
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major facilitator superfamily"
/protein-id="BAE17630.1"
/db-xref="GI:72494309"
/translation="MTQKTKIIMILMMLFGGFFG
LNLNELLTALPSLQVLDIDIDYTQ
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RIVQMGSGGIMMPLMNTLTILDFIEPHERGKMYGT
FGLVLTGLAPATGIPGSLVLYVEYF
WRSLFHVLPAPATLTFLGAIKFVKVNGVTNRKAPI
DLSLSTALSVLGGFGLGYSLLSR
DGNWDPVLTITVIGGLLVLFIFQTRLETPLL
DFSVFKNSQFVAGVIVNMAFTMIAM
IGSETVLMFQVNGIMKDTALQSGLLLPGAIVMG
IMSVASGGLYEYKGAKILAFIGML
IVVVTSSYFIPMDENTSSAILATYIARMIGIAL
GLMLPTHTMNLQSLRENNAGHSSM
TNTVQYISASTGATGLITLMSQVAKDFSPMNSDY
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QSK"

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/product="hypothetical protein"
/protein-id="BAE17631.1"
/db-xref="GI:72494310"
/translation="MKVKVDNVKVIYSDFQALLQHY
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YQNQDELHLGALATEIHLVP"
/locus-tag="SSP0487"

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note="similar to
gi|57285140|gb|AAW37234.1|
[Staphylococcus aureus subsp.
aureus COL], percent identity 68
in 407 aa, BLASTP E(): e=164"
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/transl-table=1
/product="fmhA protein"
/protein-id="BAE17632.1"
/db-xref="GI:74294311"
/translation="MFVFNLTPEEFQTFNTNHF
SYTQSRVNYEAGQYNAHLILGVKDDN
DEVIAAGMPTEARALKFKFYFYSGRQIPILYTNL
SLVDFYFSELTIKYQHNCLYVLL
DPYIENLRNADGKYSYDNRMILISTLEKLGKY
HGQYPVGVKSTQIRWLSDVLDDK
KSEQQLKEMDYQTRRNIRKTEEMGVKVRQLPIE
ETDRFLFKFLMAEEKHGFSRDEP
EYFOLKQDYGFAISOLAYILDISEYVNLKOKLD

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gene	523810..524178	TLNHQMKDVEAALQESPNKKQKT
CDS	523810..524178	KQTQLNQQIVSTQRKIDDTNKTTITTDGQVLDLAA AIYIYNDYEVYVYLLSSGSNPDPYDAY MGAYKLGWEMIKFAKNHNIDRYNFYGITGDFSED AIDYGVQFQKKGFNADVEEYIGDF VKPIKPLLYKLGKRIGKL" /locus-tag="SSP0488" /locus-tag="SSP0488" /note="similar to gi 27468906 ref NP-765543.1  [Staphylococcus epidermidis ATCC 12228], percent identity 54 in 118 aa, BLASTP E(): 5e-35" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="BAE17633.1" /db-xref="GI:72494312" /translation="MKKIITLIVISTLMAGCSS GKYADKIDKAVNQHQYQKKLAEQ HKGDIERKFDKKDANIYVYEKGKFVIIAYKPIKN DEEIHYYAYEYKDGKTIFFKDFNS RGYIQKHDPDYKENMDLDE" /locus-tag="SSP0489" /locus-tag="SSP0489" /note="similar to gi 27468905 ref NP-765542.1  [Staphylococcus epidermidis ATCC 12228], percent identity 53 in 199 aa, BLASTP E(): 3e-57" /codon-start=1 /transl-table=11 /product="putative protein-disulfide isomerase" /protein-id="BAE17634.1" /db-xref="GI:72494313" /translation="MKKAWLSIVLVLTIVLATA TNPEDTHKDDKTTSDGKIKIIEYG DFKCPYCKKVEKNVMPKLKKHYIDTDKVDYQFVN MAFLGDDSIIGSRAGHAVQRLAPE QYLKFOELMFKQOPNSEKAWITNQIVDQQIDKLG INTTLKKEIKDDYKQENSKSWVAA KKDQKQYKDNHIEAPTQVHVHGQKVEDPYDFENY KKILEKE" /locus-tag="SSP0490" /locus-tag="SSP0490" /note="similar to gi 21284057 ref NP-647145.1  [Staphylococcus aureus subsp. aureus MW2], percent identity 71 in 517 aa, BLASTP E(): 0.0" /codon-start=1 /transl-table=11 /product="putative ABC-type Mn Zn transport system periplasmic Mn Zn-binding protein" /protein-id="BAE17635.1" /db-xref="GI:72494314" /translation="MKQITYISIMVLAFMVLVLAG CGKGESDNTKSNEKIKINTIVFPL KSFAEQIGKGHVEVNSIYPAGTDLHNYEPTQKDI INASKADLFLYTDGNDLPVAKKVA
gene	524206..524811	
CDS	524206..524811	
gene	524996..526528	
CDS	524996..526528	



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STIKDKDKKLALEDKLDKSQLLTQHSHEEEHGD
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LAERYDFVQKGVQNMNAEDPSQKSLSNIVKEIKD
SGAKYILYEDNVSNKVTDTIRKET
EAKPLKFYNMESLNKSQQODYKLSYQSLMKKNII
NMDKALSDSIQTEDDKESKHKDKA
ISDGYFKDSQVKDITLGDYKGNWQSVYPYLKDG
LDEVMEHKAEDDDSMSAKAYKSY
EKGYKTDISHITISNDTITFEKDGKKETGKYVYD
GKDILKYEKGNRGVRYTFKLVDQN
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gene      526702..527223 /locus-tag="SSP0491"
CDS       526702..527223 /locus-tag="SSP0491"
/notes="similar to
gi|27467182|ref|NP-763819.1|
[Staphylococcus epidermidis ATCC
12228], percent identity 58 in 171
aa, BLASTP E(): 7e-56"
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protein"
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CDS       complement(527541..5281 /locus-tag="SSP0492"
61)
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aureus Mu50], percent identity 35
in 202 aa, BLASTP E(): 2e-34"
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SEYLLRHYPIFIWSPNQNTNFIIGIILLLTMA
ICLLKKKYFAGLILILSLPNIIIS
RIFTGGDYSNKNFLIISIVLTIISLSFIAYIVV
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gene      complement(528303..5286 /locus-tag="SSP0493"
41)
CDS       complement(528303..5286 /locus-tag="SSP0493"
41)
/notes="similar to
gi|15925682|ref|NP-373216.1|

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		/transl-table=11
		/product="putative transcriptional regulator"
		/protein-id="BAE17638.1"
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		/translation="MSISDQMMKGLLDGAILGLI AQGETYGYEILDKLKQQQFPEISD GSIYPVLLRLNKKGYVTSVSKKSMTGPGPKHKYYS ITDTGKNELNQFKANWHYLNNGMN NLMRSVNDVN"
gene	528738..529331	/locus-tag="SSP0494"
CDS	528738..529331	/locus-tag="SSP0494"
		/note="similar to gi 49484890 ref YP-042114.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 45 in 188 aa, BLASTP E(): 5e-47"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="BAE17639.1"
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		/translation="MTIDLKIGKIPATNALHHIG VKILEDIAGYDRITLLAIHGVGPK AMDILEDNLKKHNMFKEDIGDFVPHLTGDLKC DNAPKRRVMLDFLIGSALVDKDKL QAIVAEDFKWEVVDFAQLTGDAFYQELDHKET IVSIDVKMNISHGKSGALHGTQIL ENGTTIYFADMFEFTSHRKDAKVKSIYSIIMNE GES"
gene	529332..529805	/locus-tag="SSP0495"
CDS	529332..529805	/locus-tag="SSP0495"
		/note="similar to gi 27468904 ref NP-765541.1  [Staphylococcus epidermidis ATCC 12228], percent identity 48 in 154 aa, BLASTP E(): 1e-35"
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		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="BAE17640.1"
		/db-xref="GI:72494319"
		/translation="MSVKIVENNIIFTREFKATA EQIFKAYTDQNLFEKWFHPOGATT EVYEDSVQTTGGNAFFAIRAPOGTSYTVTQYTEVI OPTLIDYNDYFADKDGNDIKMAG MHNTIHIEDNDNGVAKLTSVAVLPDKAAQQLD MGVEEGMNSTFDNLETILLETIL"
gene	529892..530068	/locus-tag="SSP0496"
CDS	529892..530068	/locus-tag="SSP0496"
		/note="similar to gi 49484620 ref YP-041844.1  [Staphylococcus aureus subsp. aureus MRSA252], percent identity 46 in 58 aa, BLASTP E(): 5e-09"
		/codon-start=1
		/transl-table=11

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        /product="hypothetical protein"
        /protein-id="BAE17641.1"
        /db-xref="GI:72494320"
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        VLLNEKTLSSHTFKWFLRTLAGYG
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gene      complement(530387..5306 /locus-tag="SSP0497"
11)
CDS       complement(530387..5306 /locus-tag="SSP0497"
11)

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        /note="partial similar to
        gi|45532947|ref|ZP-00183943.1|
        [Exiguobacterium sp. 255-15],
        percent identity 80 in 61 aa,
        BLASTP E(): 3e-24"
        /codon-start=1
        /transl-table=11
        /product="putative truncated
        Beta-glucosidase"
        /protein-id="BAE17642.1"
        /db-xref="GI:72494321"
        /translation="MIIFKNAYVTYFLMGYPWG
        IDIISFTTGEMKKRYGLIYVDRD
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gene      complement(530598..5309 /locus-tag="SSP0498"
99)
CDS       complement(530598..5309 /locus-tag="SSP0498"
99)

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        /note="similar to
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        [Streptococcus suis 89/1591],
        percent identity 39 in 134 aa,
        BLASTP E(): 5e-20"
        /codon-start=1
        /transl-table=11
        /product="conserved hypothetical
        protein"
        /protein-id="BAE17643.1"
        /db-xref="GI:72494322"
        /translation="MNTQFSVSIHILLLATEKE
        PVSSQYIADSINSNATLVRKICRY
        LRDGHYIQSSQGISGYSLSSSANEIHLGDLYQLI
        FSETMHFAKIHKDTNQHCHVGKNI
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        /locus-tag="SSP0499"

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2  FILE USPATFULL
1  FILE WPIDS
1  FILE WPINDEX

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L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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L3      QUE ENTEROCOCCUS DURANS STRAIN 141-1
      -----
      SEA ENTEROCOCCUS DURANS STRAIN 152
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L4      QUE ENTEROCOCCUS DURANS STRAIN 152
      -----
      SEA ENTEROCOCCUS DRANS 141-1
      -----
L5      QUE ENTEROCOCCUS DRANS 141-1
      -----
      SEA ENTEROCOCCUS DURANS 141-1
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L6      2   FILE USPATFULL
      QUE ENTEROCOCCUS DURANS 141-1
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FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7      2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
      SEA ENTEROCOCCUS DURANS 152
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      1   FILE AGRICOLA
      1   FILE BIOENG
      1   FILE BIOSIS
      1   FILE CABA
      2   FILE CAPLUS
      1   FILE FROSTI
      1   FILE FSTA
      1   FILE HEALSAFE
      1   FILE LIFESCI
      1   FILE MEDLINE
      1   FILE PASCAL
      1   FILE SCISEARCH
      2   FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
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FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008

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## SEA LACTOCOCCUS LACTIS C-1-92

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1 FILE CAPLUS  
11 FILE GENBANK  
1 FILE PROMT  
2 FILE USPATFULL

L11 QUE LACTOCOCCUS LACTIS C-1-92

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FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC 2008

L12 15 S L11  
L13 14 DUP REM L12 (1 DUPLICATE REMOVED)

=&gt; d l13 1

L13 ANSWER 1 OF 14 CAPLUS COPYRIGHT 2008 ACS on STN DUPLICATE 1  
AN 2006:299263 CAPLUS  
DN 144:306860  
TI Foaming composition of benign microbes for competitive exclusion of  
undesired microbes  
IN Podtburg, Teresa C.; Schmidt, Bruce; Cords, Bruce; Grab, Lawrence A.;  
Halsrud, David A.  
PA USA  
SO U.S. Pat. Appl. Publ., 21 pp.  
CODEN: USXXCO  
DT Patent  
LA English  
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	US 20060067915	A1	20060330	US 2005-233922	20050922
PRAI	US 2004-612882P	P	20040924		

=&gt; d l13 2

L13 ANSWER 2 OF 14 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 1238  
INCL INCLM: 424/093.450  
NCL NCLM: 424/093.450  
IC IPCI A61K0035-74 [I,A]; A61K0035-66 [I,C\*]  
IPCR A61K0035-66 [I,C]; A61K0035-74 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=&gt; d l13 3

L13 ANSWER 3 OF 14 PROMT COPYRIGHT 2008 Gale Group on STN

ACCESSION NUMBER: 2003:81217 PROMT

TITLE: Natural Additives Kill Listeria.  
 SOURCE: Food Ingredient News, (March 2003) Vol. 11, No. 3.  
 ISSN: ISSN: 1070-1788.  
 PUBLISHER: Business Communications Company, Inc.  
 DOCUMENT TYPE: Newsletter  
 LANGUAGE: English  
 WORD COUNT: 391  
 \*FULL TEXT IS AVAILABLE IN THE ALL FORMAT\*

=> d 113 4

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)  
 GenBank ACC. NO. (GBN): AM286415  
 GenBank VERSION (VER): AM286415.1 GI:122087364  
 CAS REGISTRY NO. (RN): 917704-63-3  
 SEQUENCE LENGTH (SQL): 4615899  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 29 Oct 2008  
 DEFINITION (DEF): *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
 complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
 ORGANISM (ORGN): *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Enterobacteriales; Enterobacteriaceae; *Yersinia*  
 GenomeProject:190  
 PROJECT (PJID): 1  
 REFERENCE: 1  
 AUTHOR (AU): Delihias,N.  
 TITLE (TI): Annotation and evolutionary relationships of a small  
 regulatory RNA gene *micF* and its target *ompF* in  
*Yersinia* species  
 JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
 REFERENCE: 2  
 AUTHOR (AU): Thomson,N.R.; Howard,S.; Wren,B.W.; Holden,M.T.;  
 Crossman,L.; Challis,G.L.; Churcher,C.; Mungall,K.;  
 Brooks,K.; Chillingworth,T.; Feltwell,T.; Abdellah,Z.;  
 Hauser,H.; Jagels,K.; Maddison,M.; Moule,S.;  
 Sanders,M.; Whitehead,S.; Quail,M.A.; Dougan,G.;  
 Parkhill,J.; Prentice,M.B.  
 TITLE (TI): The complete genome sequence and comparative genome  
 analysis of the high pathogenicity *Yersinia*  
*enterocolitica* strain 8081  
 JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
 REFERENCE: 3 (bases 1 to 4615899)  
 AUTHOR (AU): Thomson,N.R.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):  

Feature Key	Location	Qualifier
source	1..4615899	/organism=" <i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081" /mol-type="genomic DNA" /strain="8081"

		/sub-species="enterocolitica" /db-xref="taxon:393305" /locus-tag="YE0001" /locus-tag="YE0001" /codon-start=1 /transl-table=11 /product="putative flavoprotein" /protein-id="CAL10146.1" /db-xref="GI:122087365" /db-xref="GOA:AlJHQ8" /db-xref="InterPro:IPR001094" /db-xref="InterPro:IPR008254" /db-xref="InterPro:IPR015702" /db-xref="UniProtKB/TrEMBL:AlJHQ8" /translation="MADITLISGSTLGSAEYVAE HLAEKLEEAGFTTETLHGPELDEL TLDGMWLIITSTHGAGDLPDNLQPLLEQIEQQR DLSQVRFGAVGLGSSEYDTFCGAV RKLDQQLIIQGAIRVGDIIEIDVIKHEIPDPAE IWKVNWINLL"
gene	complement(270..710)	
CDS	complement(270..710)	
		/locus-tag="YE0001" /inference="protein motif:PFAM:PF00258" /note="Pfam match to entry PF00258 flavodoxin, Flavodoxin, score 117.3, E-value 1.9e-32"
misc-feature	complement(273..704)	
gene	complement(802..1263)	
CDS	complement(802..1263)	/gene="asnC" /locus-tag="YE0002" /gene="asnC" /locus-tag="YE0002" /codon-start=1 /transl-table=11 /product="regulatory protein" /protein-id="CAL10147.1" /db-xref="GI:122087366" /db-xref="GOA:AlJHQ9" /db-xref="InterPro:IPR000485" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:AlJHQ9" /translation="MSEIYQIDNLDRGILNALME NARTPYAELAKNFGVSPGTIHVRV EKMRQAGIITAACVHVNPQKGLDYVCCFIGIILK SAKDYPALKKLESLEEVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP"
misc-feature	complement(868..1173)	/gene="asnC" /locus-tag="YE0002" /inference="protein motif:PFAM:PF01037" /note="Pfam match to entry PF01037 ASN-Trans-reg, AsnC family, score 61.4, E-value 1.2e-15"
misc-feature	complement(1111..1191)	/gene="asnC" /locus-tag="YE0002" /inference="protein motif:Prosites:PS00519" /note="PS00519 Bacterial regulatory proteins, asnC family signature."
misc-feature	complement(1129..1194)	/gene="asnC" /locus-tag="YE0002" /note="Predicted helix-turn-helix

		motif with score 1765.000, SD 5.20 at aa 24-45, sequence TPYAELAKNFGVSPGTIHVRVE"
gene	1449..2441	/gene="asnA" /locus-tag="YE0003" /gene="asnA" /locus-tag="YE0003" /codon-start=1 /transl-table=11 /product="aspartate-ammonia ligase" /protein-id="CAL10148.1" /db-xref="GI:122087367" /db-xref="GOA:AlJHR0" /db-xref="InterPro:IPR004618" /db-xref="InterPro:IPR006195" /db-xref="UniProtKB/Swiss-Prot:AlJ HR0" /translation="MKKQFIQKQQQISFVKSFSS RQLEQQQLGLIEVQAPILSRVGDGT QDNLSGSEKAVQVKVSLPDATFEVHSLAKWKR KTLGRDFDGADQGIYTHMKALRPD EDRLSAIHSVYVDQWDWERVMGDSERNLAYLKST VNKIYAAIKETAAIASAEFDIKPF LPEQIHFIHSESLRAKFFDLDAKGERAIKELG AVFLIGIGGKLADGKSHDVRAPDY DDWTSFSAEGFAGLNGDIIWNPVLEDAFEISSM GIRVDAEALKRQLALTSDEDRLKL EWHQSLNNGEMPQTIGGGIGQSRLVMLLLQQQHI GQVQCGVWGPEISEKVEGLL"
misc-feature	1455..2186	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:PFAM:PF03590" /note="Pfam match to entry PF03590 AsnA, Aspartate-ammonia ligase, score 597.7, E-value 4.6e-177"
misc-feature	2055..2078	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	2595..3266	/locus-tag="YE0004" /locus-tag="YE0004" /inference="similar to sequence:INSDC:AE001895" /inference="similar to sequence:INSDC:AL646078" /note="Similar to Ralstonia solanacearum probable transmembrane protein RSP0410 or RS00867 SWALL:Q8XSQ7 (EMBL:AL646078) (224 aa) fasta scores: E(): 7.3e-36, 46.54 38d in 217 aa, and to Deinococcus radiodurans hypothetical protein DR0351 SWALL:Q9RXG2 (EMBL:AE001895) (227 aa) fasta scores: E(): 3.7e-17, 31.67 38d in 221 aa" /codon-start=1
CDS	2595..3266	



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/protein-id="CAL10149.1"
/db-xref="GI:122087368"
/db-xref="InterPro:IPR009781"
/db-xref="UniProtKB/TrEMBL:A1JHR1"
/translation="MARFHLPLRHSHARPRLLS
VGAGIIAYFLPSHFTVLLRVMVS
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ASMVLISVSMACLASILVILFELS
TANQLSGSAKAFHLVLTGMTLLVSWLLLPTAFTM
HYAHLFYLSRDESDAVLPLIFPKE
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/locus-tag="YE0004"

misc-feature    join(2643..2711,
                2721..2777,2838..2906,
                2934..3002,3192..3260)

gene            complement(3276..4742)
CDS             complement(3276..4742)

/inference="protein
motif:TMHMM:2.0"
/note="5 probable transmembrane
helices predicted for YE0004 by
TMHMM2.0 at aa 17-39, 43-61,
82-104, 114-136 and 200-222"
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/codon-start=1
/transl-table=11
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/protein-id="CAL10150.1"
/db-xref="GI:122087369"
/db-xref="InterPro:IPR002035"
/db-xref="UniProtKB/Swiss-Prot:A1J
HR3"
/translation="MLSLATLDLLSISESELIE
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WRVSLTLQTTITIHQLEQEREQL
LAELQQLRALSGALEPILATNDGAAGRLWDMSQG
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VPEEVSGIHQSNDILRLLPTLVLV
LGMSELEFEFYRRLRLRRLLTYRLQGDNWQEKTL
QRPISLKSHDEQPRGPFIVCVDT
GSMGGFSEQCAKAFCLALLRIALDNRRCYIMLF
ATEIIHYELSSASGIEQAIIRLSQ
HFRGGTDLAACLSSTLSKMEERDWDYDADAVIISD
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RWKR"
/locus-tag="YE0005"
/note="Predicted helix-turn-helix
motif with score 997.000, SD 2.58
at aa 215-236, sequence
PELQQLAEQLGRSRSAKAQPTP"
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/locus-tag="YE0006"
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gene            complement(4746..6254)
CDS             complement(4746..6254)

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misc-feature	6711..8432	IELGTQVEI" /gene="kup" /locus-tag="YE0007" /inference="protein motif:PFAM:PF02705" /note="Pfam match to entry PF02705 K-trans, K+ potassium transporter, score 854.9, E-value 1.7e-254" /gene="kup"
misc-feature	join(6717..6785, 6870..6938,6966..7034, 7068..7136,7194..7262, 7299..7367,7425..7493, 7566..7634,7662..7730, 7749..7802,7830..7886)	/locus-tag="YE0007" /inference="protein motif:TMHMM:2.0" /note="11 probable transmembrane helices predicted for YE0007 by TMHMM2.0 at aa 4-26, 55-77, 87-109, 121-143,163-185, 198-220, 240-262, 287-309, 319-341, 348-365 and 375-393"
gene	8606..9025	/locus-tag="YE0008"
CDS	8606..9025	/locus-tag="YE0008" /codon-start=1 /transl-table=11 /product="ribose permease" /protein-id="CAL10153.1" /db-xref="GI:122087372" /db-xref="GOA:AlJHR8" /db-xref="InterPro:IPR007721" /db-xref="UniProtKB/Swiss-Prot:AlJ HR8" /translation="MKKGALLNSDISAVISRLGH TDQIVIGDAGLP I PATTTRIDLAL TQGVPGFLQVFVVVTQEMQVESAYLAQEIVKNNP QLHETLLAQLS QLEQHQNQIALH YISHEAFKEQTKQSRVIRSGECS PFANIILCSG VTF"
gene	9033..10535	/gene="rbsA"
CDS	9033..10535	/locus-tag="YE0009" /gene="rbsA" /locus-tag="YE0009" /inference="similar to sequence:INSDC:AL627280" /inference="similar to sequence:UniProtKB:P04983" /note="Similar to Escherichia coli ribose transport ATP-binding protein RbsA SWALL:RBSA-ECOLI (SWALL:P04983) (501 aa) fasta scores: E(): 2.7e-148, 85.83 38d in 494 aa,and to Salmonella typhi high affinity ribose transport protein STY896 SWALL:Q8ZZR4 (EMBL:AL627280) (501 aa) fasta scores: E(): 1.1e-147, 85.62 38d in 494 aa" /codon-start=1 /transl-table=11 /product="putative ribose"

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		/db-xref="InterPro:IPR015861"
		/db-xref="UniProtKB/TrEMBL:AlJHS1"
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		GREFVNHHGGIDWKKMYAEADLLARLNISSSS
		RLVGELSIGDQOMVEIAKVLSPES
		KVIIMDEPTDALTDITETASLFNVIKELKAEGRI
		VYISHRLKEIFEICDDVTVFRDQ
		FIAEKPVNILTENALIEMMVGRKLEEQYPRNLNP
		RGEKRLQVKQLCGPGVENVNFTLY
		SGEILGVAGLMGAGRTELMKIIYGALPRKSGFVM
		LDGREVVTHSPQDGLANGIVYISE
		DRKRDLGLVLMGMSVKENMSLTALRYFSRSGGSLKH
		ADEQQAADFIRLFNIKTSPMEQP
		IGLLSGGNQOKVAIARGLMTRPKVLILDEPTRGV
		DVGAKKEIYQLINQFKQEGLSIIL
		VSSMEPEVLGMSDRIIVMHEGQLSGEFSIEQATQ
		EVLMAAAVGRDLLEK"
misc-feature	9120..9683	/gene="rbsA"
		/locus-tag="YE0009"
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		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		173.1, E-value 3e-49"
misc-feature	9141..9164	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein
		motif:Prosite:PS00017"
		/note="PS00017 ATP/GTP-binding
		site motif A (P-loop)."
misc-feature	9864..10445	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein
		motif:PFAM:PF00005"
		/note="Pfam match to entry PF00005
		ABC-tran, ABC transporter, score
		134.4, E-value 1.3e-37"
misc-feature	10218..10262	/gene="rbsA"
		/locus-tag="YE0009"
		/inference="protein
		motif:Prosite:PS00211"
		/note="PS00211 ABC transporters
		family signature."
gene	10623..11588	/gene="rbsC"
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CDS	10623..11588	/gene="rbsC"
		/locus-tag="YE0010"
		/codon-start=1
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		/protein-id="CAL10155.1"
		/db-xref="GI:122087374"

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LRGVTMVYTINGSPINTGFTDVADT
FGWFGIGRPLGIPTPIWLMAIVFIAAWYMLHSTR
LGRYIYALGGNESATRLSGISVDK
VKIIVYSLCGLLAALAGIIEVARLSSAQPTAGTG
YELDAIAAVVLGGTSLAGGKGQIV
GTLIGALILGFLNNGLNLLGVSSYYQMIVKAVVI
LLAVLVDNKKQ"
/gene="rbsC"
/locus-tag="YE0010"
/note="Signal peptide predicted
for YE0010 by SignalP 2.0 HMM
(Signal peptide probability 0.969)
with cleavage site probability
0.169 between residues 42 and 43"
/gene="rbsC"

sig-peptide 10623..10748

misc-feature join(10686..10754,
10815..10883,
10911..10979,
10998..11066,
11124..11192,
11283..11351,
11445..11513)

/locus-tag="YE0010"
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motif:TMHMM:2.0"
/note="7 probable transmembrane
helices predicted for YE0010 by
TMHMM2.0 at aa 22-44, 65-87,
97-119, 126-148,168-190, 221-243
and 275-297"
/gene="rbsC"
/locus-tag="YE0010"
/inference="protein
motif:PFAM:PF02653"
/note="Pfam match to entry PF02653
BPD-transp-2,Branched-chain amino
acid transport system / permease
component, score 3.4, E-value
7.7e-07"
/gene="rbsB"
/locus-tag="YE0011"
/note="synonyms: prlB, rbsP"
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/locus-tag="YE0011"
/inference="similar to
sequence:UniProtKB:P02925"
/inference="similar to
sequence:UniProtKB:P02926"
/note="Similar to Escherichia coli
D-ribose-binding periplasmic
protein precursor RbsB or RbsP or
PrlB SWALL:RBSB-ECOLI
(SWALL:P02925) (296 aa) fasta
scores: E(): 1.7e-84, 84.74 38d in
295 aa, and to Salmonella

```

		typhimurium, and Salmonella typhi D-ribose-binding periplasmic protein precursor RbsB or RbsP or STM3884 or STY3894 SWALL:RBSB-SALTY (SWALL:P02926) (296 aa) fasta scores: E(): 5.6e-84, 84.06 38d in 295 aa" /codon-start=1 /transl-table=11 /product="putative D-ribose-binding periplasmic protein precursor" /protein-id="CAL10156.1" /db-xref="GI:122087375" /db-xref="InterPro:IPR001761" /db-xref="UniProtKB/TrEMBL:A1JHS3" /translation="MKMKKLLATLISVVALSATVS ANALAKDTIALVVS TLNPPFFVSM KDGAQKEADKLGYNLVILDSQNNPAKELANVQDL TVRGTKLLLINPTDSDAVGNVAVKM ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM AGDYIAKKVGS DAKVIQLEGIAGA SAARERGEGFKQSMKKNFKOLLASQPADFDRTKG LNVNQNLTAHPDVQAVFAQNDEM ALGALRALQTAGKTDVLVVGFDGTDGKAVESG KMGATIAQRPDQIGVIGVQTADKV LKGEKVQAVIPVDLKLVTIK"
sig-peptide	11760..11834	/gene="rbsB" /locus-tag="YE0011" /note="Signal peptide predicted for YE0011 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.933 between residues 25 and 26"
misc-feature	11835..12641	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:PFAM:PF00532" /note="Pfam match to entry PF00532 Peripla-BP-like, Periplasmic binding proteins and sugar binding domain of the LacI family, score 63.4, E-value 3.3e-16"
misc-feature	12432..12455	/gene="rbsB" /locus-tag="YE0011" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	12811..13737	/gene="rbsK" /locus-tag="YE0012"
CDS	12811..13737	/gene="rbsK" /locus-tag="YE0012" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="CAL10157.1" /db-xref="GI:122087376" /db-xref="GOA:A1JHS4" /db-xref="InterPro:IPR002139" /db-xref="InterPro:IPR002173" /db-xref="InterPro:IPR011611"

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DNIDTAPIEAVAGTTTGVALIFVN
GEGENVIGIHAGANSVTPRYLGRYQQQVIDADA
LLMQLESPLGTVIAAAKLAKOQHT
QVILNPAPARELPDELLSLVDMITPNETEAEERLT
GIHIEQDDDAKAAQILHDKGIAT
VIITLGRSGVWLSEGGQKLVAGFKVNAVDTIAA
GDTFNGALLTALLEGQAMGSAVRF
AHAAAAIAVTRPGAQPSIPWRAEIDSFLQDRV"
misc-feature 12817..13701
/gene="rbsK"
/locus-tag="YE0012"
/inference="protein
motif:PFAM:PF00294"
/note="Pfam match to entry PF00294
pfkB, pfkB family carbohydrate
kinase, score 298.8, E-value
4.4e-87"
misc-feature 12928..13002
/gene="rbsK"
/locus-tag="YE0012"
/inference="protein
motif:Prosite:PS00583"
/note="PS00583 pfkB family of
carbohydrate kinases signature 1."
misc-feature 13552..13593
/gene="rbsK"
/locus-tag="YE0012"
/inference="protein
motif:Prosite:PS00584"
/note="PS00584 pfkB family of
carbohydrate kinases signature 2."
gene 13740..14741
/gene="rbsR"
/locus-tag="YE0012A"
CDS 13740..14741
/gene="rbsR"
/locus-tag="YE0012A"
/inference="similar to
sequence:INSDC:AE008881"
/inference="similar to
sequence:UniProtKB:P25551"
/note="Similar to Escherichia
coli, and Escherichia coli O157:H7
ribose operon repressor RbsR or
b3753 or z5254 or ecs4695
SWALL:RBSR-ECOLI (SWALL:P25551)
(329 aa) fasta scores: E():
7.1e-94, 73.17 38d in 328 aa and
to Salmonella typhimurium
transcriptional repressor for rbs
operon RbsR or stm3886
SWALL:Q82KV7 (EMBL:AE008881) (332
aa) fasta scores: E(): 5.3e-95,
74.09 38d in 332 aa"
/codon-start=1
/transl-table=11
/product="ribose operon repressor"
/protein-id="CAL10158.1"
/db-xref="GI:122087377"
/db-xref="GOA:A1JHS5"
/db-xref="InterPro:IPR000843"
/db-xref="InterPro:IPR001761"

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VINKNRFVSDPIRDKVLAAIKQLN
YAPSALARSLKLNERTRTIGMLVTASSNPFYAEV
RGVERSCYERGSYLICNTEGDID
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YPSLPIIMMDWAPFEGVNDVIQDN
SLLGGEMATSYLIARGYTRIACIAGPQDKTPAKE
RLQGFRQAMDRAGLPVLPDYEVAS
DFEFGGGLVAMKQLLALPQPPEAVFTSNDAMAVG
VYQALHQAGLSIPQDMAVIGYDDI
EIAQYMTPLTTIHQPKDSLGEAIDTLIHLRLNS
PEAEPOVLILTPELIERGSVATR"

gene      complement(14738..16162 /locus-tag="YE0013"
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CDS       complement(14738..16162 /locus-tag="YE0013"
)

/codon-start=1
/transl-table=11
/product="putative membrane
transport protein"
/protein-id="CAL10159.1"
/db-xref="GI:122087378"
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/db-xref="InterPro:IPR001411"
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/db-xref="UniProtKB/TREMBL:ALJHS6"
/translation="MIKSARSMAGLPWIAAMAFF
MQALDATILNTALPSIAESLNRSP
LTMQSALIIISYTLTVAMLIPVSGWLADRFGTTRIF
ILAVSLFTLGSLLCALSGSLPFLV
ASRVIQGVGGAMMPVARLALIRAYPRSELLPVL
NEVTIPLGLIGPVMGPFLGGLLVTY
ATWHWFILNIPIGLLGIFYARKYMPDFTMPKRA
FDIIGFLFGSSLVIMISVSLEIMG
RPDIASYLPAAVLLGGLMLLIFYIFHAKGHPNPL
IGLPLFKTRTFVSGIAGNVASRLG
TGCVPFLMPLMLQVGFYSALIAAGCMMAPTIGS
MMAKSAVTQVLRSLGYRTVLVGIT
AIIIGVLIALFAFQSPGMSPLMILPLFILGMAMS
TQFTAMNTITLADLTNNASSGNS
VLAVTQQLAISFGVAISAVVLRFYDGLSFGNNID
HFHYTFITMGAVILLSSMVPELLK
PRDGDNLIQGRNVKKVTQPAKSEV"

sig-peptide complement(16052..16162 /locus-tag="YE0013"
)

/Note="Signal peptide predicted
for YE0013 by SignalP 2.0 HMM
(Signal peptide probability 0.994)
with cleavage site probability
0.74 between residues 37 and 38"

misc-feature complement(join(14816.. /locus-tag="YE0013"
14884,14927..14995,
15032..15100,
15128..15196,
15233..15301,
15344..15412,
15431..15499,
15527..15583,
15620..15679,
15689..15757,

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15791..15859,
15869..15937,
15956..16015,
16058..16126))

/inference="protein
motif:TMHMM2.0"
/notes="14 probable transmembrane
helices predicted for YE0013 by
TMHMM2.0 at aa 13-35, 50-69,
76-98, 102-124, 136-158, 162-181,
194-212, 222-244, 251-273,
288-310, 323-345, 355-377, 390-412
and 427-449"
misc-feature complement(15830..16132 /locus-tag="YE0013"
)

/inference="protein
motif:PFAM:PF00083"
/notes="Pfam match to entry PF00083
sugar-tr, Sugar (and other)
transporter, score 20.7, E-value
2.1e-06"
gene complement(16237..16926 /locus-tag="YE0014"
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CDS complement(16237..16926 /locus-tag="YE0014"
)

/codon-start=1
/transl-table=11
/product="putative GntR-family
transcriptional regulator"
/protein-id="CAL10160.1"
/db-xref="GI:122087379"
/db-xref="GOA:AlJHS7"
/db-xref="InterPro:IPR000524"
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/db-xref="UniProtKB/TREMBL:AlJHS7"
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VMQHFLILRRSLEPQACSLAAINVSGKQKALLTS
LMTMCELMHAHFNRRERWIQVDAQF
HQLIYEASGNPFLTFSANLFSSVYHSYFRSITGD
EVIKLQHHQNIQVDTILAGDSQGAL
VACQVLLKEKD"
misc-feature complement(16696..16875 /locus-tag="YE0014"
)

/inference="protein
motif:PFAM:PF00392"
/notes="Pfam match to entry PF00392
gntR, Bacterial regulatory
proteins, gntR family, score 79.0,
E-value 6.6e-21"
misc-feature complement(16744..16818 /locus-tag="YE0014"
)

/inference="protein
motif:Prosite:PS00043"
/notes="PS00043 Bacterial
regulatory proteins, gntR family
signature."
misc-feature complement(16750..16815 /locus-tag="YE0014"
)

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		/note="Predicted helix-turn-helix motif with score 1101.000, SD 2.94 at aa 38-59, sequence PGEIELGEGFGVSRITAVREAVK"
gene	17506..18994	/gene="16S rRNA"
rRNA	17506..18994	/gene="16S rRNA"
		/product="16S ribosomal RNA"
		/note="match to 16S-rRNA 1..1461 (Y.enterocolitica 16S)"
gene	19220..19295	/gene="tRNA-Glu (TTC)"
tRNA	19220..19295	/gene="tRNA-Glu (TTC)"
		/product="tRNA-Glu"
		/note="codon recognized: GAA"
gene	19674..22667	/gene="23S rRNA"
rRNA	19674..22667	/gene="23S rRNA"
		/product="23S ribosomal RNA"
		/note="match to 23S-rRNA 1..2994 (Y. enterocolitica 23S EMBL:U77925, Y.pestis KIM 98 38identity, Citrobacter freundii 23S EMBL:U77928 94 38identity)"
gene	22667..22908	/gene="5S rRNA"
rRNA	22667..22908	/gene="5S rRNA"
		/product="5S ribosomal RNA"
		/note="match to 5SrRNA 1..240 Y.enterocolitica"
gene	complement(23194..23721)	/gene="mobB"
		/locus-tag="YE0016"
CDS	complement(23194..23721)	/gene="mobB"
		/locus-tag="YE0016"
		/codon-start=1
		/transl-table=11
		/product="probable molybdopterin-guanine dinucleotide biosynthesis protein B"
		/protein-id="CAL10161.1"
		/db-xref="GI:122087380"
		/db-xref="GOA:AlJHS8"
		/db-xref="InterPro:IPR004435"
		/db-xref="UniProtKB/TrEMBL:AlJHS8"
		/translation="MSRKTPFLGIAAYSGTKT TLLKSLIPLLQQRQIRVGLIKHTH HNMEIDTPGKDSYELRKAGAYQTLVASDCRNALM TETPEQKPLDLHYLASRLDAATID LILVEGFKHEPINKIALYREAVGKPYTDLIDEYV IALASDELIETAVEQLDINQPEQI ADFICSWLQINFSQP"
misc-feature	complement(23299..23703)	/gene="mobB"
		/locus-tag="YE0016"
		/inference="protein"
		motif:PFAM:PF03205"
		/note="Pfam match to entry PF03205 MobB, Molybdopterin guanine dinucleotide synthesis protein B, score 184.3,E-value 1.3e-52"
misc-feature	complement(23662..23685)	/gene="mobB"
		/locus-tag="YE0016"
		/inference="protein"

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motif:Prosite:PS00017"
/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."
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CDS	complement(23718..24317)	<pre> /locus-tag="YE0017" /note="synonyms: chlB, mob, nar" /gene="mobA"  /locus-tag="YE0017" /codon-start=1 /transl-table=11 /product="molybdopterin-guanine dinucleotide biosynthesis protein A" /protein-id="CAL10162.1" /db-xref="GI:122087381" /db-xref="GOA:A1JHS9" /db-xref="InterPro:IPR013482" /db-xref="UniProtKB/TrEMBL:A1JHS9" /translation="MIEMQPNITGVILAGGRSSR MGGNDKGLTLLHDKPLFYQVIDRL KPQVNDLLINANRNQELYQASGVVVSIIITGV GPLAGMHAGLSYSPTEWVVFAPCD VPALPSNLVSQLWQKQQAALAYVHDSGERAHTL ALMHVSLKSLLAELYLAKSDRKLM FMDSVNAQPIIFRGKQKQFSLNLTADCDLWEQS KRGEL" /locus-tag="YE0018" /locus-tag="YE0018" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10163.1" /db-xref="GI:122087382" /db-xref="InterPro:IPR009383" /db-xref="UniProtKB/TrEMBL:A1JHT0" /translation="MKCHRVNELIELLHPAQQE PDLNLVQFLQKLSEEAGFEGEFAE LTDDILIYHLKMRGSASTEVIPGLKKDYEDFKT AILRARGIKD" /locus-tag="YE0019" /locus-tag="YE0019" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10164.1" /db-xref="GI:122087383" /db-xref="InterPro:IPR002575" /db-xref="UniProtKB/TrEMBL:A1JHT1" /translation="MNSSAFNFQTLSPDLIMDAL EGVGLRVDSGLTALNSYENRVYQF MDEDRKRYVVKFYRPERWSSEQILEEHQFSLDLA ESEIPVIAPLQLDGRTLHTHGGEF FTVFPVSGGRQYEIDNLDQLEWVGRLGRIHQVG SDALFVARSTIGIEEYLTEPRQLL ASSELVPAKQDKFLAATDLLISTIKYQWHTDWQ PLRLHGDCHPGNILWRDGPMEVDL DDARNGPAVQDLWMLLHGERREQLIQLDILLEAY GEFADFQDRELALIEPLRAMRMVY</pre>
gene	24462..24731	
CDS	24462..24731	
gene	24823..25809	
CDS	24823..25809	

		YLAWVARRWQDPAPFKSFPWMAESDFWLQQTASF TEQVKLLQAPPLQLMPMY"
gene	25856..26479	/gene="dsbA" /locus-tag="YE0020"
CDS	25856..26479	/gene="dsbA" /locus-tag="YE0020" /codon-start=1 /transl-table=11 /product="secreted thiol:disulfide interchange protein DsbA" /protein-id="CAL10165.1" /db-xref="GI:122087384" /db-xref="GOA:AlJHT2" /db-xref="InterPro:IPR001853" /db-xref="InterPro:IPR006662" /db-xref="InterPro:IPR012335" /db-xref="UniProtKB/TREMBL:AlJHT2" /translation="MKNVWLALVGMVMAFSASAA QFTDGTQYQTLNKPVTGEPQVLEF FSFYCPHCYQFEVYHVPQAVKKALPEGTKMTRY HVEFLGPLGKQLTQAWAVAMALGV EEKITPLMFEGVQKTQTVQTPDDIRNVFIKAGVS GEEFDAALNSFVVKSLVVQQQKAA EDLELRGVPAMFVNGKYMIRKNDGMTSSMDITYVK QYADVVKFLLTQK"
sig-peptide	25856..25912	/gene="dsbA" /locus-tag="YE0020" /note="Signal peptide predicted for YE0020 by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.992 between residues 19 and 20"
misc-feature	25856..26476	/gene="dsbA" /locus-tag="YE0020" /inference="protein motif:PFAM:PF01323" /note="Pfam match to entry PF01323 DSBA, DSBA oxidoreductase, score 486.2, E-value 1.7e-143"
misc-feature	25976..26032	/gene="dsbA" /locus-tag="YE0020" /inference="protein motif:Prosite:PS00194" /note="PS00194 Thioredoxin family active site."
gene	27070..29868	/gene="polA" /locus-tag="YE0021"
CDS	27070..29868	/note="synonym: resA" /gene="polA" /locus-tag="YE0021" /codon-start=1 /transl-table=11 /product="DNA polymerase I" /protein-id="CAL10166.1" /db-xref="GI:122087385" /db-xref="GOA:AlJHT3" /db-xref="InterPro:IPR001098" /db-xref="InterPro:IPR002298" /db-xref="InterPro:IPR002421" /db-xref="InterPro:IPR002562" /db-xref="InterPro:IPR003583" /db-xref="InterPro:IPR008918"

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GPQVECKEYGVPELIIDFLALMGDSSDNIPGVP
GVGKTAQALLQGLGGLDSLFLNHL
DKIPTLTFRGAKTMSAKLEQNKDVAYLSYKLATI
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PVRNEEGRRIRQAFIAPEGYRIMAADYSQIELRI
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PGVLEYMERTRKQAAEQGYVTTLDGRRLYLPDIH
SRNATRRKAAERAINAPMQGTAA
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AVPLKVDVGVGYNWDQAH"
/misc-feature 27088..27576 /gene="polA"
/locus-tag="YE0021"
/inference="protein
motif:PFAM:PF02739"
/Note="Pfam match to entry PF02739
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N-terminal resolvase-like domain,
score 316.3, E-value 2.4e-92"
/misc-feature 27580..27900 /gene="polA"
/locus-tag="YE0021"
/inference="protein
motif:PFAM:PF01367"
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exonuclease, C-terminal SAM fold,
score 194.5, E-value 1.1e-55"
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/locus-tag="YE0021"
/inference="protein
motif:PFAM:PF01612"
/Note="Pfam match to entry PF01612
3-5-exonuclease, 3'-5'
exonuclease, score 229.0, E-value
4.4e-66"
/misc-feature 28717..29862 /gene="polA"
/locus-tag="YE0021"
/inference="protein
motif:PFAM:PF00476"

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		/note="Pfam match to entry PF00476 DNA-pol-A, DNA polymerase family A, score 698.2, E-value 2.6e-207"
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misc-RNA	30017..30134	/note="Spot 42 RNA (RF00021) as predicted by Rfam, score 91.54, positions 1 to 118"
gene	complement(30302..30955	/locus-tag="YE0022"
CDS	) complement(30302..30955	/locus-tag="YE0022"
		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10167.1" /db-xref="GI:122087386" /db-xref="GOA:AlJHT4" /db-xref="InterPro:IPR002917" /db-xref="InterPro:IPR005289" /db-xref="UniProtKB/Swiss-Prot:AlJ HT4" /translation="MTIRNFNYHMTFVISAPDI RHLPRDEGIEVAFAGRSNAGKSSA LNTLTGQKSLARTSKTPGRTQLINLFEVVEGVRL VDLPGYGYAEVPEEMKLGKQWALRG EYLGKRNCLKGLVVLMDIRHPLKDLDDQMITWAV AVGTPVMLLLTAKDKLASGARKAQ LNMVREAIIPFMGDIOVEAFSSLLKIGVDKLRK LDTWFSEIPPEVMIDEXDDEEGK"
misc-feature	complement(30830..30853	/locus-tag="YE0022"
	)	/inference="protein motif:Prosites:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-RNA	31382..31582	/note="CsrC family RNA (RF00084) as predicted by Rfam, score 35.38, positions 1 to 254"
gene	31718..32284	/locus-tag="YE0023"
CDS	31718..32284	/locus-tag="YE0023" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10168.1" /db-xref="GI:122087387" /db-xref="InterPro:IPR007336" /db-xref="UniProtKB/Swiss-Prot:AlJ HT5" /translation="MKQPNKAPRADRAAPKGTAT PKRHKKTRVELDIEARERKRQKRH SGNRSGARTNIEGSKNTGSTQAQEKDPRIGSKVP VPLVVEKAKAKLTTKPVAKVEAK PRLTPEELTKLENDERLDALLDRLDNDEVLSKE DQAYVDLTLDRLDALMEQLGIELG DDEDEEREKPEDILKLLKSGNPKDTF"

gene	32467..33840	/gene="hemN"
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CDS	32467..33840	/gene="hemN"
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		/db-xref="GI:122087388"
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		/db-xref="InterPro:IPR004558"
		/db-xref="InterPro:IPR006638"
		/db-xref="InterPro:IPR007197"
		/db-xref="InterPro:IPR010723"
		/db-xref="UniProtKB/TrEMBL:AlJHT6"
		/translation="MSENAVWVWDLSLIQKYNYS GPRYTSYPTALEFSEYDESAFQQA VKRYQRPRLSLYVHIPFCHKLCYFCGCNKLVTQ QHKADEYLAVLEKEIRQRAALFAG RQVSGMHWGGGPTYLNKTQITHLMNLLRENFDF LPGAESIEVDPREIELDVLDLHLR AEGFNRLSMGVQDFNKEVQRLVNRQDEDFIFAL IARAKALGFNSTIDLIYGLPKQT PESFAFTLKRVAELNPDRLSVFNVAHLPSLFAAQ RKIKDADLPTAEQRLDILQHTISF LTESGYQFIGMDHFAFPDDELATAQREGKLHRNF QGYTTQGESDLLGLGVSIAISMLGD SYAQNEKDLKTYAVVQQRGNALWRGLTMTEDDC LRRDVIKTLICNFQISYQPIEQHY GIRFADYFAEDFELLTPFEHFDGLVERDDKSIRVT PRGRLLIRNICMCFDIYLRQARK QQFSRVI"
misc-feature	32761..33522	/gene="hemN"
		/locus-tag="YE0024"
		/inference="protein"
		motif:PFAM:PF02473"
		/note="Pfam match to entry PF02473 Coprogen-an-ox, Oxygen-independent Coproporphyrinogen III oxidase, score 555.2, E-value 2.8e-164"
gene	complement(33989..35401 )	/gene="ntrC"
		/locus-tag="YE0025"
		/note="synonyms: glnG, glnT"
CDS	complement(33989..35401 )	/gene="ntrC"
		/locus-tag="YE0025"
		/codon-start=1
		/transl-table=11
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		/db-xref="GI:122087389"
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		/db-xref="InterPro:IPR001789"
		/db-xref="InterPro:IPR002078"
		/db-xref="InterPro:IPR002197"
		/db-xref="InterPro:IPR003593"
		/db-xref="InterPro:IPR010114"
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misc-feature      complement(34001..34123 /gene="ntrC"
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                    /inference="protein
                    motif:PFAM:PF02954"
                    /note="Pfam match to entry PF02954
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                    protein, Fis family, score 64.1,
                    E-value 2e-16"
misc-feature      complement(34007..34072 /gene="ntrC"
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                    /locus-tag="YE0025"
                    /note="Predicted helix-turn-helix
                    motif with score 1763.000, SD 5.19
                    at aa 444-465, sequence
                    GHKQEAARLLGWGRNTLTRKLK"
misc-feature      complement(34313..34342 /gene="ntrC"
)
                    /locus-tag="YE0025"
                    /inference="protein
                    motif:Prosite:PS00688"
                    /note="PS00688 Sigma-54
                    interaction domain C-terminal part
                    signature."
misc-feature      complement(34316..34981 /gene="ntrC"
)
                    /locus-tag="YE0025"
                    /inference="protein
                    motif:PFAM:PF00158"
                    /note="Pfam match to entry PF00158
                    Sigma54-activat,Sigma-54
                    interaction domain, score 496.8,
                    E-value 1.1e-146"
misc-feature      complement(34676..34723 /gene="ntrC"
)
                    /locus-tag="YE0025"
                    /inference="protein
                    motif:Prosite:PS00676"
                    /note="PS00676 Sigma-54
                    interaction domain ATP-binding
                    region B signature."
misc-feature      complement(34868..34909 /gene="ntrC"
)
                    /locus-tag="YE0025"
                    /inference="protein
                    motif:Prosite:PS00675"
                    /note="PS00675 Sigma-54

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interaction domain ATP-binding
region A signature."
misc-feature complement(35033..35392 /gene="ntrC"
)
/locus-tag="YE0025"
/inference="protein
motif:PFAM:PF00072"
/note="Pfam match to entry PF00072
response-reg, Response regulator
receiver domain, score 148.5,
E-value 7.8e-42"
gene complement(35409..36458 /gene="ntrB"
)
/locus-tag="YE0026"
/note="Synonyms: glnI, glnR"
CDS complement(35409..36458 /gene="ntrB"
)
/locus-tag="YE0026"
/codon-start=1
/transl-table=11
/product="Two component regulatory
protein involved in nitrogen
assimilation"
/protein-id="CAL10171.1"
/db-xref="GI:122087390"
/db-xref="GOA:AJHT8"
/db-xref="InterPro:IPR000014"
/db-xref="InterPro:IPR003594"
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/db-xref="InterPro:IPR005467"
/db-xref="InterPro:IPR013767"
/db-xref="UniProtKB/TrEMBL:AJHT8"
/translation="MATGTLFPDAGQILNSLINSI
LLDDSLAIHYANPAAQQLAQSS
RKLEGTPLPELLGYFSLNMLMRESLASGQSFTD
NEVTLVVDGRAHILSLTAQSLAEG
FILEMAPMDNQRRLSQEQLQHAQQIAARDLVRG
LAHEIKNPLGGLRGAAQLLSKALP
DPALLEYTKVIEQADRLRNLDVRLGLGPQRPGQH
VTQSIHQVAERVCQLVLEKPDNV
TLIRDYDPSLPELAHDPDQIEQVLLNITRNALQA
LGEAGGTITLRTRTAFQITLHGVR
YRLAARIDIEDDGPVPTQLQDTILFYPMVSGREG
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WPGHTEFSVYLPIRQ"
misc-feature complement(35415..35762 /gene="ntrB"
)
/locus-tag="YE0026"
/inference="protein
motif:PFAM:PF02518"
/note="Pfam match to entry PF02518
HATPase-c, Histidine kinase-, DNA
gyrase B-, and HSP90-like ATPase,
score 104.0, E-value 1.9e-28"
misc-feature complement(35877..36074 /gene="ntrB"
)
/locus-tag="YE0026"
/inference="protein
motif:PFAM:PF00512"
/note="Pfam match to entry PF00512
HisKA, His Kinase A

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		(phosphoacceptor) domain, score 64.0, E-value 2.1e-16"
gene	complement(36607..38016 )	/gene="glnA"
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misc-feature	complement(36823..36861 )	/gene="glnA"  /locus-tag="YE0027" /inference="protein motif:Prosite:PS00182" /note="PS00182 Glutamine synthetase class-I adenylation site."
misc-feature	complement(36868..37713 )	/gene="glnA"  /locus-tag="YE0027" /inference="protein motif:PFAM:PF00120" /note="Pfam match to entry PF00120 gln-synt, Glutamine synthetase, catalytic domain, score 563.6, E-value 8.6e-167"
misc-feature	complement(37195..37242 )	/gene="glnA"  /locus-tag="YE0027" /inference="protein motif:Prosite:PS00181" /note="PS00181 Glutamine synthetase putative ATP-binding region signature."

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misc-feature    complement(37729..37977 /gene="glnA"
)
                /locus-tag="YE0027"
                /inference="protein
                motif:PFAM:PF03951"
                /note="Pfam match to entry PF03951
                gln-synt-N, Glutamine synthetase,
                beta-Grasp domain, score 169.3,
                E-value 4.1e-48"
misc-feature    complement(37813..37869 /gene="glnA"
)
                /locus-tag="YE0027"
                /inference="protein
                motif:Prosites:PS00180"
                /note="PS00180 Glutamine
                synthetase signature 1."
gene            complement(38201..38311 /locus-tag="YE0028"
)
CDS             complement(38201..38311 /locus-tag="YE0028"
)
                /inference="similar to
                sequence:INSDC:AJ414141"
                /note="Poor database matches.
                Similar to the N-terminal region
                of Yersinia pestis possible
                membrane protein YPO0025
                SWALL:Q8ZJR4 (EMBL:AJ414141) (52
                aa) fasta scores: E(): 1.8e-12,
                80.55 38d in 36 aa. Doubtful CDS"
                /codon-start=1
                /transl-table=11
                /product="hypothetical protein"
                /protein-id="CAL10173.1"
                /db-xref="GI:122087392"
                /db-xref="UniProtKB/TrEMBL:AlJHU0"
                /translation="MHTDYQQTFMWHKGVVWV
                GIDFAIDFMTQFSMNN"
gene            38529..40352
                /gene="bipA"
                /locus-tag="YE0029"
                /note="synonym: typA"
CDS             38529..40352
                /gene="bipA"
                /locus-tag="YE0029"
                /codon-start=1
                /transl-table=11
                /product="putative GTPase"
                /protein-id="CAL10174.1"
                /db-xref="GI:122087393"
                /db-xref="GOA:AlJHU1"
                /db-xref="InterPro:IPR000640"
                /db-xref="InterPro:IPR000795"
                /db-xref="InterPro:IPR004161"
                /db-xref="InterPro:IPR005225"
                /db-xref="InterPro:IPR006298"
                /db-xref="UniProtKB/TrEMBL:AlJHU1"
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                ADFGGEVERVMSVSDVLLVVDAM
                DGPMPQTRFVTKKAFANGKPIVVINKVDPRGAR
                PDWVVDQVDFDLVNLDATDEQLDF
                PIYYASALMGIAGNHDNDMAADMTPLYQAIVDHV
                SPPQVEPDAPFQMISQLDYNVYV

```

		GVIGIGRIKRGKVKPNQQVTIVDSEKTRNGKVG KVLTHMGLERIEATEAAGDIVAI TGLGELNISDTICDVNAVEALPALSVDEPTVSMY FCVNTSPFCGKEGKYVTSRQILER LNKELIHNVALRVEETEDADAFVSGRGELHLSV LIENMRREGFELAVSRPKVIVREI DGRKQEPFENVTLDIEEQHOGSVQAMGERKADL KNMDFDGKGRVRLDYILIPARGLIG FRTEFMTMTSGTGLLYSTFSHYDDVRPGEIGQRQ NGVLISNGQGKAVAFALFKLQDRG KLFIGHGTEVYEGQIIIGHSRNDLTVNCLTGKQ LTNMRASGTDEATTLVPFLKKTLE QALEFIDDDDELVEVTPQSIRIRKRLTENDRKRA GRGPKED"
misc-feature	38535..39122	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00009" /note="Pfam match to entry PF00009 GTP-EFTU, Elongation factor Tu GTP binding domain, score 258.2, E-value 7.1e-75"
misc-feature	38562..38585	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	38658..38705	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:Prosite:PS00301" /note="PS00301 GTP-binding elongation factors signature."
misc-feature	39147..39395	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF03144" /note="Pfam match to entry PF03144 GTP-EFTU-D2, Elongation factor Tu domain 2, score 71.9, E-value 8.8e-19"
misc-feature	39711..39977	/gene="bipA" /locus-tag="YE0029" /inference="protein motif:PFAM:PF00679" /note="Pfam match to entry PF00679 EFG-C, Elongation factor G C-terminus, score 112.3, E-value 6e-31"
gene	40648..41235	/locus-tag="YE0030"
CDS	40648..41235	/locus-tag="YE0030" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAL10175.1" /db-xref="GI:122087394" /db-xref="GOA:AlJHU2" /db-xref="InterPro:IPR005834" /db-xref="InterPro:IPR006402" /db-xref="UniProtKB/TrEMBL:AlJHU2"

misc-feature 40648..41208

gene 41328..42218

CDS 41328..42218

misc-feature 41409..42161

misc-feature join(41442..41510,  
41628..41687,  
41748..41816,  
41874..41933,  
41967..42035,  
42063..42131)

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QQHERGEISDEDFARQLSDEMGLSLSFQEAEGW
QAVFVALRPEVISIMQKLRAEGHR
VVVLSNTRNLHCNYWPQHYPEVAAAADHMYLSQD
LGMRKPEARIYQHVLSAENIPAEQ
AVFFDDVEANIVAARIEGITGIHVTRKVIPAYF
S"
/locus-tag="YE0030"
/inference="protein
motif:PFAM:PF00702"
/note="Pfam match to entry PF00702
Hydrolase, haloacid
dehalogenase-like hydrolase, score
61.6, E-value 1.1e-15"
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/locus-tag="YE0031"
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/codon-start=1
/transl-table=11
/product="ribonuclease BN"
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/db-xref="GI:122087395"
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/db-xref="UniProtKB/Swiss-Prot:A1J
HU3"
/translation="MASFLRFRLSASLKPYITFG
RMLYTRIDKDLTMLAGHLAYVSL
LSLVPLVTIVIFALFAFFMFADISIKLKAFIFTN
FMPATGDIQNYLEQFVANSRMT
VVGTCGLIVTALLLIYSVDSVLNIIWRSKVHRS
L
VFSFAVYWMVLTLGPILVGASMWI
SSYLLSLQWLANARVDSMIDETLRLFPLLISWVS
FWLLYSVVPTVRVPAQDALIGALV
AALFFELGKKGFTMYITLFPSYQLIYGVLAIVPI
LFLWVYWSWCIVLLGAEITVTLGE
YRAQRHQAITEKSPSQSQEI"
/gene="rbn"
/locus-tag="YE0031"
/inference="protein
motif:PFAM:PF03631"
/note="Pfam match to entry PF03631
Ribonuclease-BN, Ribonuclease
BN-like family, score 289.2,
E-value 3.5e-84"
/gene="rbn"
/locus-tag="YE0031"
/inference="protein
motif:TMHMM:2.0"
/note="6 probable transmembrane
helices predicted for YE0031 by
TMHMM2.0 at aa 39-61, 101-120,
141-163, 183-202, 214-236 and
246-268"
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gene	42225..42662	/locus-tag="YE0032"
CDS	42225..42662	/locus-tag="YE0032"
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		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAL10177.1"
		/db-xref="GI:122087396"
		/db-xref="GOA:A1JHU4"
		/db-xref="InterPro:IPR003732"
		/db-xref="UniProtKB/Swiss-Prot:A1JHU4"
		/translation="MIALIQRLASANVVVDGEVV GEIGPGLLILLGVEQQDTEQKAQR LCEKVLGYRIFGDENDKMNLVKQAGGSVLVVSQ FTLVADTQKGMRFPSFSGASPAEA DRLYQYFVAQCCEHGVKTETGLFAADMKVSLVND GPVTFWLQI"
misc-feature	42306..42659	/locus-tag="YE0032"
		/inference="protein motif:PFAM:PF02580"
		/note="Pfam match to entry PF02580 DUF154, Uncharacterized ACR, COG1490, score 261.8, E-value 6e-76"
gene	42914..43837	/locus-tag="YE0033"
CDS	42914..43837	/locus-tag="YE0033"
		/codon-start=1
		/transl-table=11
		/product="conserved membrane protein"
		/protein-id="CAL10178.1"
		/db-xref="GI:122087397"
		/db-xref="GOA:A1JHU5"
		/db-xref="InterPro:IPR000182"
		/db-xref="InterPro:IPR012660"
		/db-xref="InterPro:IPR016181"
		/db-xref="UniProtKB/TrEMBL:A1JHU5"
		/translation="MYHLRVPTTEQELKDYQFR WEMLRKPLHQPIGSEKDAYDAMAH HQMVDDEQGKPVAIGRLYINADNEAAIRFLAVDP SVRSKGLGLTVAMTLESVARQEGV KRVVCSAREDAVDFFSKLGFVSQGEITAPQITPV RHFLMIKPVVTMDDILHRPDWCGQ LQQAQYDHIPLSEKMGVIRISQYTGQRFVTMPEA GNQNPHTLFLAGSLFSLATLTGWG LIWLLLRERHLGGTIIADAHIRYSAPVTGRPRA VAELSSLSGDLDRLAGRRARVQL DVNLFGNEEAGAVFSGTYMVLVDAEGDGVN"
misc-feature	43052..43282	/locus-tag="YE0033"
		/inference="protein motif:PFAM:PF00583"
		/note="Pfam match to entry PF00583 Acetyltransf,Acetyltransferase (GNAT) family, score 63.3, E-value 3.3e-16"
misc-feature	43184..43249	/locus-tag="YE0033"
		/note="Predicted helix-turn-helix motif with score 1005.000, SD 2.61 at aa 91-112, sequence MTLESVARQEGVKRVVCSARED"
misc-feature	43517..43585	/locus-tag="YE0033"

		/inference="protein motif:TMHMM:2.0" /note="1 probable transmembrane helix predicted for YE0033 by TMHMM2.0 at aa 202-224" /note="repeat unit encoding a LuxR-family transcriptional regulator" /locus-tag="YE0035" /locus-tag="YE0035" /inference="similar to sequence:INSDC:AE004433" /inference="similar to sequence:INSDC:AE004564" /note="Similar to Pseudomonas aeruginosa probable transcriptional regulator PA1347 SWALL:Q9I3Z7 (EMBL:AE004564) (230 aa) fasta scores: E(): 3e-09, 30.43 id in 207 aa, and to the C-terminal region of Vibrio cholerae LuxR family transcriptional regulator VCA1078 SWALL:Q9KKM5 (EMBL:AE004433) (319 aa) fasta scores: E(): 2.2e-10, 27.53 38d in 207 aa" /codon-start=1 /transl-table=11 /product="LuxR family transcription regulatory protein" /protein-id="CAL10179.1" /db-xref="GI:122087398" /db-xref="GOA:AlJHU6" /db-xref="InterPro:IPR000792" /db-xref="InterPro:IPR011991" /db-xref="InterPro:IPR013656" /db-xref="UniProtKB/TrEMBL:AlJHU6" /translation="MEASLFNSLKMLIKFWECSS EPWGVKDNQSRVYANNRLHKLFA LPDKFSMEGRDTGELPTPISEFELEFQEHDCVKV LLQDRVTSVEIHAWNGHSYYQPYF FDKYPLIDEHGVSQGIISHSRPVEDVILTHLNKI KVPISLILTPPSDLFSKRENEVLF YILHSFSSMEIATKLHLSSITVDNIIQKIYKKIG ISGRQQLVDYCYENKINNYVPQSF FEYSGSFFPLV" /locus-tag="YE0035" /inference="protein motif:PFAM:PF00196" /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 41.3, E-value 1.4e-09" /locus-tag="YE0035" /note="Predicted helix-turn-helix motif with score 1060.000, SD 2.80 at aa 166-187, sequence FSSMEIATKLHLSSITVDNIIQ" /note="repeat unit encoding a LuxR-family transcriptional regulator" /locus-tag="YE0036"
repeat-region	44408..45116	
gene	44431..45117	
CDS	44431..45117	
misc-feature	44872..45069	
misc-feature	44926..44991	
repeat-region	45117..45833	
gene	45147..45833	

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CDS                45147..45833
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                    /inference="similar to
sequence:INSDC:AE004433"
                    /inference="similar to
sequence:INSDC:AE004564"
                    /note="Similar to Pseudomonas
aeruginosa probable
transcriptional regulator PA1347
SWALL:Q9I3Z7 (EMBL:AE004564) (230
aa) fasta scores: E():
2.2e-09,30.37 38d in 214 aa, and
to the C-terminal region of Vibrio
cholerae LuxR family
transcriptional regulator VCA1078
SWALL:Q9KKM5 (EMBL:AE004433) (319
aa) fasta scores: E(): 6.6e-13,
30.43 38d in 207 aa"
                    /codon-start=1
                    /transl-table=11
                    /product="LuxR family
transcription regulatory protein"
                    /protein-id="CAL10180.1"
                    /db-xref="GI:122087399"
                    /db-xref="GOA:AJJHU7"
                    /db-xref="InterPro:IPR000792"
                    /db-xref="InterPro:IPR011991"
                    /db-xref="UniProtKB/TrEMBL:AJJHU7"
                    /translation="MDKPLKNQLEILIRFWERSS
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LSDKYNLEGRLDSELPSPATAAFQMEFQAHDRKVE
LSQERITSVEIHEWDGLSYLKPNF
CDKYLPLIDESGVSGQIIFHVRPVEDIILSRLTKI
KAPTSLTFTPPSKLFTKREWEVLF
YILHSYSSKDIKKLHISPRVTSNITQSVYRKVG
VSNKRQIVDYCYENKINNVVPQSF
FEYSGSFPLM"
misc-feature       45588..45785
                    /locus-tag="YE0036"
                    /inference="protein
motif:PFAM:PF00196"
                    /note="Pfam match to entry PF00196
GerE, Bacterial regulatory
proteins, luxR family, score 49.3,
E-value 5.5e-12"
misc-feature       45642..45707
<-----User Break----->
                    )
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                    /note="synonym: kdtB"
CDS                complement(75792..76271)
                    /gene="coaD"
                    )
                    /locus-tag="YE0067"
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                    /transl-table=11
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adenylyltransferase"
                    /protein-id="CAL10209.1"
                    /db-xref="GI:122087428"
                    /db-xref="GOA:AJJHR9"
                    /db-xref="InterPro:IPR001980"
                    /db-xref="InterPro:IPR004820"
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		/db-xref="UniProtKB/Swiss-Prot:AlJHR9"
		/translation="MITKAIYPGTFDPITNGHLDLVTRASEMFSHVILAIADSSSKKPMFTLAERFVILAKQVTAPLKNVEVLGFSELMAEFAKKHNANILVRGLRSVDFEYEWQLAMNMRHLMPEKLESVFLMPSEKWSFISSSLVKEVARHGGDITPFLPAPVIKALMTKLA"
misc-feature	complement(75870..76268)	/gene="coad"
		/locus-tag="YE0067"
		/inference="protein"
		motif:PFAM:PF01467"
		/note="Pfam match to entry PF01467 CTP-transf-2, Cytidyltransferase, score 151.3, E-value 1.1e-42"
gene	complement(76268..77050)	/gene="kdtX"
		/locus-tag="YE0068"
		/note="synonym: waaE"
CDS	complement(76268..77050)	/gene="kdtX"
		/locus-tag="YE0068"
		/codon-start=1
		/transl-table=11
		/product="lipopolysaccharide core biosynthesis glycosyl transferase"
		/protein-id="CAL10210.1"
		/db-xref="GI:122087429"
		/db-xref="GOA:AlJHS0"
		/db-xref="InterPro:IPR001173"
		/db-xref="UniProtKB/TrEMBL:AlJHS0"
		/translation="MSAKRLRSVVMIVKNEASLLADCLASVTWADEIVVLDSGSEDETVALAEQYGAKVYSNTEWPGYGKQRQLAQYATGDYILMLDADERVTPELKSAIETVLLAPEEGAVYSCARRNLFGRFMRHSGWYPDRVTRLYPREQYRYNDDLHVHESLDSGSAAVILLAGDLLHLTCRDFFAFQRKQLNYAQAWANQRHQGKSCRYFAIISHTLGAFCKTWLIRAGFLDGGKQGLLLAVVNAQYTFNKYAALWALSHQYQKSENS"
sig-peptide	complement(76961..77050)	/gene="kdtX"
		/locus-tag="YE0068"
		/note="Signal peptide predicted for YE0068 by SignalP 2.0 HMM (Signal peptide probability 0.844) with cleavage site probability 0.843 between residues 30 and 31"
misc-feature	complement(76565..77029)	/gene="kdtX"
		/locus-tag="YE0068"
		/inference="protein"
		motif:PFAM:PF00535"
		/note="Pfam match to entry PF00535 Glycos-transf-2, Glycosyl transferase, score 88.5, E-value 8.8e-24"
gene	complement(77051..78328)	/gene="kdtA"
		/locus-tag="YE0069"

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CDS      complement(77051..78328)
)
/note="synonym: waaA"
/gene="kdtA"

/locus-tag="YE0069"
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/product="3-deoxy-D-manno-octuloso
nic-acid transferase"
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/db-xref="UniProtKB/TrEMBL:AlJHX3"
/translation="MLLRLYQVLLYLIQPLIWLRL
LLRSRKAPAYRKRWGERYGFCAG
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HVYLPYDLPGSVNRFLDQVNPFLVIIMETELWPN
LINALHRRKIPLVIANARLSARSA
AGYKKIGSFIRNMLQRITLIAAQNQEDGDRFIEL
GLRRSOLTVTGSKLKFDISVTELA
ARAVTLRRQWAPHRFVWIATSTHDGEETILLEAH
RQLLQQFPTLLLLVPRHPERFFK
AIELTQKAGLSYTLRSKGEVPPSSQTQVIGDTMG
ELMLLYGIADLAFVGGSLVERGGH
NPLEAAAAHAIPVLMGPHTFNFKDICKALEQAEG
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/misc-feature complement(77126..77638)
)
/gene="kdtA"

/locus-tag="YE0069"
/inference="protein
motif:PFAM:PF00534"
/note="Pfam match to entry PF00534
Glycos-transf-1,Glycosyl
transferases group 1, score 20.0,
E-value 1.6e-06"
/gene="rfaC"
/gene complement(78869..79834)
)
/locus-tag="YE0070"
/note="synonyms: rfa-2, waaC"
/gene="rfaC"

CDS      complement(78869..79834)
)
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with cleavage site probability
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<-----User Break----->

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L13 ANSWER 5 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM236080 GenBank (R)  
 GenBank ACC. NO. (GBN): AM236080  
 GenBank VERSION (VER): AM236080.1 GI:115254414  
 CAS REGISTRY NO. (RN): 906734-09-6  
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 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 14 Nov 2006  
 DEFINITION (DEF): Rhizobium leguminosarum bv. viciae chromosome complete  
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 KEYWORDS (ST): complete genome  
 SOURCE: Rhizobium leguminosarum bv. viciae 3841  
 ORGANISM (ORGN): Rhizobium leguminosarum bv. viciae 3841  
 Bacteria; Proteobacteria; Alphaproteobacteria;  
 Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium  
 group; Rhizobium  
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 REFERENCE:  
 AUTHOR (AU): Young,J.W.; Crossman,L.C.; Johnston,A.W.B.;  
 Thomson,N.R.; Ghazoui,Z.F.; Hull,K.H.; Wexler,M.;  
 Curson,A.R.J.; Todd,J.D.; Poole,F.S.; Mauchline,T.H.;  
 East,A.K.; Quail,M.A.; Churcher,C.; Arrowsmith,C.;  
 Cherevach,A.; Chillingworth,T.; Clarke,K.; Cronin,A.;  
 Davis,P.; Fraser,A.; Hance,Z.; Hauser,H.; Jagels,K.;  
 Moule,S.; Mungall,K.; Norbertczak,H.; Rabinowitsch,E.;  
 Sanders,M.; Simmonds,M.; Whitehead,S.; Parkhill,J.  
 TITLE (TI): The genome of Rhizobium leguminosarum has recognizable  
 core and accessory components  
 JOURNAL (SO): Genome Biol., 7, R4-R4 (2006)  
 OTHER SOURCE (OS): CA 145:307927  
 REFERENCE: 2 (bases 1 to 5057142)  
 AUTHOR (AU): Crossman,L.C.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (21-FEB-2006) Crossman L.C., Pathogen  
 Sequencing Unit, The Wellcome Trust Sanger Institute,  
 Hinxton, Cambridge, Cambridgeshire, CB10 1SA, UNITED  
 KINGDOM

FEATURES (FEAT):

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(EMBL:SME591782); Rhizobium
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gene 2778..3389  
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Escherichia coli; DNA polymerase
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243 aa; 244 aa overlap; query
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similarity:fasta; SWALL:Q92TE8
(EMBL:AL591782); Rhizobium
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iii, epsilon chain protein; length
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/inference="protein

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		motif:Pfam:PF00929.11" /note="Pfam match to entry PF00929.11 Exonuc-X-T"
gene	complement(4172..4654)	/gene="secB" /locus-tag="RL0006"
CDS	complement(4172..4654)	/gene="secB" /locus-tag="RL0006" /inference="similar to sequence:INSDC:AE008975" /inference="similar to sequence:UniProtKB:P15040" /note="similarity:fasta; SWALL:SECB-ECOLI (SWALL:P15040); Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, and Shigella flexneri; protein-export protein SecB; secB; length 155 aa; 151 aa overlap; query 1-151 aa; subject 1-145 aa similarity:fasta; SWALL:Q8UJC2 (EMBL:AE008975); Agrobacterium tumefaciens; protein-export protein; secB; length 160 aa; 160 aa overlap; query 1-160 aa; subject 1-160 aa" /codon-start=1 /transl-table=11 /product="putative SecB protein export protein" /protein-id="CAK05494.1" /db-xref="GI:115254420" /db-xref="GOA:Q1MNF1" /db-xref="UniProtKB/TrEMBL:Q1MNF1" /translation="MADDNNSNGAANPTLSILAQ YTKDLSFENPGAPRSLQARDKAPT ININNVNANPLSDTDFDVVLSLNAEAKDGDKTV FHAELTYGGVFRVAGFPQEHMLPV LFIECPRMILFFPARQIIADVTRNGGFPPLMIDPI DFTQMFQQRVAEEQARAKVQAVPN
misc-feature	complement(4202..4654)	/gene="secB" /locus-tag="RL0006" /inference="protein motif:Pfam:PF02556.4" /note="Pfam match to entry PF02556.4 SecB"
gene	complement(4756..5271)	/locus-tag="RL0007"
CDS	complement(4756..5271)	/locus-tag="RL0007" /inference="similar to sequence:INSDC:AE007943" /inference="similar to sequence:INSDC:ECUW93" /note="similarity:fasta; with=UniProt:FXSA-ECOLI (EMBL:ECUW93); Escherichia coli.; fxsA; FxsA protein (Suppressor of F exclusion of phage T7).; length=158; id 36.364; 132 aa overlap; query 4-132; subject 1-129 similarity:fasta; with=UniProt:Q8UJC1 (EMBL:AE007943); Agrobacterium tumefaciens (strain C58/ATCC 33970).; fxsA; Hypothetical

		protein fxsA (AGR-C-11p).; length=178; id 48.521; 169 aa overlap; query 4-167; subject 1-169" /codon-start=1 /transl-table=11 /product="putative transmembrane FxsA-family protein" /protein-id="CAK05495.1" /db-xref="GI:115254421" /db-xref="GOA:Q1MNF0" /db-xref="UniProtKB/TrEMBL:Q1MNF0" /translation="MTDMRFSILPAFILLLPFAE IAGFVVVGQAIGLWLTLLVLMVGLF VLGVVLLRRQGIGILRRMSSEGRNGVMPGRDLLR PAMNVIASLLLIIPGFLTDIIAIL ILIPPVRDLVWRAIAKRFVVVNAKGGSSSGPQPD FRDRKFPNSKVVDLEEDYHREPD NSPWSGRHLGD"
misc-feature	complement(4879..5244)	/locus-tag="RL0007" /inference="protein motif:Pfam:PF04186.2" /note="Pfam match to entry PF04186.2 FxsA"
misc-feature	complement(join(4957..5025,5116..5184,5194..5253))	/locus-tag="RL0007"  /inference="protein motif:TMHMM:2.0" /note="3 probable transmembrane helices predicted at aa 7-26, 30-52 and 83-105"
gene	5394..6098	/locus-tag="RL0008"
CDS	5394..6098	/locus-tag="RL0008" /inference="similar to sequence:INSDC:AL591782" /note="similarity:fasta; SWALL:Q92TE6 (EMBL:AL591782); Rhizobium meliloti; putative translocase transmembrane protein; length 233 aa; 234 aa overlap; query 1-233 aa; subject 1-233 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAK05496.1" /db-xref="GI:115254422" /db-xref="GOA:Q1MNE9" /db-xref="UniProtKB/TrEMBL:Q1MNE9" /translation="MSSNDITLFFLVAAVLIFF QLRSVLGRRTGNEKPPRDLYTPRD AAPAEAAADAGKVVTLPRRDATTEDEDRFAAIDAF AAPGTPLNESLRALNKADPAFSFK EFLNGARMAYEMIVMAYADGDRKTLKNLLSREVI DGFDAIIGEREARGEKVKSTFVGI DKAEITHAETKGSEAQITVRIASQLISATYDKAD VLIEGDAENVAEVNDVWTFARDTR SRDPNWKLVATESEHE" /locus-tag="RL0008" /inference="protein motif:Pfam:PF04280.4"
misc-feature	5646..6086	

		/note="Pfam match to entry PF04280.4 Tim44" /gene="mItA" /locus-tag="RL0009" /gene="mItA" /locus-tag="RL0009" /inference="similar to sequence:INSDC:AL591782" /inference="similar to sequence:UniProtKB:P46885" /note="similarity:fasta; SWALL:MLTA-ECOLI (SWALL:P46885); Escherichia coli, and Escherichia coli O157:H7; membrane-bound lytic murein transglycosylase a precursor; mItA; length 365 aa; 282 aa overlap; query 92-369 aa; subject 112-360 aa similarity:fasta; SWALL:Q92TE5 (EMBL:AL591782); Rhizobium meliloti; putative lytic murein transglycosylase a protein; length 372 aa; 365 aa overlap; query 8-371 aa; subject 3-365 aa" /codon-start=1 /transl-table=11 /product="putative membrane-bound lytic murein transglycosylase a precursor" /protein-id="CAK05497.1" /db-xref="GI:115254423" /db-xref="GOA:Q1MNE8" /db-xref="UniProtKB/TrEMBL:Q1MNE8" /translation="MSDHASDFVLQAI SFDTL EG WKDDDP SGLFEVMRSCRRQITDVK FYRTGSLGLSSEDL LPLAAAE DFTPSSPASARA FFETHCRPFLIRRDGNSGFVTAF YEPDIDVSRPDEIFRFFFYRRPDDLIDLDDANR PAGLDKAYAFGRLEHGHVTA YPDR RAIDQGFLEGRGLEIAWAKSKVDVFFVHVQGAAR LRYQDGRIGRITYAAKAGHAFSAI GKLLIERGEIDRAEISMQAIRAWLARNPERVDEV LWNHRSYIFFRDAPVADPQAGPIA AAKVPLLAGRS LAVDRITHTFGFFFI RAESLTH LDQGRPFRRMLALD TGSAIVGFA RGDIFTGSGDIAGESAGTVRNQADFVILIPNAAA GRFD" /gene="mItA" /locus-tag="RL0009" /inference="protein motif:Pfam:PF03562.4" /note="Pfam match to entry PF03562.4 MItA" /gene="mItA" /locus-tag="RL0009" /inference="protein motif:Pfam:PF06725.1" /note="Pfam match to entry PF06725.1 3D" /locus-tag="RL0010" /locus-tag="RL0010" /inference="similar to
gene	6091..7209	
CDS	6091..7209	
misc-feature	6310..6936	
misc-feature	6946..7179	
gene	7209..7775	
CDS	7209..7775	

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/note="similarity:fasta;
with=UniProt:Q92KV6
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02784.; length=188; id 62.766;
188 aa overlap; query 1-185;
subject 1-185"
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protein"
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AAEREQEKRTPATPTPLQPTAPSMAPKSAGVHHP
LEKPVKKRIAKGRLALEARIDLHG
LVQSEAHITILLDFLIRAHERSMRHVLVITGKGS
MGSDGALKRAVPLWFSKPEFRLI
SSYESAAQHHGGEGALYIRLSRRHGERP"
misc-feature 7500..7751
/locus-tag="RL0010"
/inference="protein
motif:Pfam:PF01713.8"
/note="Pfam match to entry
PF01713.8 Smr"
gene 7772..8149
CDS 7772..8149
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/locus-tag="RL0011"
/inference="similar to
sequence:INSDC:AE008975"
/note="similarity:fasta;
SWALL:Q8UJB7 (EMBL:AE008975);
Agrobacterium tumefaciens;
transcriptional regulator; length
121 aa; 121 aa overlap; query
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regulator"
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/db-xref="UniProtKB/TrEMBL:Q1MNE6"
/translation="MTPFGAEAVRRLRARKGVSQK
EMAEALNVSPAYLSALEHGKRLP
TFDLLQRIAGYFNIIWDEAEELFLLARSSDPV
IDTSGLPPEYTEFANRLARRIRNL
DSAEIGRLSALLENGKGDGKAS"
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motif:Pfam:PF01381.9"
/note="Pfam match to entry
PF01381.9 HTH-3"
gene 8285..10720
CDS 8285..10720
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sequence:INSDC:AE007943"

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/note="similarity:fasta;
with=UniProt:GYRB-ECOLI
(EMBL:CEK132C8R); Shigella
flexneri.; gyrB; DNA gyrase
subunit B (EC 5.99.1.3).;
length=EC 5.99.1 ( 803; id 58.612;
807 aa overlap; query 12-811;
subject 1-803 similarity:fasta;
with=UniProt:Q8UJB6
(EMBL:AE007943); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; gyrB; DNA gyrase subunit
B (AGR-C-19p).; length=AGR-C-19p;
id 86.190; 811 aa overlap; query
1-811; subject 6-816"
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subunit B"
/protein-id="CAK05500.1"
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/db-xref="UniProtKB/TrEMBL:Q1MNE5"
/translation="MSDISATENGVSLEYGADSI
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GLHHMVYEVVDNAIDEALAGHADIVTVTLNPDGS
VTVTDNNGRGIPDTIHTGEGVSAAE
VIMTQLHAGGKFDQNSYKVSGLHGVSVVNAL
SVWLKLRIRRHDKIHEMSFTHGVA
DAPLKVTGDAPNETGTEVSFMPSTDTFTMTTEFDY
GTLEHRLRELAFNLNSGVRILLTDK
RHSDIKQEELRYDGGLEAFVAYLDRAKKSIVDKP
VAIHGEKDGITVEVAMWVNDSEYHE
NVLCFTNNIPQRDGGTHMAGFRAALTRQVVSAD
SSGITKREKVTILQGEDCREGLTAV
LSVKVPDPKFSSQTKDKLVSSSEVRPVVESLVNEA
LNTWFEHPSEAKILVGKVVEAAA
AREAARKARELTRRKALDIASLPGLADCSERD
PTKSEVFLVEGDSAGGSAKQGRSR
ENQAILPLRGKILNVERARFDMKMLSSQEIIGTLIT
ALGTGIGKDEFNVEKLYRHKIIM
TDADV DGAHIRTLLLTFFFRQMPQLIERGHLIYA
QPPLYKVSRGKSVQYLKDEKALEE
YLISQGLEDA SLRLGSGEV RAGQDLREVILDALR
MRALLDNLHSR YNRSAVEQA AIAG
ALNAELASDPARALALANEVAGRLDIAEETERG
WRGDVTTDGGRLRLRMVRGVREL V
VLDMALIGSSDARHIDQLTARLKEIYQTPPSLHR
REGDIEISGPRALLDAIFASGRKG
LTMQRYKGLGEMNAEQ LWETTLPNVRSLLQVRV
NDATDADGLFARLMGDEVEPRREF
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/locus-tag="RL0012"
/inference="protein
motif:Pfam:PF02518.9"
/note="Pfam match to entry
PF02518.9 HATPase-c"
/gene="gyrB"
/locus-tag="RL0012"

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misc-feature 8405..8839

misc-feature 8981..9493



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misc-feature	9662..9910	
misc-feature	10487..10684	
gene	complement(10828..11427	/locus-tag="RL0013"
CDS	) complement(10828..11427 )	/locus-tag="RL0013"
		/inference="similar to sequence:INSDC:AE007944" /note="similarity:fasta; with=UniProt:Q8UJB5 (EMBL:AE007944); Agrobacterium tumefaciens (strain C58/ATCC 33970).; NAD(P)H-flavin oxidoreductase (AGR-C-21p).; length=P; id 60.204; 196 aa overlap; query 1-196; subject 1-195" /codon-start=1 /transl-table=11 /product="putative oxidoreductase" /protein-id="CAK05501.1" /db-xref="GI:115254427" /db-xref="GOA:Q1MNE4" /db-xref="UniProtKB/TrEMBL:Q1MNE4" /translation="MTKSNHRESDYPIIDPFELDR WSPRAFTGEIIIEEAQLLLDLAAH WAPSSANHQPWFRIYGLKGSEHWEIFVALLNDSN QEWARNASALIFVVSRAFTGAAGS TEEKPSYTHSFDAAGWGHIAIQARLSGLYAHGM GGIKHEEIRQAFAIPEGYRVEAGV AIGRLADKSVLSERNQAREFPQQRKPLSEVAFNG RFVAN"
misc-feature	complement(10936..11379	/locus-tag="RL0013"
	)	
		/inference="protein motif:Pfam:PF00881.10" /note="Pfam match to entry PF00881.10 Nitroreductase"
gene	complement(11473..11769	/locus-tag="RL0014"
	)	
CDS	complement(11473..11769 )	/locus-tag="RL0014"
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5-96 aa; subject 1-92 aa"
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protein"
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/db-xref="UniProtKB/TrEMBL:Q1MNE3"
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IDDLHKRF AFREELDIVVTN"
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with=UniProt:P74752 (EMBL:SSD917);
Synecocystis sp. (strain PCC
6803).; Slr0605 protein.;
length=319; id 56.013; 316 aa
overlap; query 1-315; subject
1-314"
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glutathione-S-transferase"
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/db-xref="UniProtKB/TrEMBL:Q1MNE2"
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EKGGFVRQTSSFRNVPTDGSAGP
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GLEDIISVSVEFLLGKQGNRFEGD
YPGATEDHVNVTYMHETIYTRAAPDFTGRATVPI
LWDKQKTTIVNNESADILRMLNSG
FGGLAKNPIDLVPVRCETIEAFNDRIPDLNNG
VYRAGFATTQIAYEEAFADVFACL
DWVEQQQFEGRTFLFADHPTESDIRLFVTLVRFVDV
AYHGIFKCNLRLRLSDYANLRAFCR
RMLDWP GIGETVNLDHKRGYYISLNPTKIIP
SGPDLAEIFRA"
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sequence:INSDC:AE007944"
/inference="similar to
sequence:INSDC:AF169302"
/note="similarity:fasta;
with=UniProt:Q8VUC7
(EMBL:AF169302); Burkholderia
cepacia (Pseudomonas cepacia).;
DntG.; length=281; id 38.267; 277
aa overlap; query 5-279; subject
13-279 similarity:fasta;
with=UniProt:Q8UJB4

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gene	11922..12887
CDS	11922..12887
misc-feature	12531..12767
gene	13031..13873
CDS	13031..13873

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(EMBL:AE007944); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hpcE;
2-hydroxyhepta-2,4-diene-1,7-dioat
e isomerase (AGR-C-22p).;
length=280; id 87.097; 279 aa
overlap; query 1-279; subject
1-279"
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VTEAEALDYVAGYCVSNDVSEAF
QTERSGQWTKGKSCDTFGPIGPWLVTKDEIPEPQ
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motif:Pfam:PF01557.8"
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with=UniProt:Q71KW6
(EMBL:AF474374); Azospirillum
brasiliense.; phaZ; PHB
depolymerase.; length=603; id
57.471; 348 aa overlap; query
61-406; subject 257-602
similarity:fasta;
with=UniProt:Q92TD3
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; Hypothetical protein
SMc02770.; length=424; id 76.000;
425 aa overlap; query 1-424;
subject 1-423 Codons 60 to the
C-terminus are similar to codons
255 to the C-terminus of
Azospirillum brasiliense PHB
depolymerase phaZ UniProt:Q92TD3
(EMBL:SME591782) (603 aa), and
entire protein is similar to
Rhizobium meliloti (Sinorhizobium
meliloti) Hypothetical protein
SMc02770 UniProt:Q92TD3
(EMBL:SME591782) (424 aa)"

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misc-feature	13286..13783
gene	14079..15356
CDS	14079..15356

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misc-feature	14694..15299	
gene	15502..15936	
CDS	15502..15936	
		/codon-start=1 /transl-table=11 /product="putative PHB depolymerase" /protein-id="CAK05505.1" /db-xref="GI:115254431" /db-xref="UniProtKB/TrEMBL:Q1MNE0" /translation="MFYQLYELNHAAMAFRAAA DIMRFAYANPLNPFSSHTPFGRITMA ASLEMFERTTTRYGKPEFGLKQTTIGDKTVSVRE EVVWSRPFENLLHFARNAPAAARGN DPRILIVAPMSGHYATLLRGTVALLPSADIYIT DWIDARMVPMTEGTFDFDDYIDYV IEMLHFLGHDTHVAVACQPSVPVLA AAAVMEEAR DPLSPASMTLMGGPIDTRINPTAV NKLAQERSLQWFSNDVIMNVFPWQPGFVRPVYPG FLQLSGFMSMNLDRLHVAHKEFFM HLVKNDGEPEHRHDFYDEYLAVMDLTAEFYLQTV EEVFIKHS LPKGELMHRGKRVDP AIRNVALLTVEGENDDISGVGTMAAQITCVNIP EDMRMHYLQPDVGHYGVFNGSRFR REIAPRIIDFVRQHSRS AVKFPQIPRVIKGGRTG" /locus-tag="RL0017" /inference="protein motif;Pfam:PF06850.1" /note="Pfam match to entry PF06850.1 PHB-depo-C" /locus-tag="RL0018" /locus-tag="RL0018" /inference="similar to sequence:INSDC:AL591782" /note="similarity:fasta; SWALL:Q92TD2 (EMBL:AL591782); Rhizobium meliloti; conserved hypothetical transmembrane protein; length 141 aa; 143 aa overlap; query 1-143 aa; subject 1-140 aa" /codon-start=1 /transl-table=11 /product="putative transmembrane protein" /protein-id="CAK05506.1" /db-xref="GI:115254432" /db-xref="GOA:Q1MND9" /db-xref="UniProtKB/TrEMBL:Q1MND9" /translation="MNQSALLRPDWT PATIALMI LGFMVFWPLGLAMLAYIIFGDRLR GFKRDVNEATDGFASCRPHGRHRPHFSTGNVA FDDWRKAELDRMEERKRLDEMRE EFDYSYLRRLRAKDQEEFDRFMRDRRAKRRDNG PVAEYQTP" /locus-tag="RL0018" /inference="protein motif;TMHMM:2.0" /note="1 probable transmembrane helix predicted at aa 15-37" /locus-tag="RL0019" /locus-tag="RL0019" /inference="similar to sequence:INSDC:HS360250" /note="similarity:fasta;
misc-feature	15544..15612	
gene	16044..16802	
CDS	16044..16802	

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(EMBL:HS360250); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; Hypothetical protein
Atu0016 (AGR-C-25p).; length=AGR-C
( 255; id 68.482; 257 aa overlap;
query 1-252; subject 1-255"
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protein"
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/db-xref="GI:115254433"
/db-xref="UniProtKB/TrEMBL:Q1MND8"
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TKLAKFSTDTGLRDGGEILLRGVS
HRIQHSGSLRGLTEAVSIDGRPVLRVSGMPEHVG
RRIAAFLKKEARADLARLATMHAA
TIRAPIRSISMKDTRSRWGSCSEGNLSFSWRIV
MAPPSVIDYLAAEVAHLKEMNHG
PHFWALCRKLCPGMEEAQSWLKRHGSQHLHAIDFD
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/locus-tag="RL0019"
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motif:Pfam:PF01863.6"
/note="Pfam match to entry
PF01863.6 DUF45"
/gene 16969..17637
CDS 16969..17637
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/locus-tag="RL0020"
/inference="similar to
sequence:UniProtKB:Q8UJB1"
/inference="similar to
sequence:UniProtKB:Q9X4E3"
/note="similarity:fasta;
SWALL:TRPF-RHOSH (SWALL:Q9X4E3);
Rhodobacter sphaeroides;
n-(5'-phosphoribosyl)anthranilate;
trpF; length 212 aa; 206 aa
overlap; query 5-209 aa; subject
6-210 aa similarity:fasta;
SWALL:TRPF-AGRT5 (SWALL:Q8UJB1);
Agrobacterium tumefaciens;
n-(5'-phosphoribosyl)anthranilate;
trpF; length 220 aa; 210 aa
overlap; query 1-210 aa; subject
1-210 aa"
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N-(5'-phosphoribosyl)anthranilate"
/protein-id="CAK05508.1"
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/db-xref="UniProtKB/TrEMBL:Q1MND7"
/translation="MRPDIKICGLKTPEAVDRAL
KRGATHIGIFFEKSPRIEPLA
AKLAEPARGKAKIVAVVDPDNDDELDEIVSLLKP
DMLQLHGNESPEHVLTIKALYGLP
VMKVFSVRTADDLKRVEAYIGIADRFLLDAPKAPK
GSELPGGNGISFDWLLSWLDGVS

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misc-feature	16981..17595	DYMLSGGLNKDNVAEALFVTKAPGIDVSSSGVETA PGVKSVAKIDEFFDAVEKANAPMM ASGS" /locus-tag="RL0020" /inference="protein motif:Pfam:PF00697.10" /note="Pfam match to entry PF00697.10 PRAI"
gene	17640..18860	/gene="trpB" /locus-tag="RL0021" /gene="trpB" /locus-tag="RL0021" /EC-number="4.2.1.20" /inference="similar to sequence:UniProtKB:P56929" /inference="similar to sequence:UniProtKB:Q9X4E5" /note="similarity:fasta; SWALL:TRPB-RHOSH (SWALL:Q9X4E5); Rhodobacter sphaeroides; tryptophan synthase beta chain; trpB; length 409 aa; 401 aa overlap; query 8-406 aa; subject 7-407 aa similarity:fasta; SWALL:TRPB-RHIET (SWALL:P56929); Rhizobium etli; tryptophan synthase beta chain; trpB; length 406 aa; 406 aa overlap; query 1-406 aa; subject 1-406 aa" /codon-start=1 /transl-table=11 /product="putative tryptophan synthase beta chain" /protein-id="CAK05509.1" /db-xref="GI:115254435" /db-xref="GOA:Q1MND6" /db-xref="UniProtKB/TrEMBL:Q1MND6" /translation="MNETPKPNSFRSGPDEDGRF GIYGGRFVAETLMLPLILDLDQDEWN RAKNDPAFQAEKHLGAHYIGRPSPLYFAERLTA ELGGAKIYFKREELNHTGSHKINN CIGQILLAKRMGKTIRIAETGAGQHGVASATVAA RFGLPCVVYMGATDVERQAPNVFR MKLLGAEVKPVTAGSGTLKDAMNEALRDWVTNVE DTYYLIGTAAGHPYPPEMVRDFQS VIGIEAKEQMLAAEGRPLDLVIAAVGGGSNAIGI FHPFLDDPSVKIVGVEAGGKGLQG DEHCASITAGSPGVLHGNRTYLLQDSQDQIKEGH SISAGLDYPGIGPEHSWLDNTRGV DYVPIMDHEALEAFQTLTRLEGIIPALEPSHAIA EVIKRAPTMGKDEIILMNLSSGRGD KDIFTVGKILGMGL"
misc-feature	17820..18809	/gene="trpB" /locus-tag="RL0021" /inference="protein motif:Pfam:PF00291.10" /note="Pfam match to entry PF00291.10 PALP"
gene	18864..19703	/gene="trpA" /locus-tag="RL0022" /gene="trpA" /locus-tag="RL0022" /inference="similar to
CDS	18864..19703	

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sequence:INSDC:AE007944"
/inference="similar to
sequence:INSDC:AF107094"
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with=UniProt:TRPA-RHOSH
(EMBL:AF107094); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; trpA; Tryptophan
synthase alpha chain (EC
4.2.1.20).; length=263; id 62.214;
262 aa overlap; query 4-265;
subject 3-259 similarity:fasta;
with=UniProt:TRPA-AGRT5
(EMBL:AE007944); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; trpA; Tryptophan synthase
alpha chain (EC 4.2.1.20).;
length=279; id 84.229; 279 aa
overlap; query 1-279; subject
1-279; putative tryptophan
synthase, alpha subunit"
/codon-start=1
/transl-table=11
/product="Tryptophan synthase
alpha chain."
/protein-id="CAK05510.1"
/db-xref="GI:115254436"
/db-xref="GOA:Q1MND5"
/db-xref="UniProtKB/TrEMBL:Q1MND5"
/translation="MTARMDKRFALKAEGRPAL
VTYFMGGDPDYDTSLGIMKALPEA
GSDIIELGMPFSDPMADGPAIQLAGQRALKGGQT
LKKTLQLAADFRKTNDAATPIVMMG
YNNPIYIYGVEKFLDDALLAGIDGLIVVDLPPEM
DDELCPAIRKGINFIRLATPTTD
EKRLPKVLKNTSGFVYIVSMNGITGSALPDPFSLV
SGAVERIKQHTKLPVCVGFVGVKTA
EHAKVIGGSADGVVGTAVNQVATSLTHDGKAT
ADTVQAVATLVRLSTGTRSARLV AAE"

misc-feature      18888..19676
/gene="trpA"
/locus-tag="RL0022"
/inference="protein
motif;Pfam:PF00290.9"
/note="Pfam match to entry
PF00290.9 Trp-syntA"

gene              19845..20750
CDS               19845..20750
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sequence:INSDC:HS028244"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:ACCD-ECOLI
(EMBL:HS028244); Escherichia coli
O157:H7.; accD; Acetyl-coenzyme A
carboxylase carboxyl transferase
subunit beta (EC 6.4.1.2) (ACCase
beta chain).; length=304; id
46.831; 284 aa overlap; query
1-283; subject 1-281
similarity:fasta;
with=UniProt:Q92TC7

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```

(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PROBABLE
ACETYL-COENZYME A CARBOXYLASE
CARBOXYL TRANSFERASE SUBUNIT BETA
PROTEIN (EC 6.4.1.2).; length=304;
id 85.526; 304 aa overlap; query
1-301; subject 1-304; putative
acetyl-coenzyme A carboxylase
carboxyl transferase subunit"
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/transl-table=11
/product="Acetyl-coenzyme A
carboxylase carboxyl transferase
subunit beta (ACCase beta chain).
/protein-id="CAK05511.1"
/db-xref="GI:11525443/"
/db-xref="GOA:Q1MND4"
/db-xref="UniProtKB/TREMBL:Q1MND4"
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KVAQDPLKFRDSKKYSRLRDRSL
KTEQEDTILAGVGKVGQKLKLVAVVHEFNFIGGSL
GMAAGEAIVKAFAERATAEKCPLVM
FPASGGARMQEGILSLMQLPRTTVAVDMLKESGQ
FYIVVLNTPTTGGVTASYAMLGDI
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LLEHGMVDMVVKRHDIPETLARLL
KILTKKPVSAANDMNGGAILAASA"
/locus-tag="RL0023"
/inference="protein
motif:Pfam:PF01039.9"
/note="Pfam match to entry
PF01039.9 Carboxyl-trans"
/gene="folC"
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/gene="folC"
/locus-tag="RL0024"
/inference="similar to
sequence:INSDC:ECD862"
/inference="similar to
sequence:INSDC:SME591782"
/note="similarity:fasta;
with=UniProt:FOLC-ECOLI
(EMBL:ECD862); Escherichia coli.;
folC; FolC bifunctional protein
[Includes: Folylpolyglutamate
synthase (EC 6.3.2.17)
(Folylpoly-gamma-glutamate
synthetase) (FPGS); Dihydrofolate
synthase (EC 6.3.2.12)].;
length=422; id 31.757; 444 aa
overlap; query 1-442; subject
2-411 similarity:fasta;
with=UniProt:Q92TC6
(EMBL:SME591782); Rhizobium
meliloti (Sinorhizobium
meliloti).; PROBABLE FOLC
BIFUNCTIONAL PROTEIN INCLUDES:
FOLYLPOLYGLUTAMATE SYNTHASE AND
DIHYDROFOLATE SYNTHASE (EC

```

misc-feature	20172..20372
gene	20778..22130
CDS	20778..22130



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6.3.2.17) (EC 6.3.2.12).;
length=447; id 75.901; 444 aa
overlap; query 7-450; subject
4-447"
/codon-start=1
/transl-table=11
/product="putative FolC
bifunctional protein [Includes:
Folylpolyglutamate synthase (EC
6.3.2.17)
(Folylpoly-gamma-glutamate
synthetase) (FPGS); Dihydrofolate
synthase]."
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misc-feature 20877..21641

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/db-xref="UniProtKB/TrEMBL:Q1MND3"
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HVHTSPHLVNWHERYRIGVKGGRG
QLVDDAVFAEAVRRVADANAGQHITVFEILTAVT
FILFSEHPADAAIIEVGLGGRFDA
TNVISDPAVSVIMPISLDHQPYLGDRLVIAAEK
AGIMKPGFPVVIGHQEYDAALDVL
MSTAERLHCPSAVFGQDFMAHEEYGRLVYQDEFG
LADLPLRLPGRHQYANAAAAIRA
VKAAGFTVTETMMEKAMSSVEWFGRLQRLSEGL
LSHAPAGAEIWDGGHNPAGAGEVI
AEAMANFEERQSRPLFLIIGMINTKDPVGYFKAF
AGLVEKVFCVPVIRGSEAMIDPVIL
SNAAYDAGLVAEPMSTVGDALAEAKAVADPEALP
PRILVGGSYLVGDVLDNGTTPPK
/gene="folC"
/locus-tag="RL0024"
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motif:Pfam:PF01225.11"
/note="Pfam match to entry
PF01225.11 Mur-ligase"
gene complement(22203..22523
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CDS complement(22203..22523
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/locus-tag="RL0025"
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sequence:INSDC:A35135"
/inference="similar to
sequence:INSDC:AE008976"
/note="similarity:fasta;
with=UniProt:THIO-RHOSH
(EMBL:A35135); Rhodobacter
sphaeroides (Rhodopseudomonas
sphaeroides).; trxA; Thioredoxin
(TRX).; length=TRX; id 57.692; 104
aa overlap; query 2-105; subject
1-104 similarity:fasta;
with=UniProt:Q8UJA6
(EMBL:AE008976); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; trxA; Thioredoxin C-1.;
length=133; id 91.509; 106 aa
overlap; query 1-106; subject
28-133 Similar to entire protein
```

```

of Rhodobacter sphaeroides
(Rhodopseudomonas sphaeroides)
Thioredoxin (TRX) trxA (104 aa),
and similar, but truncated at the
N-terminus, to Agrobacterium
tumefaciens (strain C58/ATCC
33970) Thioredoxin C-1 trxA (133
aa)"
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/db-xref="UniProtKB/TrEMBL:Q1MND2"
/translation="MATVKVDINNFAQSEVLESSE
PVVVDFWAEWCGPCKMIAPSLSEI
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IFKGGEVADISVGAKPKTALSNWI SSAA"
misc-feature complement(22206..22520
) /locus-tag="RL0025"

/inference="protein
motif:Pfam:PF00085.8"
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PF00085.8 Thioredoxin"
gene complement(22599..26150
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CDS complement(22599..26150
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/inference="similar to
sequence:INSDC:AE008977"
/note="similarity:fasta;
with=UniProt:Q8UJA5
(EMBL:AE008977); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; uvrD; ATP-dependant DNA
helicase.; length=1185; id 62.203;
1180 aa overlap; query 6-1183;
subject 8-1185"
/codon-start=1
/transl-table=11
/product="putative ATP-dependent
UvrD family DNA helicase"
/protein-id="CAK05514.1"
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/db-xref="UniProtKB/TrEMBL:Q1MND1"
/translation="MSDVTALPNDDDPGAWIGWT
TIQQAIASDPLRSANVANSAGSGK
THVLTQVRVIRLLLSGARPSAILCLTYTKAAASEM
SNRVFERLAEWVVLDDDELSRRIT
QIEGMADPDLGLAEARRLFAKALETTPGGLKIQTI
HAFCEALLHQFPLEANVAGHFSVL
DDRAAVALLSDARRALLTATAPDEDSALAEAFAY
VLNLGDESGLENLLGDIVANRNAI
RRFTAAAEQQGGVMVLRKRLGLAVGDTEDRIEA
QYWPLPELSGSVLELYLSLADQKG
GAKAQEVAYGLRLAGRERDDARRAQFLEKIFLTV
KGEPKADSQFFVKAMLAEPQLA
AIAIARAHVAASDRRLKLMRMYGATHAALVLADR
LNHDYELKKQRSQLDFEDILITRT
ADLLTKSGVGVPWIHYKLDGRDGHILVDEAQDTSP

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IQWSVIQSLAEDFFSGESARPIVR  
 TLFAVGDEKQSIYSFQGARPFRFSESDRTRRRV  
 SDSGQSFSSVRLPLSFRSTADVLE  
 AVDHIFKTPENARGLSALGEPVVRSSRIGHPGA  
 VDLWEMIAPEAVVKEEDWTAPFDA  
 TPESAPAAILARRIAHSIGTLVGRETIVDKGKER  
 LIEAGDILVLVRKRDAFVNALTRA  
 LKRRGDIPVAGADRLVLTSIAVQDLLALGRFLL  
 LPEDDLSLAAVLKSPFLDLSDDI  
 FAIAALRGDNEFWSHLRSFAADGTFLFRAAVER  
 LELFLRQSRSLSVHDFYARVLGSY  
 GGRQFLARLGTVEVDILDEFLTFTLDHESSGLP  
 GLQSFISTLELEAPVMKREQDKGR  
 NEVRIMTVHASKGLEAPIVFLVDGGSKAFTHTHL  
 PKRLRIETRPDEPPMPVWVPVSDL  
 ANSLTQDDAARIQMLAEEYRRLLYVAMTRAADR  
 LVVCGYRGVRVNDTWHMMISTAL  
 HDDHPHVEATTFSGSDGEWPGIKWRVPRVERSF  
 RIDRSQERGSEETLPDGLLRPLFP  
 QALPRPLSPSGAGTIIIDEDEGLLVVSPLFGEK  
 EHSRSLSEKGRLIHRMLQALPEIP  
 LAERPDAASRYAERARFWPEVERRKLVDVSLKL  
 LDEEGLQAVLGAAQOPEVSMIGTL  
 TLEDRRYAVSGRIDRLAVLADRVVILDYKTRNRP  
 PATEEAIPFAHRAQLAIYREILT  
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 KTK"

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/inference="protein  
 motif:Pfam:PF00580.8"  
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CDS complement(43056..44051 /gene="coaA"
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 with=UniProt:COAA-ECOLI  
 (EMBL:A45727); Escherichia coli  
 O157:H7.; coaA; Pantothenate  
 kinase (EC 2.7.1.33) (Pantothenic  
 acid kinase) (Rts protein).;  
 length=EC 2.7.1.3 ( 316; id  
 53.526; 312 aa overlap; query  
 23-330; subject 10-316  
 similarity:fasta;  
 with=UniProt:COAA-AGRT5  
 (EMBL:AE007946); Agrobacterium  
 tumefaciens (strain C58/ATCC  
 33970).; coaA; Pantothenate kinase  
 (EC 2.7.1.33) (Pantothenic acid  
 kinase).; length=EC 2.7.1.3 ( 322;  
 id 81.988; 322 aa overlap; query  
 10-331; subject 1-322; putative

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pantothenate kinase"
/codon-start=1
/transl-table=11
/product="Pantothenate kinase
(Pantothenic acid kinase) (Rts
protein)."
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db-xref="UniProtKB/TrEMBL:Q1MNG0"  
/translation="MSIATEIIGVPETLDFQSE  
SYSPYHFFSSEQWAKFRADTPLTL  
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FVIGIAGSVAVGKSTTARILKELLGRWPSSPKVD  
LVTTDGFLEHNAVLQREKLMQRKG  
FPESYDTGAILRFLSAIKAGRDPVKAPSYSHLVY  
DVLDEYKIVDRPDILIFEGINVL  
QSRDLPAGGKIVPMVSDFDFSIYIDAAEDEIHN  
WYVTRFMRLETAFRDPNSYFHR  
ASISDAEALIEADLWANINLKNLRQNILPTRPR  
ADLLKKGKDHLIEQVALRKL"

misc-feature complement(43080..43742 /gene="coaA"  
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/locus-tag="RL0040"  
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motif:Pfam:PF00485.7"  
/note="Pfam match to entry  
PF00485.7 PRK"

gene complement(44048..44371 /locus-tag="RL0041"  
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CDS complement(44048..44371 /locus-tag="RL0041"  
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sequence:INSDC:ECRFBM"  
/note="similarity:fasta;  
with=UniProt:HIS2-ECOLI  
(EMBL:ECRFBM); Escherichia coli.;  
hisI; Histidine biosynthesis  
bifunctional protein hisIE  
[Includes: Phosphoribosyl-AMP  
cyclohydrolase (EC 3.5.4.19)  
(PRA-CH); Phosphoribosyl-ATP  
pyrophosphatase (EC 3.6.1.31)  
(PRA-PH)].; length=203; id 47.126;  
87 aa overlap; query 6-92; subject  
115-201 similarity:fasta;  
with=UniProt:HIS2-AGRT5  
(EMBL:AE007946); Agrobacterium  
tumefaciens (strain C58/ATCC  
33970).; hisE; Phosphoribosyl-ATP  
pyrophosphatase (EC 3.6.1.31)  
(PRA-PH)].; length=107; id 71.698;  
106 aa overlap; query 1-106;  
subject 1-106"  
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/transl-table=11  
/product="putative histidine  
biosynthesis bifunctional protein"  
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misc-feature complement(44090..44356 /locus-tag="RL0041"
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/inference="protein
motif: Pfam:PF01503.6"
/note="Pfam match to entry
PF01503.6 PRA-PH"
gene complement(44389..45177 /gene="hisF"
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/locus-tag="RL0042"
CDS complement(44389..45177 /gene="hisF"
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/locus-tag="RL0042"
/inference="similar to
sequence: INSDC:ABHISHAFE"
/inference="similar to
sequence: INSDC:AE007946"
/note="similarity:fasta;
with=UniProt:HIS6-AZOBR
(EMBL:ABHISHAFE); Azospirillum
brasiliense.; hisF; Imidazole
glycerol phosphate synthase
subunit hisF (EC 4.1.3.-) (IGP
synthase cyclase subunit) (IGP
synthase subunit hisF) (ImGP
synthase subunit hisF) (IGPS
subunit hisF).; length=261; id
69.767; 258 aa overlap; query
3-260; subject 2-251
similarity:fasta;
with=UniProt:HIS6-AGRT5
(EMBL:AE007946); Agrobacterium
tumefaciens (strain C58/ATCC
33970).; hisF; Imidazole glycerol
phosphate synthase subunit hisF
(EC 4.1.3.-) (IGP synthase cyclase
subunit) (IGP synthase subunit
hisF) (ImGP synthase subunit hisF)
(IGPS subunit hisF).; length=258;
id 82.129; 263 aa overlap; query
1-262; subject 1-258"
/codon-start=1
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/product="putative imadazole
glycerol phosphate synthase
sununit"
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/db-xref="GI:115254456"
/db-xref="GOA:Q1MNF7"
/db-xref="UniProtKB/TrEMBL:Q1MNF7"
/translation="MTLKARVIFPCLDVKGDRVVK
GVNFLNLVDAGDPVEAAKAYDAAG
ADELCFLDLITASDNRRETFIDVVSRTADQCFMPL
TVGGGVRTIADIRKLLLCGADKVS
INSAAVSNPDFVTEADKFGDQCIVVSDIAKRRR
TQAVGGDNLSAWEIYTHGGRNATG

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misc-feature    complement(44446..45162 /gene="hisF"
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                /inference="protein
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                /note="Pfam match to entry
                PF00977.8 His-biosynth"
gene            complement(45178..45924 /gene="hisA"
)
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CDS             complement(45178..45924 /gene="hisA"
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                sequence:INSDC:SME591782"
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                with=UniProt:HIS4-ECOLI
                (EMBL:ECD840); Escherichia coli.;
                hisA;
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                ribosylamino)methylidene amino]
                imidazole-4-carboxamide isomerase
                (EC 5.3.1.16)
                (Phosphoribosylformimino-5-aminoim
                idazole carboxamide ribotide
                isomerase).;
                length=5-phosphoribosyl; id
                35.081; 248 aa overlap; query
                2-242; subject 1-245
                similarity:fasta;
                with=UniProt:HIS4-RHIME
                (EMBL:SME591782); Rhizobium
                meliloti (Sinorhizobium
                meliloti).; hisA;
                1-(5-phosphoribosyl)-5-[(5-phospho
                ribosylamino)methylidene amino]
                imidazole-4-carboxamide isomerase
                (EC 5.3.1.16)
                (Phosphoribosylformimino-5-aminoim
                idazole carboxamide ribotide
                isomerase).;
                length=5-phosphoribosyl; id
                88.066; 243 aa overlap; query
                1-243; subject 1-243"
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 DIVISION CODE (CI): Bacteria  
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 KEYWORDS (ST): complete genome  
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 ORGANISM (ORGN): Bacteroides fragilis NCTC 9343  
 Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales;  
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 PROJECT (PJID): GenomeProject:46  
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 AUTHOR (AU): Cerdeno-Tarraga,A.M.; Patrick,S.; Crossman,L.C.;  
 Blakely,G.; Abratt,V.; Lennard,N.; Foxton,I.;  
 Duerden,B.; Harris,B.; Quail,M.A.; Barron,A.; Clark,L.;  
 Corton,C.; Doggett,J.; Holden,M.T.; Larke,N.; Line,A.;  
 Lord,A.; Norbertczak,H.; Ormond,D.; Price,C.;  
 Rabinowitsch,E.; Woodward,J.; Barrell,B.; Parkhill,J.  
 TITLE (TI): Extensive DNA inversions in the B. fragilis genome  
 control variable gene expression  
 JOURNAL (SO): Science, 307 (5714), 1463-1465 (2005)  
 OTHER SOURCE (OS): CA 142:234199  
 REFERENCE: 2 (bases 1 to 5205140)  
 AUTHOR (AU): Cerdeno-Tarraga,A.M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (29-JUL-2004) Cerdeno-Tarraga A.M., submitted  
 on behalf of the Pathogen Sequencing Unit, Sanger  
 Institute, Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA E-mail: amct@sanger.ac.uk

# FEATURES (FEAT):

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 3398627..3398695, 289-311, 346-368, 414-436 and  
 3398732..3398800, 472-494"  
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 3399410..3399478))  
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 3423779..3423847, 486-508, 549-568, 874-893,  
 3423866..3423925, 900-922, 932-954, 974-996 and  
 3424841..3424900, 1011-1033"  
 3425021..3425089,  
 3425132..3425200,  
 3425267..3425335,  
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 3425432..3425500,  
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 3468847..3468906, 468-490, 534-556, 913-932,  
 3468925..3468984, 939-958, 968-987, 1008-1030 and  
 3470053..3470121, 1045-1067"  
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 3470527..3470595,  
 3470614..3470667,  
 3471592..3471660))  
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	7..3473305, 3473348..3473407, 3473528..3473596, 3473639..3473707, 3474632..3474691, 3474812..3474880, 3474899..3474967, 3475064..3475132, 3475145..3475204, 3475214..3475273, 3476198..3476266))	helices predicted for BF2986 by TMHMM2.0 at aa 10-32, 341-360, 364-383, 388-410, 443-465, 472-494, 535-554, 863-885, 900-922, 963-982 and 997-1019"
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misc-feature	complement(order(349713 7..3497196, 3498223..3498282))	/note="2 probable transmembrane helices predicted for BF3007 by TMHMM2.0 at aa 13-32 and 375-394"
misc-feature	complement(order(351045 2..3510520, 3510554..3510622, 3510632..3510688))	/note="3 probable transmembrane helices predicted for BF3020 by TMHMM2.0 at aa 21-39, 43-65 and 77-99"
misc-feature	complement(order(352811 1..3528179, 3528216..3528284, 3528327..3528395, 3528432..3528500, 3528543..3528611, 3528669..3528737, 3528774..3528842, 3528903..3528971))	/note="8 probable transmembrane helices predicted for BF3033 by TMHMM2.0 at aa 218-240, 261-283, 296-318, 338-360, 375-397, 410-432, 447-469 and 482-504"
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misc-feature	complement(order(353789 1..3537959, 3537978..3538046, 3538056..3538115, 3538176..3538244, 3538272..3538340))	/note="5 probable transmembrane helices predicted for BF3041 by TMHMM2.0 at aa 34-56, 66-88, 109-128, 132-154 and 161-183"
misc-feature	complement(order(354037 5..3540443, 3540480..3540548, 3540591..3540659, 3540678..3540743))	/note="4 probable transmembrane helices predicted for BF3044 by TMHMM2.0 at aa 10-31, 38-60, 75-97 and 110-132"

misc-feature	complement(order(354684 /note="2 probable transmembrane 5..3546901, 3546914..3546982))	helices predicted for BF3050 by TMHMM2.0 at aa 34-56 and 61-79"
misc-feature	complement(order(356408 /note="6 probable transmembrane 4..3564152, 3564162..3564221, 3564258..3564326, 3564354..3564422, 3564492..3564560, 3564624..3564692))	helices predicted for BF3062 by TMHMM2.0 at aa 13-35, 57-79, 103-125, 135-157, 170-189 and 193-215"
misc-feature	complement(order(356568 /note="3 probable transmembrane 1..3565740, 3565759..3565827, 3566128..3566184))	helices predicted for BF3064 by TMHMM2.0 at aa 21-39, 140-162 and 169-188"
misc-feature	complement(order(357948 /note="4 probable transmembrane 5..3579553, 3579566..3579634, 3579695..3579763, 3579776..3579844))	helices predicted for BF3076 by TMHMM2.0 at aa 27-49, 54-76, 97-119 and 124-146"
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misc-feature	complement(order(364252 /note="3 probable transmembrane 1..3642574, 3642587..3642655, 3642734..3642802))	helices predicted for BF3123 by TMHMM2.0 at aa 15-37, 64-86 and 91-108"
misc-feature	complement(order(370108 /note="2 probable transmembrane 4..3701137, 3701165..3701224))	helices predicted for BF3161 by TMHMM2.0 at aa 9-28 and 38-55"
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 3737299..3737367, 227-249, 254-276, 297-319,  
 3737428..3737496, 347-369, 376-398 and 438-460"  
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 3738178..3738237))  
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 3744940..3744999, 463-485, 525-544, 885-904,  
 3745018..3745077, 911-930, 934-956, 986-1008 and  
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 3753109..3753168))  
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 3800397..3800465, 118-140 and 145-167"  
 3800478..3800537))  
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3841494..3841550, 268-290, 302-319, 323-341,
3841560..3841613, 348-370, 385-404 and 411-433"
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3842686..3842754, 91-108, 123-145, 157-179 and
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3905850..3905906, 231-253, 273-295, 308-326,
3905943..3906011, 341-363, 376-398 and 402-424"
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3937552..3937620, 87-109, 119-138, 151-173, 188-210,
3937648..3937716, 222-244, 274-293, 300-322,
3937855..3937923, 358-380, 427-449, 459-481, 502-524
3938029..3938097, and 529-548"
3938116..3938175,
3938263..3938331,
3938365..3938433,
3938476..3938544,
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3938668..3938736,
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 4088311..4088379, 335-357, 370-392 and 397-419"  
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 4249453..4249521, 244-266, 273-295, 321-343,  
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4265809..4265877, 212-231 and 257-279"
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4336135..4336194, and 514-531"
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4355819..4355887, 397-419, 439-456 and 460-482"  
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4400276..4400344,  
4400363..4400431))

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4428947..4429006))

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4539116..4539184,      467-489, 523-545, 866-884,
4539203..4539259,      891-913, 923-942, 963-985 and
4540220..4540288,      1000-1022"
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4540484..4540552,
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4540799..4540858,
4541777..4541836))
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4544527..4544595, 705-727, 747-769 and 779-801"
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4545025..4545093,
4545199..4545267))
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4553745..4553813, 159-181, 191-208, 343-365,
4553856..4553924, 380-402, 683-705 and 709-731"
4554327..4554380,
4554408..4554476,
4554513..4554581,
4554594..4554662))
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4561533..4561601, 102-124 and 139-161"
4561614..4561682))
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7..4608176, helices predicted for BF3912 by
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4608309..4608368, 133-150, 171-193, 203-225,
4608603..4608656, 232-249, 259-278, 285-302,
4608675..4608734, 381-400, 413-435 and 445-464"
4608762..4608815,
4608834..4608902,
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4609428..4609496))
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4611786..4611854))
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=> d l13 4 tit

'TIT' IS NOT A VALID FORMAT

In a multifile environment, a format can only be used if it is valid in at least one of the files. Refer to file specific help messages or the STNGUIDE file for information on formats available in individual files.

REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):.

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM286415 GenBank (R)  
GenBank ACC. NO. (GBN): AM286415  
GenBank VERSION (VER): AM286415.1 GI:122087364  
CAS REGISTRY NO. (RN): 917704-63-3  
SEQUENCE LENGTH (SQL): 4615899  
MOLECULE TYPE (CI): DNA; circular  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 29 Oct 2008  
DEFINITION (DEF): *Yersinia enterocolitica* subsp. *enterocolitica* 8081 complete genome.  
KEYWORDS (ST): complete genome  
SOURCE: *Yersinia enterocolitica* subsp. *enterocolitica* 8081  
ORGANISM (ORGN): *Yersinia enterocolitica* subsp. *enterocolitica* 8081 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Yersinia*  
PROJECT (PJID): GenomeProject:190  
REFERENCE: 1  
AUTHOR (AU): Delihias, N.  
TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene *micF* and its target *ompF* in *Yersinia* species  
JOURNAL (SO): (er) BMC Microbiol., 3, 13 (2003)  
REFERENCE: 2  
AUTHOR (AU): Thomson, N.R.; Howard, S.; Wren, B.W.; Holden, M.T.; Crossman, L.; Challis, G.L.; Churcher, C.; Mungall, K.; Brooks, K.; Chillingworth, T.; Feltwell, T.; Abdellah, Z.; Hauser, H.; Jagels, K.; Maddison, M.; Moule, S.; Sanders, M.; Whitehead, S.; Quail, M.A.; Dougan, G.; Parkhill, J.; Prentice, M.B.  
TITLE (TI): The complete genome sequence and comparative genome analysis of the high pathogenicity *Yersinia enterocolitica* strain 8081  
JOURNAL (SO): PLoS Genet., 2 (12), E206 (2006)  
REFERENCE: 3 (bases 1 to 4615899)  
AUTHOR (AU): Thomson, N.R.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (30-JUN-2006) Thomson N.R., Pathogen Sequencing Unit, The Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge, CB10 1SA, UNITED KINGDOM

FEATURES (FEAT):

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CDS	complement(270..710)	/locus-tag="YE0001"

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CDS	complement(802..1263)	/gene="asnC" /locus-tag="YE0002" /codon-start=1 /transl-table=11 /product="regulatory protein" /protein-id="CAL10147.1" /db-xref="GI:122087366" /db-xref="GOA:AlJHQ9" /db-xref="InterPro:IPR000485" /db-xref="InterPro:IPR011991" /db-xref="UniProtKB/TrEMBL:AlJHQ9" /translation="MSEIYQIDNLDRGILNALME NARTPYAELAKNFGVSPGTIHVRV EKMRQAGIITAACVHVNPKQLGYDVCCFIGIILK SAKDYPSALKKLESLEEVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP"
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gene	1449..2441	/gene="asnA"

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misc-feature	2055..2078	/gene="asnA" /locus-tag="YE0003" /inference="protein motif:Prosite:PS00017" /note="PS00017 ATP/GTP-binding site motif A (P-loop)." /locus-tag="YE0004" /locus-tag="YE0004" /inference="similar to sequence:INSDC:AE001895" /inference="similar to sequence:INSDC:AL646078" /note="Similar to Ralstonia solanacearum probable transmembrane protein RSP0410 or RS00867 SWALL:Q8XSQ7 (EMBL:AL646078) (224 aa) fasta scores: E(): 7.3e-36, 46.54 38d in 217 aa, and to Deinococcus radiodurans hypothetical protein DR0351 SWALL:Q9RXG2 (EMBL:AE001895) (227 aa) fasta scores: E(): 3.7e-17, 31.67 38d in 221 aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAL10149.1"
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TANQLSGSAKAFHLVLTGMTLLVSWLLLPFTAFTM
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82-104, 114-136 and 200-222"
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MRIHTSEMESGQIYIPVINWTLYLAVVLVIVGF
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misc-feature	6711..8432

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7068..7136,7194..7262,
7299..7367,7425..7493,
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7749..7802,7830..7886)

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87-109, 121-143,163-185, 198-220,
240-262, 287-309, 319-341, 348-365
and 375-393"

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CDS             8606..9025

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VTF"

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CDS             9033..10535

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sequence:UniProtKB:P04983"
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protein RbsA SWALL:RBSA-ECOLI
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scores: E(): 2.7e-148, 85.83 38d
in 494 aa,and to Salmonella typhi
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misc-feature	9864..10445	/gene="rbsA" /locus-tag="YE0009" /inference="protein motif:PFAM:PF00005" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 134.4, E-value 1.3e-37"
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gene	10623..11588	/gene="rbsC" /locus-tag="YE0010" /gene="rbsC" /locus-tag="YE0010" /codon-start=1 /transl-table=11 /product="putative sugar transport system, permease protein" /protein-id="CAL10155.1" /db-xref="GI:122087374" /db-xref="GOA:AlJHS2" /db-xref="InterPro:IPR001851" /db-xref="UniProtKB/TrEMBL:AlJHS2" /translation="MSSQTINTKRWFSSKEWLLEQ
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/protein-id="CAL10156.1"
/db-xref="GI:122087375"
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/db-xref="UniProtKB/TrEMBL:A1JHS3"
/translation="MKMKKLATLISVVALSATVS
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TVRGTKLLLINPTDSDAVGNVAKM
ANQANIPVITLDRLANAGTVVSHVASDNRFGGKM
AGDYIAKKVGSDAKVIQLEGIAGA
SAARERGEFGKQSMKKNFQLLASQPADFDRTKG
LNVMQNLLTAHPDVQAVFAQNDEM
ALGALRALQTAGKTDVLVVGFDGTDGKAVEG
KMGATIAQRPDQIGVIGVQTADKV
LKGEKVQAVIPVDLKLKLVK"
/genes="rbsB"
/locus-tag="YE0011"
/note="Signal peptide predicted
for YE0011 by SignalP 2.0 HMM
(Signal peptide probability 1.000)
with cleavage site probability
0.933 between residues 25 and 26"
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/inference="protein
motif:PFAM:PF00532"
/note="Pfam match to entry PF00532
Peripla-BP-like, Periplasmic
binding proteins and sugar binding
domain of the LacI family, score
63.4, E-value 3.3e-16"
misc-feature 12432..12455
/genes="rbsB"
/locus-tag="YE0011"
/inference="protein
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/note="PS00017 ATP/GTP-binding
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/transl-table=11
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/protein-id="CAL10157.1"
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misc-feature	13552..13593	/gene="rbsK" /locus-tag="YE0012" /inference="protein" motif:Prosite:PS00584" /note="PS00584 pfkB family of carbohydrate kinases signature 2."
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<-----User Break----->

LCEKVLGYRIFGDENDKMNLNVKQAGGSVLVVSQ  
FTLVADITQKGMRFPSFRGASPAEA

=> d l14 4 ti

L14 NOT FOUND

The L-number entered has not been defined in this session, or it has been deleted. To see the L-numbers currently defined in this session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> d l13 4 ti

L13 ANSWER 4 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene micF and its target ompF in Yersinia species

TITLE (TI): The complete genome sequence and comparative genome analysis of the high pathogenicity Yersinia enterocolitica strain 8081

TITLE (TI): Direct Submission

=> d l13 5 ti

L13 ANSWER 5 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome of Rhizobium leguminosarum has recognizable core and accessory components

TITLE (TI): Direct Submission

=> d l13 6-14 ti

L13 ANSWER 6 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Whole genome sequence of Staphylococcus saprophyticus reveals the pathogenesis of uncomplicated urinary tract infection

TITLE (TI): Direct Submission

L13 ANSWER 7 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The Chlamydomonas reinhardtii genome sequence reveals an array of variable proteins that contribute to interspecies variation

TITLE (TI): Direct Submission

L13 ANSWER 8 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Extensive DNA inversions in the B. fragilis genome control variable gene expression

TITLE (TI): Direct Submission

L13 ANSWER 9 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater

TITLE (TI): Direct Submission

L13 ANSWER 10 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Genomic plasticity of the causative agent of  
melioidosis, *Burkholderia pseudomallei*

TITLE (TI): Direct Submission

L13 ANSWER 11 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome sequence of the enterobacterial  
phytopathogen *Erwinia carotovora* subsp. *atroseptica*  
SCRI1043 and functional genomic identification of novel  
virulence factors

TITLE (TI): Direct Submission

L13 ANSWER 12 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus*  
strains: evidence for the rapid evolution of virulence  
and drug resistance

TITLE (TI): Direct Submission

L13 ANSWER 13 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus*  
strains: evidence for the rapid evolution of virulence  
and drug resistance

TITLE (TI): Direct Submission

L13 ANSWER 14 OF 14 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genome sequence of the model actinomycete  
*Streptomyces coelicolor* A3(2)

TITLE (TI): Direct Submission

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDE

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S LI

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

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L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

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                SEA ENTEROCOCCUS DURANS STRAIN 152
L4  -----
    QUE ENTEROCOCCUS DURANS STRAIN 152
    -----
                SEA ENTEROCOCCUS DRANS 141-1
L5  -----
    QUE ENTEROCOCCUS DRANS 141-1
    -----
                SEA ENTEROCOCCUS DURANS 141-1
L6  -----
    2   FILE USPATFULL
    QUE ENTEROCOCCUS DURANS 141-1
    -----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7  2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
    SEA ENTEROCOCCUS DURANS 152
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    1   FILE AGRICOLA
    1   FILE BIOENG
    1   FILE BIOSIS
    1   FILE CABA
    2   FILE CAPLUS
    1   FILE FROSTI
    1   FILE FSTA
    1   FILE HEALSAFE
    1   FILE LIFESCI
    1   FILE MEDLINE
    1   FILE PASCAL
    1   FILE SCISEARCH
    2   FILE USPATFULL
L8  QUE ENTEROCOCCUS DURANS 152
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FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9  15 S L8
L10 3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
    SEA LACTOCOCCUS LACTIS C-1-92
    -----
    1   FILE CAPLUS
    11  FILE GENBANK
    1   FILE PROMT
    2   FILE USPATFULL
L11 QUE LACTOCOCCUS LACTIS C-1-92
    -----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12 15 S L11
L13 14 DUP REM L12 (1 DUPLICATE REMOVED)

```

=> index bioscience  
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED  
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
110.65	153.92

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view  
search error messages that display as 0\* with SET DETAIL OFF.

=> s Lactococcus lactis C-1-152

31 FILES SEARCHED...

7 FILE GENBANK

60 FILES SEARCHED...

2 FILE USPATFULL

1 FILE WPIDS

1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L14 QUE LACTOCOCCUS LACTIS C-1-152

=> file genbank uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
2.60	156.52

FULL ESTIMATED COST

FILE 'GENBANK' ENTERED AT 16:49:45 ON 16 DEC 2008

FILE 'USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l14

L15 9 L14

=> rem dup l15

DUP IS NOT VALID HERE

The DELETE command is used to remove various items stored by the  
system.

To delete a saved query, saved answer set, saved L-number list, SDI  
request, batch request, mailing list, or user-defined cluster, format,  
or search field, enter the name. The name may include ? for left,  
right, or simultaneous left and right truncation.

Examples:

DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field

DELETE NAMELIST MYLIST - delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C    - delete print request
DELETE D134002C    - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21          - delete a single L-number
DELETE L3-L6        - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-         - delete L33 and any higher L-number
DELETE -L55         - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER      - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                  and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l15
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L15
L16          9 DUP REM L15 (0 DUPLICATES REMOVED)
```

```
=> d l16 1 ti
```

```
L16 ANSWER 1 OF 9 USPATFULL on STN
TI    Composition and method for inhibition of microorganisms
```



=> d 116 1 bib

L16 ANSWER 1 OF 9 USPATFULL on STN  
AN 2006:86130 USPATFULL  
TI Composition and method for inhibition of microorganisms  
IN Doyle, Michael P, Peachtree City, GA, UNITED STATES  
Zhao, Tong, Peachtree City, GA, UNITED STATES  
PI US 20060073129 A1 20060406  
AI US 2003-535357 A1 20031124 (10)  
WO 2003-US37526 20031124  
20050518 PCT 371 date  
PRAI US 2002-428863P 20021125 (60)  
DT Utility  
FS APPLICATION  
LREP Barnes & Thornburg, 11 South Meridian Street, Indianapolis, IN, 46204, US  
CLMN Number of Claims: 35  
ECL Exemplary Claim: 1  
DRWN 1 Drawing Page(s)  
LN.CNT 1238  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 116 2 bib

L16 ANSWER 2 OF 9 USPATFULL on STN  
AN 2006:79924 USPATFULL  
TI Foaming composition of competitive exclusion microbes and method of  
using same  
IN Podtburg, Teresa C., Waconia, MN, UNITED STATES  
Schmidt, Bruce, Apple Valley, MN, UNITED STATES  
Cords, Bruce, Inver Grove Heights, MN, UNITED STATES  
Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF  
Halsrud, David A., Minneapolis, MN, UNITED STATES  
PI US 20060067915 A1 20060330  
AI US 2005-233922 A1 20050922 (11)  
PRAI US 2004-612882P 20040924 (60)  
DT Utility  
FS APPLICATION  
LREP MERCHANT & GOULD PC, P.O. BOX 2903, MINNEAPOLIS, MN, 55402-0903, US  
CLMN Number of Claims: 23  
ECL Exemplary Claim: 1  
DRWN 1 Drawing Page(s)  
LN.CNT 1878  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 116 3 bib

'BIB' IS NOT A VALID FORMAT  
In a multifile environment, a format can only be used if it is valid  
in at least one of the files. Refer to file specific help messages  
or the STNGUIDE file for information on formats available in  
individual files.  
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d 116 3 ti  
'D' IS NOT A VALID FORMAT  
In a multifile environment, a format can only be used if it is valid  
in at least one of the files. Refer to file specific help messages  
or the STNGUIDE file for information on formats available in  
individual files.  
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):ti

L16 ANSWER 3 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The complete genome, comparative and functional analysis of *Stenotrophomonas maltophilia* reveals an organism heavily shielded by drug resistance determinants

TITLE (TI): Direct Submission

=> d l16 4-9 ti

L16 ANSWER 4 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene *micF* and its target *ompF* in *Yersinia* species

TITLE (TI): The complete genome sequence and comparative genome analysis of the high pathogenicity *Yersinia enterocolitica* strain 8081

TITLE (TI): Direct Submission

L16 ANSWER 5 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

TITLE (TI): Direct Submission

L16 ANSWER 6 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): The genome of *Rhizobium leguminosarum* has recognizable core and accessory components

TITLE (TI): Direct Submission

L16 ANSWER 7 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Extensive DNA inversions in the *B. fragilis* genome control variable gene expression

TITLE (TI): Direct Submission

L16 ANSWER 8 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Genome sequence of *Yersinia pestis*, the causative agent of plague

TITLE (TI): Annotation and evolutionary relationships of a small regulatory RNA gene *micF* and its target *ompF* in *Yersinia* species

TITLE (TI): Direct Submission

L16 ANSWER 9 OF 9 GENBANK® COPYRIGHT 2008 on STN

TITLE (TI): Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance

TITLE (TI): Direct Submission

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,

DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O  
-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1  
-----

SEA ENTEROCOCCUS DURANS STRAIN 152  
-----

L4 QUE ENTEROCOCCUS DURANS STRAIN 152  
-----

SEA ENTEROCOCCUS DRANS 141-1  
-----

L5 QUE ENTEROCOCCUS DRANS 141-1  
-----

SEA ENTEROCOCCUS DURANS 141-1  
-----

2 FILE USPATFULL

L6 QUE ENTEROCOCCUS DURANS 141-1  
-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008

L7 2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS 152

-----  
1 FILE AGRICOLA  
1 FILE BIOENG  
1 FILE BIOSIS  
1 FILE CABA  
2 FILE CAPLUS  
1 FILE FROSTI  
1 FILE FSTA  
1 FILE HEALSAFE  
1 FILE LIFESCI  
1 FILE MEDLINE  
1 FILE PASCAL  
1 FILE SCISEARCH  
2 FILE USPATFULL

L8 QUE ENTEROCOCCUS DURANS 152  
-----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,  
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16

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DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
SEA LACTOCOCCUS LACTIS C-1-92
-----
1      FILE CAPLUS
11     FILE GENBANK
1      FILE PROMT
2      FILE USPATFULL
L11    QUE LACTOCOCCUS LACTIS C-1-92
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FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12     15 S L11
L13     14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
SEA LACTOCOCCUS LACTIS C-1-152
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7      FILE GENBANK
2      FILE USPATFULL
1      FILE WPIDS
1      FILE WPINDEX
L14    QUE LACTOCOCCUS LACTIS C-1-152
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FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008
L15     9 S L14
L16     9 DUP REM L15 (0 DUPLICATES REMOVED)

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                               SINCE FILE      TOTAL
                                                    ENTRY      SESSION
FULL ESTIMATED COST                               30.05      186.57

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008

69 FILES IN THE FILE LIST IN STINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s food(p)process? and inhibit? (p)pathogen? and surface
0*      FILE ADISNEWS
11      FILE AGRICOLA
2*      FILE ANTE
1*      FILE AQUALINE
4        FILE AQUASCI
11*     FILE BIOENG

```

```

32 FILE BIOSIS
11* FILE BIOTECHABS
11* FILE BIOTECHDS
12* FILE BIOTECHNO
13 FILE CABA
15 FILE CAPLUS
0* FILE CEABA-VTB
16 FILES SEARCHED...
0* FILE CIN
1 FILE CROPV
6 FILE DISSABS
12 FILE EMBASE
16* FILE ESBIOBASE
30 FILES SEARCHED...
0* FILE FOMAD
0* FILE FOREGE
20* FILE FROSTI
45* FILE FSTA
1 FILE GENBANK
1 FILE HEALSAFE
39 FILE IFIPAT
0* FILE KOSMET
13 FILE LIFESCI
12 FILE MEDLINE
0* FILE NTIS
1* FILE NUTRACEUT
18* FILE PASCAL
47 FILES SEARCHED...
1* FILE PHARMAML
24 FILE PROMT
14 FILE SCISEARCH
16 FILE TOXCENTER
2042 FILE USPATFULL
5 FILE USPATOLD
620 FILE USPAT2
64 FILES SEARCHED...
1* FILE WATER
32 FILE WPIDS
1 FILE WPIFV
32 FILE WPINDEX

```

35 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

=> s L17 and (Enterococcus durans or Lactococcus lactis)

```

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
22 FILES SEARCHED...
1 FILE DISSABS
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI

```

```

0* FILE FSTA
35 FILES SEARCHED...
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
47 FILES SEARCHED...
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER
68 FILES SEARCHED...

```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

```

=> \file caplus dissabs uspatfull
\FILE IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

```

```

=> file caplus dissabs uspatfull
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          5.85      192.42

```

FILE 'CAPLUS' ENTERED AT 17:00:10 ON 16 DEC 2008  
 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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```

=> file baplus dissabs uspatfull uspat2
'BAPLUS' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available. If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):.
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          2.40      194.82

```

FILE 'DISSABS' ENTERED AT 17:00:27 ON 16 DEC 2008  
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FILE 'USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008  
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```

=> file caplus dissabs uspatfull uspat2
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION

```

FULL ESTIMATED COST

3.42

198.24

FILE 'CAPLUS' ENTERED AT 17:00:43 ON 16 DEC 2008  
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PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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FILE 'USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> d l18

L18 HAS NO ANSWERS

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURF  
ACE  
L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

=> s l18

L19 109 L18

=> s l19 and treat?(p)surface

L20 46 L19 AND TREAT?(P) SURFACE

=> s l20 and inhibit(p)pathogen(p)?organis?

L21 3 L20 AND INHIBIT(P) PATHOGEN(P) ?ORGANIS?

=> d l21 1-3

L21 ANSWER 1 OF 3 USPATFULL on STN

AN 2006:303630 USPATFULL

TI Proteases, nucleic acids encoding them and methods for making and using them

IN Cayouette, Michelle, 3812 PARK BOULEVARD #505, SAN DIEGO, CA, UNITED STATES 92103

Hansen, Connie Jo, San Diego, CA, UNITED STATES

McClure, Amy, San Diego, CA, UNITED STATES

Sun, May, San Diego, CA, UNITED STATES

Gramatikova, Svetlana, San Diego, CA, UNITED STATES

Dycaico, Mark, San Diego, CA, UNITED STATES

Barton, Nelson R., San Diego, CA, UNITED STATES

Stege, Justin T., San Diego, CA, UNITED STATES

Aboushadi, Nahla M., Oceanside, CA, UNITED STATES

PA DIVERSA CORPORATION (U.S. corporation)

PI US 20060259995 A1 20061116

AI US 2003-530643 A1 20031010 (10)

WO 2003-US32819

20031010

20060407 PCT 371 date

PRAI US 2002-418467P 20021010 (60)

US 2003-471423P 20030516 (60)

DT Utility

FS APPLICATION

LN.CNT 7319

INCL INCLM: 800/018.000

INCLS: 435/069.100; 435/226.000; 435/320.100; 435/325.000; 435/006.000;

536/023.200; 800/288.000

NCL NCLM: 800/018.000

NCLS: 435/006.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;  
536/023.200; 800/288.000  
IC IPCI A01K0067-027 [I,A]; C12Q0001-68 [I,A]; C07H0021-04 [I,A];  
C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C12N0009-64 [I,A];  
A01H0001-00 [I,A]  
IPCR A01K0067-027 [I,C]; A01K0067-027 [I,A]; A01H0001-00 [I,C];  
A01H0001-00 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
C12N0009-64 [I,C]; C12N0009-64 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]; C12Q0001-68 [I,C]; C12Q0001-68 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L21 ANSWER 2 OF 3 USPATFULL on STN  
AN 2004:12970 USPATFULL  
TI Polynucleotides, materials incorporating them, and methods for using  
them  
IN Glenn, Matthew, Whenuapai, NEW ZEALAND  
Havukkala, Ilkka J., Remuera, NEW ZEALAND  
Lubbers, Mark, Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND  
PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND  
(non-U.S. corporation)  
PI US 20040009490 A1 20040115  
US 7125698 B2 20061024  
AI US 2002-264213 A1 20021003 (10)  
RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
2000, GRANTED, Pat. No. US 6544772  
PRAI US 1999-147853P 19990809 (60)  
US 1999-147852P 19990809 (60)  
US 1999-152032P 19990901 (60)  
US 1999-152031P 19990901 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 5375  
INCL INCLM: 435/006.000  
INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200  
NCL NCLM: 435/193.000; 435/006.000  
NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
435/252.300; 435/320.100; 536/023.200  
IC [7]  
ICM C12Q001-68  
ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335  
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
IPCI-2 C12N0009-10 [I,A]  
IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L21 ANSWER 3 OF 3 USPAT2 on STN  
AN 2004:12970 USPAT2  
TI Polynucleotides, materials incorporating them, and methods for using  
them  
IN Glenn, Matthew, 14 Waimarie Road, Whenuapai, Auckland, NEW ZEALAND  
Havukkala, Ilkka J., 19 Liley Place, Remuera, Auckland, NEW ZEALAND  
Lubbers, Mark, 397 Ruahine Street, Palmerston North, NEW ZEALAND  
Dekker, James, 135 Russel Street, Palmerston North, NEW ZEALAND  
PI US 7125698 B2 20061024  
AI US 2002-264213 20021003 (10)



RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
 2000, Pat. No. US 6544772

PRAI US 1999-152032P 19990901 (60)  
 US 1999-152031P 19990901 (60)  
 US 1999-147853P 19990809 (60)  
 US 1999-147852P 19990809 (60)

DT Utility  
 FS GRANTED

LN.CNT 5273

INCL INCLM: 435/193.000  
 INCLS: 435/183.000; 435/194.000; 426/534.000; 530/350.000

NCL NCLM: 435/193.000; 435/006.000  
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
 435/252.300; 435/320.100; 536/023.200

IC IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
 IPCI-2 C12N0009-10 [I,A]  
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
 A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
 C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]

EXF 435/193; 435/183; 435/194; 426/534; 530/350  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
 SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
 1 FILE IFIPAT  
 2 FILE USPATFULL  
 1 FILE WPIDS  
 1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O  
 -----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
 AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
 DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
 SEA ENTEROCOCCUS DURANS STRAIN 141-1

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

-----  
 SEA ENTEROCOCCUS DURANS STRAIN 152

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

-----  
 SEA ENTEROCOCCUS DRANS 141-1

L5 QUE ENTEROCOCCUS DRANS 141-1

```

-----
SEA ENTEROCOCCUS DURANS 141-1
-----
L6      2   FILE USPATFULL
        QUE ENTEROCOCCUS DURANS 141-1
        -----

L7      FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
        2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
SEA ENTEROCOCCUS DURANS 152
-----
1   FILE AGRICOLA
1   FILE BIOENG
1   FILE BIOSIS
1   FILE CABA
2   FILE CAPLUS
1   FILE FROSTI
1   FILE FSTA
1   FILE HEALSAFE
1   FILE LIFESCI
1   FILE MEDLINE
1   FILE PASCAL
1   FILE SCISEARCH
2   FILE USPATFULL
L8      QUE ENTEROCOCCUS DURANS 152
        -----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9      15 S L8
L10     3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
SEA LACTOCOCCUS LACTIS C-1-92
-----
1   FILE CAPLUS
11  FILE GENBANK
1   FILE PROMT
2   FILE USPATFULL
L11     QUE LACTOCOCCUS LACTIS C-1-92
        -----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12     15 S L11
L13     14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
SEA LACTOCOCCUS LACTIS C-1-152
-----

```

7 FILE GENBANK  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX  
L14 QUE LACTOCOCCUS LACTIS C-1-152  
-----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008  
L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008  
SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE

-----  
0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG  
32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIODASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
1 FILE HEALSFAE  
39 FILE IFIPAT  
0\* FILE KOSMET  
13 FILE LIFESCI  
12 FILE MEDLINE  
0\* FILE NTIS  
1\* FILE NUTRACEUT  
18\* FILE PASCAL  
1\* FILE PHARMAML  
24 FILE PROMT  
14 FILE SCISEARCH  
16 FILE TOXCENTER  
2042 FILE USPATFULL  
5 FILE USPATOLD  
620 FILE USPAT2  
1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE  
-----  
SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

```

-----
0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE DISSABS
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER
L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
-----

FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC
2008
L19 109 S L18
L20 46 S L19 AND TREAT?(P)SURFACE
L21 3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?

=> s L21 and (Enterococcus durans)\
MISSING OPERATOR DURANS)\
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s L21 and (Enterococcus durans or Lactococcus lactis)
L22 3 L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

=> s L22 and inhibit?(p)first population of microorganism
L23 0 L22 AND INHIBIT?(P) FIRST POPULATION OF MICROORGANISM

=> s L22 and (C-1-152 or C-1-92 or 152 or 141-1)
L24 3 L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)

=> d L24

L24 ANSWER 1 OF 3 USPATFULL on STN
AN 2006:303630 USPATFULL
TI Proteases, nucleic acids encoding them and methods for making and using
them
IN Cayouette, Michelle, 3812 PARK BOULEVARD #505, SAN DIEGO, CA, UNITED
STATES 92103
Hansen, Connie Jo, San Diego, CA, UNITED STATES
McClure, Amy, San Diego, CA, UNITED STATES

```

Sun, May, San Diego, CA, UNITED STATES  
 Gramatikova, Svetlana, San Diego, CA, UNITED STATES  
 Dyaico, Mark, San Diego, CA, UNITED STATES  
 Barton, Nelson R., San Diego, CA, UNITED STATES  
 Stege, Justin T., San Diego, CA, UNITED STATES  
 Aboushadi, Nahla M., Oceanside, CA, UNITED STATES  
 PA DIVERSA CORPORATION (U.S. corporation)  
 PI US 20060259995 A1 20061116  
 AI US 2003-530643 A1 20031010 (10)  
 WO 2003-US32819 20031010  
 20060407 PCT 3/1 date  
 PRAI US 2002-418467P 20021010 (60)  
 US 2003-471423P 20030516 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 7319  
 INCL INCLM: 800/018.000  
 INCLS: 435/069.100; 435/226.000; 435/320.100; 435/325.000; 435/006.000;  
 536/023.200; 800/288.000  
 NCL NCLM: 800/018.000  
 NCLS: 435/006.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;  
 536/023.200; 800/288.000  
 IC IPCI A01K0067-027 [I,A]; C12Q0001-68 [I,A]; C07H0021-04 [I,A];  
 C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C12N0009-64 [I,A];  
 A01H0001-00 [I,A]  
 IPCR A01K0067-027 [I,C]; A01K0067-027 [I,A]; A01H0001-00 [I,C];  
 A01H0001-00 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
 C12N0009-64 [I,C]; C12N0009-64 [I,A]; C12P0021-06 [I,C];  
 C12P0021-06 [I,A]; C12Q0001-68 [I,C]; C12Q0001-68 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 124 1 ti

L24 ANSWER 1 OF 3 USPATFULL on STN  
 TI Proteases, nucleic acids encoding them and methods for making and using them

=> d 124 1 kwic

L24 ANSWER 1 OF 3 USPATFULL on STN  
 AB . . . therapeutic, and industrial contexts. The polypeptides of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver.  
 . .  
 SUMM . . . therapeutic, and industrial contexts. The polypeptides of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver.  
 . .  
 SUMM Enzymes are used within a wide range of applications in industry, research, and medicine. Through the use of enzymes, industrial processes can be carried out at reduced temperatures and pressures and with less dependence on the use of corrosive or toxic. .

. substances. The use of enzymes can thus reduce production costs, energy consumption, and pollution as compared to non-enzymatic products and processes. An important group of enzymes is the proteases. Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of. . . The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in. . . milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases. . .

SUMM . . . in laundry detergents to aid in the removal of proteinaceous stains (e.g., Crabb, ACS Symposium Series 460:82-94, 1991). In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products (Kida et al., Journal of Fermentation and Bioengineering 80:478-484, 1995; Haard and Simpson, in Martin, A. M., ed., Fisheries Processing: Biotechnological Applications, Chapman and Hall, London, 1994, 132-154; Bos et al., European Patent Office Publication 494 149 A1).

SUMM	206	207-209	210
211			
C	231	232-233	234
D	160	161-163	164
E	195	196-198	199
F	224	225-228	229
G	152	153-157	158
159			
H	189	190-192	193
I	220	221	222
J	173	174-178	179
K	212	213-217	218
L	148. . .		219

SUMM . . . acid of the invention, wherein the polypeptide has a protease activity. The protease can be a nonsurface-active protease or a surface-active protease. The protease can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, . . .

DETD . . . defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

DETD . . . Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Pat. Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.

DETD Inhibition of protease expression can have a variety of industrial applications. For example, inhibition of protease expression can slow or prevent spoilage. Spoilage can occur when polypeptides, e.g., structural polypeptides, are enzymatically degraded. This. . . lead to the deterioration, or rot, of fruits and vegetables. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of proteases, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. . . to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a protease gene of the

invention). The compositions of the invention for the inhibition of protease expression (e.g., antisense, iRNA, ribozymes, antibodies) can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., anti-inflammatory or skin or digestive aid treatments. For example, proteases are attractive antimalarial targets. . . especially in the processes of host erythrocyte rupture, invasion and hemoglobin degradation; see, e.g., Wu (2003) Genome Res. 13:601-616. Selective inhibition of the mosquito angiotensin-converting enzyme (ACE) (a dipeptidyl carboxypeptidase) involved in the activation/inactivation of a peptide regulating egg-laying activity can be an effective anti-mosquito method; see, e.g., Ekbote (2003) Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 134:593-598. Inhibition of matrix metalloproteases (e.g., metalloproteinases) and collagenases, which can degrade extracellular matrices and promote cancer cell migration and metastases, can. . .

DETD . . . include gram negative bacteria, such as *Escherichia coli* and *Pseudomonas fluorescens*; gram positive bacteria, such as *Streptomyces diversus*, *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces*. . .

DETD . . . comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

DETD . . . formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a protease of the. . . invention. Alternatively, a protease of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes. . .

DETD Treating Foods and Food Processing

DETD The proteases of the invention have numerous applications in food processing industry. For example, in one aspect, the proteases of the invention are used to improve the extraction of oil from. . .

DETD Proteases of the present invention, in the modification of animal feed or a food, can process the food or feed either in vitro (by modifying components of the feed or food) or in vivo. Proteases can be added to animal feed or food compositions containing high amounts of arabinogalactans or galactans, e.g. feed or food containing plant material from soy bean, rape seed, lupin and the like. When added to the feed or food the protease significantly improves the in vivo break-down of plant cell wall material, whereby a better utilization of the plant. . . more digestible by the animal. Thus, proteases of the invention can contribute to the available energy of the feed or food. Also, by contributing to the degradation of galactan-comprising proteins, a protease of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

DETD The proteases of the invention can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using proteases of the invention. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking. . . proteases of the invention can be used in combination with cellulases, pectate lyases or other enzymes. The paper can be treated by the following three processes: 1) disintegration in the presence of

proteases of the invention, 2) disintegration with a deinking chemical and proteases of the invention, and/or 3) disintegration after soaking with proteases of the invention. The recycled paper treated with proteases can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of proteases of the invention may be due to its behavior as surface-active agents in pulp suspension.

DETD . . . from the well bore; reducing the flow of production fluids from the formation below expected flow rates; formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, protein-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack protein in cell walls.

CLM What is claimed is:

. . . polypeptide as set forth in claim 60, wherein the polypeptide has a protease activity, wherein optionally the protease is a non-surface-active protease or a surface-active protease, and optionally the protease is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate. . .

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIIDS  
1 FILE WPINDEX

L1 QUE ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S LI

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

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L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

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SEA ENTEROCOCCUS DURANS STRAIN 152

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L4 QUE ENTEROCOCCUS DURANS STRAIN 152

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SEA ENTEROCOCCUS DRANS 141-1

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L5 QUE ENTEROCOCCUS DRANS 141-1

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SEA ENTEROCOCCUS DURANS 141-1



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2   FILE USPATFULL
L6   QUE ENTEROCOCCUS DURANS 141-1
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FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7   2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
      SEA ENTEROCOCCUS DURANS 152
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1   FILE AGRICOLA
1   FILE BIOENG
1   FILE BIOSIS
1   FILE CABA
2   FILE CAPLUS
1   FILE FROSTI
1   FILE FSTA
1   FILE HEALSAFE
1   FILE LIFESCI
1   FILE MEDLINE
1   FILE PASCAL
1   FILE SCISEARCH
2   FILE USPATFULL
L8   QUE ENTEROCOCCUS DURANS 152
-----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9   15 S L8
L10  3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-92
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1   FILE CAPLUS
11  FILE GENBANK
1   FILE PROMT
2   FILE USPATFULL
L11  QUE LACTOCOCCUS LACTIS C-1-92
-----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12  15 S L11
L13  14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-152
-----
7   FILE GENBANK
2   FILE USPATFULL

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1 FILE WPIDS  
1 FILE WPINDEX  
L14 QUE LACTOCOCCUS LACTIS C-1-152  
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FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008

SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE

-----  
0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG  
32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIOBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
1 FILE HEALSAFE  
39 FILE IFIPAT  
0\* FILE KOSMET  
13 FILE LIFESCI  
12 FILE MEDLINE  
0\* FILE NTIS  
1\* FILE NUTRACEUT  
18\* FILE PASCAL  
1\* FILE PHARMAML  
24 FILE PROMT  
14 FILE SCISEARCH  
16 FILE TOXCENTER  
2042 FILE USPATFULL  
5 FILE USPATOLD  
620 FILE USPAT2  
1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

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SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

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0\* FILE ADISNEWS

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0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE DISSABS
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER
L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
-----

FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008
FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008
FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC
2008
L19 109 S L18
L20 46 S L19 AND TREAT?(P)SURFACE
L21 3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22 3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23 0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24 3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)

=> s l24 and strain
L25 3 L24 AND STRAIN

=> d l25 1 kwic

L25 ANSWER 1 OF 3 USPATFULL on STN
AB . . . therapeutic, and industrial contexts. The polypeptides of the
invention can be used as, e.g., an additive for a detergent, for
processing foods and for chemical synthesis utilizing a reverse
reaction. Additionally, the polypeptides of the invention can be used in
food processing, brewing, bath additives, alcohol
production, peptide synthesis, enantioselectivity, hide preparation in
the leather industry, waste management and animal degradation, silver.
. . .
SUMM . . . therapeutic, and industrial contexts. The polypeptides of the
invention can be used as, e.g., an additive for a detergent, for
processing foods and for chemical synthesis utilizing a reverse
reaction. Additionally, the polypeptides of the invention can be used in
food processing, brewing, bath additives, alcohol
production, peptide synthesis, enantioselectivity, hide preparation in
the leather industry, waste management and animal degradation, silver.
. . .
SUMM Enzymes are used within a wide range of applications in industry,

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research, and medicine. Through the use of enzymes, industrial processes can be carried out at reduced temperatures and pressures and with less dependence on the use of corrosive or toxic substances. The use of enzymes can thus reduce production costs, energy consumption, and pollution as compared to non-enzymatic products and processes. An important group of enzymes is the proteases. Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of. . . The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in. . . milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases. . . .

SUMM . . . in laundry detergents to aid in the removal of proteinaceous stains (e.g., Crabb, ACS Symposium Series 460:82-94, 1991). In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products (Kida et al., Journal of Fermentation and Bioengineering 80:478-484, 1995; Haard and Simpson, in Martin, A. M., ed., Fisheries Processing: Biotechnological Applications, Chapman and Hall, London, 1994, 132-154; Bos et al., European Patent Office Publication 494 149 A1).

SUMM . . . e.g., an archeal source, a bacterial source, a fungal source (e.g., filamentous ascomycetes, such as *Cochliobolus heterostrophus*, e.g., *C. heterostrophus* strain C4, having ATCC accession no. 48331), or an environmental source, e.g., a mixed environmental source, e.g., as set forth below. . . .

SUMM 187, 188 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 210, 211 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 234, 235 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 164, 165 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 199, 200 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 229, 230 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 158, 159 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 193, 194 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 222, 223 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 179, 180 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 218, 219 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 150, 151 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 171, 172 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 204, 205 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 254, 255 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 248, 249 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)  
 SUMM 241, 242 *Cochliobolus heterostrophus* strain C4 (ATCC 48331)

85, 86 Environmental  
 11, 12 Environmental  
 121, 122 Environmental  
 117, 118 Environmental  
 119, 120 Environmental  
 83, 84 Environmental  
 9, 10 Environmental  
 93, 94. . . .

SUMM . . . 206 207-209 210  
 211

C 231 232-233 234 235

D	160	161-163	164	165
E	195	196-198	199	200
F	224	225-228	229	230
G	152	153-157	158	
	159			
H	189	190-192	193	194
I	220	221	222	223
J	173	174-178	179	180
K	212	213-217	218	219
L	148. . .			
SUMM	. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .			
SUMM	. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .			
SUMM	. . . a newly engineered phenotype. In another aspect, the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.			
SUMM	. . . acid of the invention, wherein the polypeptide has a protease activity. The protease can be a nonsurface-active protease or a surface-active protease. The protease can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form. . .			
DETD	. . . defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.			
DETD	. . . as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction). . .			
DETD	. . . Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Pat. Nos. 4,683,195 and 4,683,202; Sooknanan (1995) Biotechnology 13:563-564.			
DETD	Inhibition of protease expression can have a variety of industrial applications. For example, inhibition of protease expression can slow or prevent spoilage. Spoilage can occur when polypeptides, e.g., structural polypeptides, are enzymatically degraded. This. . . lead to the deterioration, or rot, of fruits and vegetables. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of proteases, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. . . to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a protease gene of the invention). The compositions of the invention for the inhibition of protease expression (e.g., antisense, iRNA, ribozymes, antibodies)			

can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., anti-inflammatory or skin or digestive aid treatments. For example, proteases are attractive antimalarial targets. . . especially in the processes of host erythrocyte rupture, invasion and hemoglobin degradation; see, e.g., Wu (2003) Genome Res. 13:601-616. Selective inhibition of the mosquito angiotensin-converting enzyme (ACE) (a dipeptidyl carboxypeptidase) involved in the activation/inactivation of a peptide regulating egg-laying activity can be an effective anti-mosquito method; see, e.g., Ekbote (2003) Comp. Biochem. Physiol. B. Biochem. Mol. Biol. 134:593-598. Inhibition of matrix metalloproteases (e.g., metalloproteinases) and collagenases, which can degrade extracellular matrices and promote cancer cell migration and metastases, can. . .

DETD . . . (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .

DETD . . . some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an E. coli strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation. . .

DETD . . . include gram negative bacteria, such as *Escherichia coli* and *Pseudomonas fluorescens*; gram positive bacteria, such as *Streptomyces* diversa, *Lactobacillus gasserii*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces*. . .

DETD . . . simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. "Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins. . . comprising a defined amount of one or more biological molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

DETD . . . methods of the invention provide whole cell evolution, or whole cell engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified protease activity, by modifying the genetic composition of the cell. The. . .

DETD Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome. . .

DETD . . . formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a protease of the. . . invention. Alternatively, a protease of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes. . .

DETD . . . or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives in order to. . .

DETD Treating Foods and Food Processing

DETD The proteases of the invention have numerous applications in

food processing industry. For example, in one aspect, the proteases of the invention are used to improve the extraction of oil from. . .

DETD Proteases of the present invention, in the modification of animal feed or a food, can process the food or feed either in vitro (by modifying components of the feed or food) or in vivo. Proteases can be added to animal feed or food compositions containing high amounts of arabinogalactans or galactans, e.g. feed or food containing plant material from soy bean, rape seed, lupin and the like. When added to the feed or food the protease significantly improves the in vivo break-down of plant cell wall material, whereby a better utilization of the plant. . . more digestible by the animal. Thus, proteases of the invention can contribute to the available energy of the feed or food. Also, by contributing to the degradation of galactan-comprising proteins, a protease of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

DETD The proteases of the invention can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using proteases of the invention. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking. . . proteases of the invention can be used in combination with cellulases, pectate lyases or other enzymes. The paper can be treated by the following three processes: 1) disintegration in the presence of proteases of the invention, 2) disintegration with a deinking chemical and proteases of the invention, and/or 3) disintegration after soaking with proteases of the invention. The recycled paper treated with proteases can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of proteases of the invention may be due to its behavior as surface-active agents in pulp suspension.

DETD . . . from the well bore; reducing the flow of production fluids from the formation below expected flow rates; formulating an enzyme treatment by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous, protein-containing, damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack protein in cell walls.

CLM What is claimed is:

. . . comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer. . .

CLM What is claimed is:

. . . polypeptide as set forth in claim 60, wherein the polypeptide has a protease activity, wherein optionally the protease is a non-surface-active protease or a surface-active protease, and optionally the protease is formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate. . .

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

-----  
QUE ENTEROCOCCUS DURANS STRAIN 141-1

L3

-----  
SEA ENTEROCOCCUS DURANS STRAIN 152

L4

-----  
QUE ENTEROCOCCUS DURANS STRAIN 152

-----  
SEA ENTEROCOCCUS DRANS 141-1

L5

-----  
QUE ENTEROCOCCUS DRANS 141-1

-----  
SEA ENTEROCOCCUS DURANS 141-1

L6

-----  
2 FILE USPATFULL  
QUE ENTEROCOCCUS DURANS 141-1

-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008

L7 2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS 152

-----  
1 FILE AGRICOLA  
1 FILE BIOENG  
1 FILE BIOSIS  
1 FILE CABA  
2 FILE CAPLUS  
1 FILE FROSTI  
1 FILE FSTA  
1 FILE HEALSAFE  
1 FILE LIFESCI  
1 FILE MEDLINE  
1 FILE PASCAL  
1 FILE SCISEARCH  
2 FILE USPATFULL



L8                    QUE ENTEROCOCCUS DURANS 152

-----  
FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,  
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16  
DEC 2008

L9                    15 S L8  
L10                   3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008  
SEA LACTOCOCCUS LACTIS C-1-92

-----  
1     FILE CAPLUS  
11    FILE GENBANK  
1     FILE PROMT  
2     FILE USPATFULL  
L11                   QUE LACTOCOCCUS LACTIS C-1-92  
-----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC  
2008

L12                   15 S L11  
L13                   14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008  
SEA LACTOCOCCUS LACTIS C-1-152

-----  
7     FILE GENBANK  
2     FILE USPATFULL  
1     FILE WPIDS  
1     FILE WPINDEX  
L14                   QUE LACTOCOCCUS LACTIS C-1-152  
-----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

L15                   9 S L14  
L16                   9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008  
SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE

-----  
0\*    FILE ADISNEWS  
11    FILE AGRICOLA  
2\*    FILE ANTE  
1\*    FILE AQUALINE  
4     FILE AQUASCI  
11\*   FILE BIOENG  
32    FILE BIOSIS  
11\*   FILE BIOTECHABS  
11\*   FILE BIOTECHDS  
12\*   FILE BIOTECHNO  
13    FILE CABA  
15    FILE CAPLUS

0\* FILE CEABA-VTB  
 0\* FILE CIN  
 1 FILE CROFU  
 6 FILE DISSABS  
 12 FILE EMBASE  
 16\* FILE ESBIOBASE  
 0\* FILE FOMAD  
 0\* FILE FOREGE  
 20\* FILE FROSTI  
 45\* FILE FSTA  
 1 FILE GENBANK  
 1 FILE HEALSAFE  
 39 FILE IFIPAT  
 0\* FILE KOSMET  
 13 FILE LIFESCI  
 12 FILE MEDLINE  
 0\* FILE NTIS  
 1\* FILE NUTRACEUT  
 18\* FILE PASCAL  
 1\* FILE PHARMAML  
 24 FILE PROMT  
 14 FILE SCISEARCH  
 16 FILE TOXCENTER  
 2042 FILE USPATFULL  
 5 FILE USPATOLD  
 620 FILE USPAT2  
 1\* FILE WATER  
 32 FILE WPIDS  
 1 FILE WPIFV  
 32 FILE WPINDEX

L17           QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

-----  
 SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)  
 -----

0\* FILE ADISNEWS  
 0\* FILE ANTE  
 0\* FILE AQUALINE  
 0\* FILE BIOENG  
 0\* FILE BIOTECHABS  
 0\* FILE BIOTECHDS  
 0\* FILE BIOTECHNO  
 1 FILE CAPLUS  
 0\* FILE CEABA-VTB  
 0\* FILE CIN  
 1 FILE DISSABS  
 0\* FILE ESBIOBASE  
 0\* FILE FOMAD  
 0\* FILE FOREGE  
 0\* FILE FROSTI  
 0\* FILE FSTA  
 0\* FILE KOSMET  
 0\* FILE NTIS  
 0\* FILE NUTRACEUT  
 0\* FILE PASCAL  
 0\* FILE PHARMAML  
 92 FILE USPATFULL  
 15 FILE USPAT2  
 0\* FILE WATER

L18           QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

-----

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

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L19      109 S L18
L20      46 S L19 AND TREAT?(P)SURFACE
L21      3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22      3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23      0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24      3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)
L25      3 S L24 AND STRAIN
```

```
=> s l25 and strain 152
L26      0 L25 AND STRAIN 152
```

```
=> s l25 and strain 141-1
L27      0 L25 AND STRAIN 141-1
```

```
=> s l25 and strain C-1-152
L28      0 L25 AND STRAIN C-1-152
```

```
=> s l25 and strain C-1-92
L29      0 L25 AND STRAIN C-1-92
```

=> d hist

(FILE 'HOME' ENTERED AT 16:31:09 ON 16 DEC 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:31:20 ON 16 DEC 2008  
SEA (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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-----
1  FILE IFIPAT
2  FILE USPATFULL
1  FILE WPIDS
1  FILE WPINDEX
```

L1 QUE (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----

FILE 'USPATFULL, IFIPAT' ENTERED AT 16:32:25 ON 16 DEC 2008

L2 3 S L1

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:33:15 ON 16 DEC 2008  
SEA ENTEROCOCCUS DURANS STRAIN 141-1

-----

L3 QUE ENTEROCOCCUS DURANS STRAIN 141-1

-----

SEA ENTEROCOCCUS DURANS STRAIN 152

-----

L4 QUE ENTEROCOCCUS DURANS STRAIN 152

-----

SEA ENTEROCOCCUS DRANS 141-1

-----

L5 QUE ENTEROCOCCUS DRANS 141-1

-----

SEA ENTEROCOCCUS DURANS 141-1

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-----
2   FILE USPATFULL
L6   QUE ENTEROCOCCUS DURANS 141-1
-----

FILE 'USPATFULL' ENTERED AT 16:36:57 ON 16 DEC 2008
L7   2 S L6

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:37:29 ON 16 DEC 2008
      SEA ENTEROCOCCUS DURANS 152
      -----
      1   FILE AGRICOLA
      1   FILE BIOENG
      1   FILE BIOSIS
      1   FILE CABA
      2   FILE CAPLUS
      1   FILE FROSTI
      1   FILE FSTA
      1   FILE HEALSAFE
      1   FILE LIFESCI
      1   FILE MEDLINE
      1   FILE PASCAL
      1   FILE SCISEARCH
      2   FILE USPATFULL
L8   QUE ENTEROCOCCUS DURANS 152
      -----

FILE 'AGRICOLA, BIOENG, BIOSIS, CABA, CAPLUS, FROSTI, FSTA, HEALSAFE,
LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL' ENTERED AT 16:38:26 ON 16
DEC 2008
L9   15 S L8
L10  3 DUP REM L9 (12 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:40:04 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-92
      -----
      1   FILE CAPLUS
      11  FILE GENBANK
      1   FILE PROMT
      2   FILE USPATFULL
L11  QUE LACTOCOCCUS LACTIS C-1-92
      -----

FILE 'CAPLUS, GENBANK, PROMT, USPATFULL' ENTERED AT 16:41:04 ON 16 DEC
2008
L12  15 S L11
L13  14 DUP REM L12 (1 DUPLICATE REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:47:33 ON 16 DEC 2008
      SEA LACTOCOCCUS LACTIS C-1-152
      -----
      7   FILE GENBANK
      2   FILE USPATFULL

```

1 FILE WPIDS  
1 FILE WPINDEX  
L14 QUE LACTOCOCCUS LACTIS C-1-152  
-----

FILE 'GENBANK, USPATFULL' ENTERED AT 16:49:45 ON 16 DEC 2008

L15 9 S L14  
L16 9 DUP REM L15 (0 DUPLICATES REMOVED)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 16:55:03 ON 16 DEC 2008

SEA FOOD(P)PROCESS? AND INHIBIT? (P)PATHOGEN? AND SURFACE

-----  
0\* FILE ADISNEWS  
11 FILE AGRICOLA  
2\* FILE ANTE  
1\* FILE AQUALINE  
4 FILE AQUASCI  
11\* FILE BIOENG  
32 FILE BIOSIS  
11\* FILE BIOTECHABS  
11\* FILE BIOTECHDS  
12\* FILE BIOTECHNO  
13 FILE CABA  
15 FILE CAPLUS  
0\* FILE CEABA-VTB  
0\* FILE CIN  
1 FILE CROPU  
6 FILE DISSABS  
12 FILE EMBASE  
16\* FILE ESBIOBASE  
0\* FILE FOMAD  
0\* FILE FOREGE  
20\* FILE FROSTI  
45\* FILE FSTA  
1 FILE GENBANK  
1 FILE HEALSAFE  
39 FILE IFIPAT  
0\* FILE KOSMET  
13 FILE LIFESCI  
12 FILE MEDLINE  
0\* FILE NTIS  
1\* FILE NUTRACEUT  
18\* FILE PASCAL  
1\* FILE PHARMAML  
24 FILE PROMT  
14 FILE SCISEARCH  
16 FILE TOXCENTER  
2042 FILE USPATFULL  
5 FILE USPATOLD  
620 FILE USPAT2  
1\* FILE WATER  
32 FILE WPIDS  
1 FILE WPIFV  
32 FILE WPINDEX

L17 QUE FOOD(P) PROCESS? AND INHIBIT? (P) PATHOGEN? AND SURFACE

-----  
SEA L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)

-----  
0\* FILE ADISNEWS

```

0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
1 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN
1 FILE DISSABS
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
92 FILE USPATFULL
15 FILE USPAT2
0* FILE WATER
L18 QUE L17 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
-----

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FILE 'CAPLUS, DISSABS, USPATFULL' ENTERED AT 17:00:10 ON 16 DEC 2008

FILE 'DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:27 ON 16 DEC 2008

FILE 'CAPLUS, DISSABS, USPATFULL, USPAT2' ENTERED AT 17:00:43 ON 16 DEC 2008

```

L19      109 S L18
L20      46 S L19 AND TREAT?(P)SURFACE
L21      3 S L20 AND INHIBIT(P)PATHOGEN(P)?ORGANIS?
L22      3 S L21 AND (ENTEROCOCCUS DURANS OR LACTOCOCCUS LACTIS)
L23      0 S L22 AND INHIBIT?(P)FIRST POPULATION OF MICROORGANISM
L24      3 S L22 AND (C-1-152 OR C-1-92 OR 152 OR 141-1)
L25      3 S L24 AND STRAIN
L26      0 S L25 AND STRAIN 152
L27      0 S L25 AND STRAIN 141-1
L28      0 S L25 AND STRAIN C-1-152
L29      0 S L25 AND STRAIN C-1-92

```

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
113.40	311.64

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 17:08:01 ON 16 DEC 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS 1 Web Page for STN Seminar Schedule - N. America  
NEWS 2 DEC 01 ChemPort single article sales feature unavailable  
NEWS 3 JAN 06 The retention policy for unread STNmail messages  
will change in 2009 for STN-Columbus and STN-Tokyo  
NEWS 4 JAN 07 WPIDS, WPINDEX, and WPIX enhanced Japanese Patent  
Classification Data  
NEWS 5 FEB 02 Simultaneous left and right truncation (SLART) added  
for CERAB, COMPUAB, ELCOM, and SOLIDSTATE  
NEWS 6 FEB 02 GENBANK enhanced with SET PLURALS and SET SPELLING  
NEWS 7 FEB 06 Patent sequence location (PSL) data added to USGENE  
NEWS 8 FEB 10 COMPENDEX reloaded and enhanced  
NEWS 9 FEB 11 WTEXTILES reloaded and enhanced  
NEWS 10 FEB 19 New patent-examiner citations in 300,000 CA/CAPLUS  
patent records provide insights into related prior  
art  
NEWS 11 FEB 19 Increase the precision of your patent queries -- use  
terms from the IPC Thesaurus, Version 2009.01  
NEWS 12 FEB 23 Several formats for image display and print options  
discontinued in USPATFULL and USPAT2  
NEWS 13 FEB 23 MEDLINE now offers more precise author group fields  
and 2009 MeSH terms  
NEWS 14 FEB 23 TOXCENTER updates mirror those of MEDLINE - more  
precise author group fields and 2009 MeSH terms  
NEWS 15 FEB 23 Three million new patent records blast AEROSPACE into  
STN patent clusters  
NEWS 16 FEB 25 USGENE enhanced with patent family and legal status  
display data from INPADOCDB  
NEWS 17 MAR 06 INPADOCDB and INPAFAMDB enhanced with new display  
formats  
NEWS 18 MAR 11 EPFULL backfile enhanced with additional full-text  
applications and grants  
NEWS 19 MAR 11 ESBIOBASE reloaded and enhanced  
NEWS 20 MAR 20 CAS databases on STN enhanced with new super role  
for nanomaterial substances  
NEWS 21 MAR 23 CA/CAPLUS enhanced with more than 250,000 patent  
equivalents from China  
NEWS 22 MAR 30 IMSPATENTS reloaded and enhanced  
NEWS 23 APR 03 CAS coverage of exemplified prophetic substances  
enhanced  
NEWS 24 APR 07 STN is raising the limits on saved answers  
NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.  
NEWS HOURS STN Operating Hours Plus Help Desk Availability  
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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 13:45:18 ON 09 APR 2009

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.22	0.22

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDEFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:45:46 ON 09 APR 2009

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s (Enterococcus duras or Lactococcus lactis) and (PTA-4759 or PTA-4758 or PTA-4760 or PTA-4761)

1 FILE IFIPAT

54 FILES SEARCHED...

2 FILE USPATFULL

1 FILE WPIDS

1 FILE WPINDEX

4 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STNINDEX

L1 QUE (ENTEROCOCCUS DURNAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 OR PTA-4758 OR PTA-4760 OR PTA-4761)

=> file ifipat uspatfull

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
4.76	4.98

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 13:49:59 ON 09 APR 2009

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FILE 'USPATFULL' ENTERED AT 13:49:59 ON 09 APR 2009

CA INDEXING COPYRIGHT (C) 2009 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l1

L2 3 L1

=> rem dup l2

DUP IS NOT VALID HERE

The DELETE command is used to remove various items stored by the system.

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:



DELETE BIO?/Q	- delete query names starting with BIO
DELETE ?DRUG/A	- delete answer set names ending with DRUG
DELETE ?ELEC?/L	- delete L-number lists containing ELEC
DELETE ANTICOAG/S	- delete SDI request
DELETE ENZYME/B	- delete batch request
DELETE .MYCLUSTER	- delete user-defined cluster
DELETE .MYFORMAT	- delete user-defined display format
DELETE .MYFIELD	- delete user-defined search field
DELETE NAMELIST MYLIST	- delete mailing list

To delete an ordered document or an offline print, enter its number.

Examples:

DELETE P123001C	- delete print request
DELETE D134002C	- delete document order request

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

DELETE L21	- delete a single L-number
DELETE L3-L6	- delete a range of L-numbers
DELETE LAST 4	- delete the last 4 L-numbers
DELETE L33-	- delete L33 and any higher L-number
DELETE -L55	- delete L55 and any lower L-number
DELETE L2-L6 RENUMBER	- delete a range of L-numbers and renumber remaining L-numbers
DELETE RENUMBER	- renumber L-numbers after deletion of intermediate L-numbers

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

DELETE SAVED/Q	- delete all saved queries
DELETE SAVED/A	- delete all saved answer sets
DELETE SAVED/L	- delete all saved L-number lists
DELETE SAVED	- delete all saved queries, answer sets, and L-number lists
DELETE SAVED/S	- delete all SDI requests
DELETE SAVED/B	- delete all batch requests
DELETE CLUSTER	- delete all user-defined clusters
DELETE FORMAT	- delete all user-defined display formats
DELETE FIELD	- delete all user-defined search fields
DELETE SELECT	- delete all E-numbers
DELETE HISTORY	- delete all L-numbers and restart the session at L1

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
PROCESSING COMPLETED FOR L2
```

L3 2 DUP REM L2 (1 DUPLICATE REMOVED)

=> d 13 1-2

L3 ANSWER 1 OF 2 IFIPAT COPYRIGHT 2009 IFI on STN DUPLICATE 1

AN 11124117 IFIPAT;IFIUDB;IFICDB

TI Composition and method for inhibition of microorganisms

IN Doyle Michael P; Zhao Tong

PA Unassigned Or Assigned To Individual (68000)

PPA Georgia, University of Research Foundation Inc (Probable)

PI US 20060073129 A1 20060406

AI US 2003-535357 20031124

WO 2003-US37526 20031124

20050518 PCT 3/1 date

20050518 PCT 102(e) date

PRAI US 2002-428863P 20021125 (Provisional)

FI US 20060073129 20060406

DT Utility; Patent Application - First Publication

FS CHEMICAL

APPLICATION

ED Entered STN: 10 Apr 2006

Last Updated on STN: 10 Apr 2006

CLMN 35

GI 1 Figure(s).

FIG. 1 illustrates the results of analyzing four probiotic isolates for their DNA fingerprinting by pulsed field-gel electrophoresis; lane 1 Lambda ladder DNA standard, lane 2 C-1-92 [*L. lactis* subsp. *lactis*], lane 3 C-1-152 [*L. lactis* subsp. *lactis*], lane 4 141-1 [*E. durans*], and lane 5 152 [*E. durans*].

L3 ANSWER 2 OF 2 USPATFULL on STN

AN 2006:79924 USPATFULL

TI Foaming composition of competitive exclusion microbes and method of using same

IN Podtburg, Teresa C., Waconia, MN, UNITED STATES

Schmidt, Bruce, Apple Valley, MN, UNITED STATES

Cords, Bruce, Inver Grove Heights, MN, UNITED STATES

Grab, Lawrence A., Dusseldorf, GERMANY, FEDERAL REPUBLIC OF

Halsrud, David A., Minneapolis, MN, UNITED STATES

PI US 20060067915 A1 20060330

AI US 2005-233922 A1 20050922 (11)

PRAI US 2004-612882P 20040924 (60)

DT Utility

FS APPLICATION

LN.CNT 1878

INCL INCLM: 424/093.400

INCLS: 435/243.000

NCL NCLM: 424/093.400

NCLS: 435/243.000

IC IPCI A01N0063-00 [I,A]

IPCR A01N0063-00 [I,A]; A01N0063-00 [I,C]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d hist

(FILE 'HOME' ENTERED AT 13:45:18 ON 09 APR 2009)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:45:46 ON 09 APR 2009

SEA (ENTEROCOCCUS DURNAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

-----  
1 FILE IFIPAT  
2 FILE USPATFULL  
1 FILE WPIDS  
1 FILE WPINDEX

L1 QUE (ENTEROCOCCUS DURNAS OR LACTOCOCCUS LACTIS) AND (PTA-4759 O

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FILE 'IFIPAT, USPATFULL' ENTERED AT 13:49:59 ON 09 APR 2009

L2 3 S L1

L3 2 DUP REM L2 (1 DUPLICATE REMOVED)

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

6.95

11.93

STN INTERNATIONAL LOGOFF AT 13:50:26 ON 09 APR 2009